

```

XX 10-FEB-1998; 98US-00021701.
PR (SHAN/) SHANNON K W.
XX (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINCA/) KINCAID R H.
XX Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
PI WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
XX Example 2; SEQ ID NO 733; 423bp; English.
XX
XX The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridize to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridize
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridize to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
XX Sequence 20 BP; 1 A; 8 C; 0 G; 11 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5700 TTGCTTCCTTTCTCTTC 5719
Db 1 TTCCCTTCCTTTCCATTTC 20
XX
XX RESULT 2557
XX ADD81659
XX ID ADD81659 standard; DNA; 20 BP.
XX
XX ADD81659;
XX
XX 29-JAN-2004 (first entry)
XX
XX HIV PRT antisense derived probe #588.
XX
XX ss; oligonucleotide hybridisation potential; efficient hybridisation;
XX large array; minimum oligonucleotide synthesis; probe.
XX
XX Human immunodeficiency virus.
XX
XX US2003054346-A1.
XX
XX 20-MAR-2003.
XX
XX 15-FEB-2001; 2001US-00784674.
XX
XX 10-FEB-1998; 98US-00021701.
XX
XX (SHAN/) SHANNON K W.
XX (WOLB/) WOLBER P K.
XX (DELE/) DELENSTARR G C.
XX (WEBB/) WEBB P G.
XX (KINCA/) KINCAID R H.
XX
XX Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

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XX WPI; 2003-743746/70.
XX
XX Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
XX Example 2; SEQ ID NO 732; 423bp; English.
XX
XX The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridize to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridize
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridize to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
XX Sequence 20 BP; 1 A; 7 C; 0 G; 12 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 1.7e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5699 TTGCTTCCTTTCTCTTC 5718
Db 1 TTCCCTTCCTTTCCATTTC 20
XX
XX RESULT 2558
XX ADE50858/C
XX ID ADE50858 standard; DNA; 20 BP.
XX
XX ADE50858;
XX
XX 29-JAN-2004 (first entry)
XX
XX ESE gene SNP primer #16.
XX
XX
XX ss; single nucleotide polymorphism; immunosuppressive; antidiabetic;
XX neuroprotective; antineuritic; antiarthritic; thyromimetic;
XX antiasthenic; antileukemic; antiinflammatory; dermatological; antipsoriatic;
XX antiaesthetic; diagnosis; autoimmune disease; ESE-3; ESE-2; ESE-1;
XX diabetes; multiple sclerosis; rheumatoid arthritis; lupus; psoriasis;
XX asthma; myasthenia gravis; Sjogren's syndrome; Hashimoto's thyroiditis;
XX Pemphigus vulgaris; atherosclerosis; rheumatoid arthritis; restenosis;
XX primer.
XX
XX Homo sapiens.
XX
XX WO2003034896-A2.
XX
XX 01-MAY-2003.
XX
XX 15-OCT-2002; 2002WO-US032116.
XX
XX 12-OCT-2001; 2001US-0329158P.
XX
XX 26-APR-2002; 2002US-0376139P.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Libermann T, Tautu O, Grall F, Gu X;
XX
XX WPI; 2003-441218/41.
XX
XX Diagnosing the presence, predisposition or susceptibility to an
PT autoimmune disease e.g. diabetes or multiple sclerosis, comprises
PT detecting a polymorphism in the ESE-3, ESE-1 or ESE-1 genes.
XX

```

PS Example 2; SEQ ID NO 72; 96bp; English.

XX The invention relates to the diagnosis of an autoimmune disease, a  
 CC predisposition or a susceptibility to the disease, by detecting a  
 CC polymorphism in the ESR-3, ESR-2 or ESR-1 genes, which is correlated with  
 CC an alteration in the activity or expression of a polypeptide encoded by  
 CC these genes. Detection of the polymorphism is indicative of the  
 CC occurrence, predisposition or susceptibility to autoimmune disease. The  
 CC method is useful for diagnosing the presence, predisposition to, or  
 CC susceptibility to an autoimmune disease, e.g. diabetes (e.g. Type 1  
 CC diabetes or Type II diabetes), multiple sclerosis, rheumatoid arthritis,  
 CC lupus, psoriasis, asthma, myasthenia gravis, Sjogren's syndrome,  
 CC Hashimoto's thyroiditis, pemphigus vulgaris, or inflammation (e.g.  
 CC atherosclerosis, rheumatoid arthritis, or inflammation associated with  
 CC restenosis). The method is also useful for preventing or treating any of  
 CC these diseases. This sequence corresponds to a primer used in the method  
 CC to detect the single nucleotide polymorphisms in the ESR genes,  
 CC especially correlated with multiple sclerosis.

XX Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5581 CTTTGCTCATGTGATTTG 5600  
 DB 20 CATTGGCTCATTTGCAATTG 1

RESULT 2559  
 ADE43461  
 ID ADE43461 standard; DNA; 20 BP.

XX ADE43461;  
 XX 29-JUN-2004 (first entry)

DE Human SNCG sequencing primer, SEQ ID 66.  
 XX  
 XX Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;  
 KM Alzheimer's disease; neuroprotective; neurotrophic; gene therapy;  
 KM Chromosome 10; PCR; primer; ss.

OS Homo sapiens.  
 OS  
 XX WO2003054143-A2.  
 PN  
 XX 03-JUL-2003.

PD 25-OCT-2002; 2002WO-US034679.  
 PF  
 XX 25-OCT-2001; 2001US-0339525P.  
 PR 08-NOV-2001; 2001US-0336929P.  
 PR 08-NOV-2001; 2001US-0338010P.  
 PR 09-NOV-2001; 2001US-0338363P.  
 PR 04-DEC-2001; 2001US-0337052P.  
 PR 28-MAR-2002; 2002US-0368919P.

XX (NEUR-) NEUROGENETICS INC.  
 PA (GENO) GEN HOSPITAL CORP.  
 XX  
 XX Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;  
 PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;  
 XX  
 XX WPI; 2003-559131/52.

XX Determining a predisposition for or the occurrence of neurodegenerative  
 PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid  
 PT the presence or absence of an allelic variant of one or more polymorphic  
 XX regions.  
 XX Example 2; Page 267; 848bp; English.

XX The present invention relates to a method (M1) for determining a  
 CC predisposition for or the occurrence of neurodegenerative disease in a  
 CC subject. The method comprises detecting in a target nucleic acid obtained  
 CC from the subject the presence or absence of an allelic variant of one or  
 CC more polymorphic regions of one or more genes selected from uPA  
 CC (urokinase plasminogen activator), SNCG (gamma-gynuclein), IDE (insulin-  
 CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid  
 CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-sF6), where the  
 CC presence of at least one of the allelic variant of one or more  
 CC polymorphic regions is indicative of a predisposition for or the  
 CC occurrence of neurodegenerative disease. The genes are all located on  
 CC chromosome 10. M1 is useful for determining a predisposition for or the  
 CC occurrence of, and for treating neurodegenerative disease, particularly  
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used  
 CC in the method of the invention.

XX Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3627 GGCGGTGCGAGAGAGGTAG 3646  
 DB 1 GGAAGTGCGAGAGAGGTAG 20

RESULT 2560  
 AAQ29595/c  
 ID AAQ29595 standard; DNA; 21 BP.

XX AAQ29595;  
 XX 25-MAR-2003 (revised)  
 DT 10-MAR-1993 (first entry)

DE Pol 67/70 region sequencing primer 90-417.  
 XX  
 XX Amplify; HIV; pol; resistance; azidothymidine; AZT; 3SR; probe;  
 KM self-sustained sequence replication; mutation; inosine; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9216180-A2.  
 PN  
 XX 01-OCT-1992.

PD 12-MAR-1992; 92WO-US002037.  
 PF  
 XX 13-MAR-1991; 91US-00668549.  
 PR 03-SEP-1991; 91US-00754146.

XX (SISK-) SISKRA DIAGNOSTICS INC.  
 PA (REGC) UNIV CALIFORNIA.  
 XX  
 XX Gingersas TR, Barringer KJ, Richman DD, Prodanovich PC, Davis GR;  
 PI WPI; 1992-348902/42.

XX Assay for detecting genotype of AZT resistance - utilizes series of  
 PT probes which anneal to amplified region of HIV-1 gene.  
 XX  
 XX Disclosure; Page 17; 57pp; English.

XX The sequences given in AAQ29591-601 are sequencing primers which were  
 CC used in the method of the invention to determine the sequence of regions  
 CC of the HIV pol gene which are involved with resistance to azidothymidine  
 CC (AZT). Resistance to AZT is caused by the accumulation of four mutations  
 CC grouped within two regions of the HIV pol gene. The primers AAQ29591-96  
 CC are used to determine the sequence around the mutations at amino acids  
 CC positions 67 and 70, and primers AAQ29597-601 are used to determine the  
 CC sequence around the mutations at positions 215 and 219. The region of

CC interest was amplified by self-sustained sequence replication (3SR).  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 11 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5703 CCTTCCTTTCTCTCTCTCT 5722

DB 20 CCTTCCTTTCTCTCTCTCT 1

RESULT 2561

AAQ79211/c

AAQ79211; standard; DNA; 21 BP.

AC AAQ79211;

DT 25-MAR-2003 (revised)

DT 17-JUL-1995 (first entry)

XX Guanosine rich oligonucleotide used to treat viral infection.

XX Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;

XX Infection; herpes simplex virus; human papilloma virus;

XX Epstein-Barr virus; HIV; adenovirus; respiratory syncytial virus;

XX hepatitis B virus; human cytomegalovirus; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX misc\_feature 21

XX 25-APR-1994; 94WO-US004529.

XX 23-APR-1993; 93US-00053027.

XX 28-OCT-1993; 93US-00145704.

XX (TRIP-) TRIPLEX PHARM CORP.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Rando RF, Fennwald S, Zendequi JG, Ojwang JO, Hogan ME;

XX WPI; 1994-357890/44.

XX Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used

XX to treat viral infections, e.g. herpes-virus and HIV.

XX Claim 41; Page 49; 10pp; English.

XX The oligonucleotides (see AAQ79201-52) can be used to treat viral

XX infections. The oligonucleotides inhibit viral replication by forming

XX guanosine tetrads which form a stabilised 3D structure. Preferred

XX oligonucleotides contain at least 2 runs of at least 2 guanosine bases

XX and may be capped at the 3' terminus with a modifier selected from

XX polyamine, poly-L-lysine, cholesterol and propanolamine. They may also

XX have a modified phosphodiester linkage or be modified to contain a

XX phosphorothioate linkage. They are used to treat infections with viruses

XX such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,

XX HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human

XX cytomegalovirus. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2398 CCCCCCCTCACCACATC 3017

DB 21 CCCCCCCTCACCACATC 2

RESULT 2562

AA116460

ID AA116460 standard; DNA; 21 BP.

AC AA116460;

DT 05-SEP-1996 (first entry)

DE PCR primer, p53-BP2, for human p53 gene (position 805 to 825).

XX Polymerase chain reaction; p53; cancer; neoplasia; diagnosis; prognosis;

XX Tumour suppressor gene; Li-Fraumeni syndrome; sequencing; ss.

XX Synthetic.

XX W09602671-A1.

XX 01-FEB-1996.

XX 29-JUN-1995; 95WO-SE000804.

XX 15-JUL-1994; 94SE-00002487.

XX 16-NOV-1994; 94SE-00003953.

XX (PHAA) PHARMACIA BIOTECH AB.

XX Bywater M, Lindstroem P, Inganäs M;

XX WPI; 1996-105932/11.

XX Sequence-based diagnosis of a human neoplastic tissue, blood or body

XX fluid - useful for the diagnosis or prognosis of neoplasia.

XX Example 1; Page 24; 46pp; English.

XX AA116454-T16469 are PCR primers used to amplify human p53 genomic DNA.

XX The primers are used to demonstrate a method of sequence-based diagnosis

XX of a human neoplastic tissue, blood or other body fluid. The method

XX determines the presence, nature and location of any mutations and their

XX influence on the biological function of the p53 protein (or other cancer-

XX related protein), and hence the properties of the neoplasia (e.g.

XX metastatic potential). The method allows a reliable, accurate diagnosis

XX of neoplasia, allowing clinicians to form a prognosis on the development

XX of the neoplasia and guidance for its treatment

XX Sequence 21 BP; 1 A; 2 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7307 CTTTGAGATTGCTTTGCTG 7326

DB 2 CTTTGAGATTGCTTTGCTG 21

RESULT 2563

AA151629/c

ID AA151629 standard; DNA; 21 BP.

AC AA151629;

DT 12-NOV-1997 (first entry)

DE Viral integrase inhibiting oligonucleotide.  
 XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;  
 KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;  
 KM respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;  
 KM integrase inhibition; guanosine tetrad; ss.  
 XX Synthetic.  
 OS  
 PN MO9703997-A1.  
 XX  
 PD 06-FEB-1997.  
 XX  
 PF 17-JUL-1996; 96MO-US011786.  
 XX  
 PR 19-JUL-1995; 95US-0001505P.  
 PR 23-OCT-1995; 95US-00535168.  
 PR 19-MAR-1996; 96US-0013688P.  
 PR 25-MAR-1996; 96US-0014007P.  
 PR 17-APR-1996; 96US-0015714P.  
 PR 23-APR-1996; 96US-0016271P.  
 XX  
 PA (ARON-) ARONEX PHARM INC.  
 XX  
 PI Rando RF, Fennwald S, Zendegui JG, Ojwang JO, Hogan ME;  
 PI Pommer Y, Mazumder A;  
 DR WPI; 1997-132569/12.  
 XX  
 PT Oligo:nucleotide(s) capable of forming guanosine tetrad - inhibit viral  
 PT enzyme responsible for integrating viral nucleic acid into the host  
 PT genome.  
 XX  
 PS Claim 3; Page 145; 245pp; English.  
 XX  
 CC AAT51619-T51698 are oligonucleotides used to inhibit the production of  
 CC viruses within a host cell. The oligonucleotides may form guanosine  
 CC tetrads (structures formed of eight hydrogen bonds by coordination of the  
 CC four oxygen atoms of guanine with alkali cations believed to bind to the  
 CC centre of a quadruplex, and by strong stacking interactions) and are used  
 CC to prevent the integration of viral nucleic acid into a host genome. The  
 CC oligonucleotides inhibit functioning of the integrase enzyme and hence  
 CC prevent viral infection. Viral infections that may be treated include  
 CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes  
 CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory  
 CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),  
 CC especially HIV-1 infection  
 CC  
 SQ Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 2998 CCCCCACCCCTACCCGCATC 3017  
 Db 21 CCCCCACCCACCCACCCACC 2  
 RESULT 2564  
 AAT74344/C  
 ID AAT74344 standard; DNA; 21 BP.  
 XX  
 AC AAT74344;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-AUG-1997 (first entry)  
 XX  
 DE Oligo for use in p11n gene hybridisation assay.  
 XX  
 KW promoter; template probe; signal amplifier; hybridisation assay; detect;  
 KW functional domain; DNA-dependent RNA polymerase; quantifying; analyte;  
 KW ligand receptor; amplification; hepatitis B virus; Neisseria gonorrhoeae;

KM bacterial beta-lactamase TEM-1 gene; Chlamydia; HIV; hepatitis C virus;  
 KM bacterial tet M determinant; consensus; T7 promoter; ss.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_base 1  
 FT /\*tag= a  
 FT /note= "Y4-(6-aminocaproyl-2-aminoethyl) derivative of 5-  
 FT methyl cytidine"  
 XX  
 XX US5629153-A.  
 PN  
 PD 13-MAY-1997.  
 XX  
 PF 08-MAR-1994; 94US-00207901.  
 XX  
 PR 10-JAN-1990; 90US-00463022.  
 PR 10-JAN-1991; 91US-00639560.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Urdea MS;  
 DR WPI; 1997-280266/25.  
 XX  
 PT DNA construct for use as signal amplifier in hybridisation assays -  
 PT containing DNA-dependent RNA polymerase promoter and template sequences.  
 XX  
 PS Example 2; Col 25; 45pp; English.  
 XX  
 CC A novel DNA construct (referred to as a "template probe") for use as a  
 CC signal amplifier in hybridisation assays to detect a target comprises 3  
 CC functional domains (A, B and C) orientated A-B-C or B-C-A. (A) is single-  
 CC stranded and is designed to hybridise to complementary target sequence.  
 CC (B) is double-stranded and functions as a DNA-dependent RNA polymerase  
 CC promoter. (C) is single- or double-stranded, and functions as a template  
 CC for the promoter activity of domain B. It consists of a nucleotide  
 CC sequence not found in the template. The DNA construct is used in a method  
 CC for detecting and quantifying an oligonucleotide analyte or a ligand  
 CC receptor by amplification of a biological signal in a nucleic acid  
 CC hybridisation assay. The method is especially useful for determination of  
 CC nucleic acid segments characteristic of hepatitis B virus, Neisseria  
 CC gonorrhoeae, bacterial beta-lactamase TEM-1 gene, Chlamydia, Neisseria  
 CC tet M determinant, HIV or hepatitis C virus. A hybridisation assay for  
 CC the p11n gene DNA of Neisseria gonorrhoeae was performed using a  
 CC microtitre dish assay procedure and the T7 RNA polymerase. The present  
 CC sequence is a 21 base oligomer synthesised for use in the assay. (Updated  
 CC on 25-MAR-2003 to correct PF field.)  
 CC  
 SQ Sequence 21 BP; 7 A; 8 C; 2 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3609 TTCTTGGGGAATGGGTTGG 3628  
 Db 20 TTCTTGGAGAAATGGGTTGG 1  
 RESULT 2565  
 AAT95441/C  
 ID AAT95441 standard; DNA; 21 BP.  
 XX  
 AC AAT95441;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-1998 (first entry)  
 XX  
 DE Primer for breast cancer susceptibility gene BRCA2 exon 11-7.  
 XX  
 KW Human; breast cancer; susceptibility; gene; BRCA2; diagnosis; screening;



KM treatment; gene therapy; PCR primer; exon 11-7; ss.  
 XX  
 OS Synthetic.  
 XX Homo sapiens.  
 XX  
 PN W09722689-A1.  
 XX  
 PD 26-JUN-1997.  
 XX  
 PF 17-DEC-1996; 96WO-US019598.  
 XX  
 PR 18-DEC-1995; 95US-00573779.  
 PR 20-DEC-1995; 95US-00575359.  
 PR 21-DEC-1995; 95US-00576559.  
 PR 11-JAN-1996; 96US-00585391.  
 PR 29-APR-1996; 96US-00639501.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 PA (UYBE-) UNIV PENNSYLVANIA.  
 PA (HSCR-) HSC RES & DEV LP.  
 PA (ENDO-) ENDO RECH INC.  
 XX  
 PI Tavligian SV, Kamb A, Simard J, Couch F, Rommens JM, Weber BL;  
 XX WPI, 1997-341680/31.  
 XX  
 DR Human breast cancer susceptibility gene BRCA2 - useful for diagnosing  
 PT breast cancer and screening for compounds to treat breast cancer.  
 XX  
 PS Example 3; Page 60; 189pp; English.  
 XX  
 CC The present sequence is a primer for the human breast cancer  
 CC susceptibility gene BRCA2, which can be used to diagnose breast cancer  
 CC and screen for compounds to treat breast cancer. BRCA2 can also be used  
 CC in gene therapy to restore wild type BRCA2 gene function to a cell, which  
 CC has lost its or has altered (i.e. by virtue of a mutation in BRCA2) BRCA2  
 CC gene function. (updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SO Sequence 21 BP; 9 A; 3 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4947 TTACTTTTCTCTGCTGCT 4966  
 DB 21 TAACTTTTCTCCGCTAGCT 2  
 RESULT 2566  
 AAT80147/c  
 ID AAT80147 standard; DNA; 21 BP.  
 XX  
 AC AAT80147;  
 XX  
 DT 08-FEB-1998 (first entry)  
 XX  
 DE Immunoglobulin signal sequence reverse PCR primer.  
 XX  
 DE CTLA4; IgG1; immunoglobulin; antibody; autoimmune disease;  
 KM diabetes mellitus; rheumatoid arthritis; multiple sclerosis;  
 KM myasthenia gravis; systemic lupus erythematosus; thyroiditis;  
 KM transplant rejection; graft versus host disease; allergy; therapy;  
 KM immunosuppressant; human; primer; PCR; signal peptide; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09728267-A1.  
 XX  
 PD 07-AUG-1997.  
 XX  
 PF 03-FEB-1997; 97WO-US001698.  
 XX

XX  
 PR 02-FEB-1996; 96US-00595590.  
 XX  
 PA (REPK ) REPLIGEN CORP.  
 XX  
 PI Gray GS, Carson J, Javaherian K, Jellis CL, Rennert PD, Silver S;  
 XX WPI, 1997-402620/37.  
 XX  
 DR New CTLA4-modified immunoglobulin fusion proteins - used for e.g.  
 PT treating auto-immune diseases and allergies, or for inhibiting  
 PT transplantation rejection.  
 XX  
 PS Example 1; Page 46; 105pp; English.  
 XX  
 CC A forward primer (AAT80146) and a reverse primer (AAT80147) were used for  
 CC the PCR amplification of the immunoglobulin (Ig) signal sequence from  
 CC template plasmid pSP7219G1. The reverse primer corresponds to the C-  
 CC terminal of the natural Ig signal peptide. The 208 bp PCR product  
 CC contains the entire Ig signal sequence. Novel CTLA4-antibody fusions have  
 CC the heavy and light chain variable domains of an antibody molecule  
 CC replaced with the extracellular domain of CTLA4. The resulting antibody-  
 CC like protein binds to B7-1, B7-2 and CTLA4 ligands with high affinity.  
 CC Novel CTLA4-Ig constructs (see AAT80131-83) encode fusion proteins (see  
 CC AAT80131-83) useful in claimed methods for suppressing an immune response  
 CC in a subject  
 XX  
 SO Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 6020 TTTCACACCTGTCACCTCC 6039  
 DB 20 TTTCACACGAGTCCACTCC 1  
 RESULT 2567  
 AAX79218/c  
 ID AAX79218 standard; DNA; 21 BP.  
 XX  
 AC AAX79218;  
 XX  
 DT 31-AUG-1999 (first entry)  
 XX  
 DE Oligonucleotide #11 forms an intramolecular stacked tetrad structure.  
 XX  
 KM Column; box; stacked tetrad; inhibition; replication; pathophysiological;  
 KM herpes simplex virus; HSV; human papilloma virus; Epstein Barr Virus;  
 KM HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCMV;  
 KM respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;  
 KM human T-cell leukaemia virus; HTLV; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key  
 FT modified\_base 1.21  
 FT Location/Qualifiers  
 FT 1.21  
 FT /tag= a  
 FT /note= "optionally contains phosphodiester  
 FT internucleotide linkages"  
 FT misc\_structure 1.21  
 FT /tag= b  
 FT /note= "forms intramolecular stacked tetrad or 3D  
 FT columnar box structure"  
 XX  
 PN W09833807-A1.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 03-FEB-1998; 98WO-US001974.  
 XX  
 PR 04-FEB-1997; 97US-0037374P.  
 XX

PR 09-DEC-1997; 97US-00987574.  
XX (ARON-) ARONEX PHARM INC.  
PA  
PI Rando RF, Ojwang JO, Hogan ME, Wallace TL, Coesum PA;  
XX WPI; 1998-446809/38.  
DR  
PT New guanosine-rich tetrad forming oligonucleotide(s) - used for  
PT inhibiting virus replication for treating e.g. herpes simplex, papilloma,  
PT HIV, adenovirus or hepatitis B virus infection.  
XX  
PS Disclosure; Page 137; 140pp; English.  
XX  
CC Sequences AAY79210-X79275 represent oligonucleotides (ON) which are able  
CC to form a columnar box or "stacked tetrad" structure by intramolecular  
CC internucleotide binding. The ONs are used to inhibit the replication of  
CC viruses. They are able to suppress virus production for prolonged periods  
CC after an initial short treatment regimen. They can be used for treating  
CC pathophysiological states caused by viruses such as herpes simplex virus,  
CC human papilloma virus, Epstein Barr Virus, HIV, adenovirus, respiratory  
CC syncytial virus, hepatitis B virus, human cytomegalovirus and HTLV I and  
CC II  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 17 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2998 CCCCCACCCCTCACCCTGC 3017  
DB 21 CCCCCACCCACCCACCCAC 2  
RESULT 2568  
AAZ26573/C  
ID AAZ26573 standard; DNA; 21 BP.  
XX  
AC AAZ26573;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 762.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX WPI; 1998-521232/44.  
XX  
DR Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-226825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 14 A; 1 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 5744 TTTTCTCTATTCACCTGC 5763  
DB 20 TTTTCTCTATTCACCTGC 1  
RESULT 2569  
AAZ26268  
ID AAZ26268 standard; DNA; 21 BP.  
XX  
AC AAZ26268;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 457.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX WPI; 1998-521232/44.  
XX  
DR Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is

CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AA25812-226825 represent  
CC human polymorphic sites described in the method of the invention  
SQ Sequence 21 BP; 5 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACCTTTTCTTTTCTTTT 4481  
DB 1 AATTTTCTTTTCTTTTAT 20

RESULT 2570  
AA26511  
ID AA26511 standard; DNA; 21 BP.  
XX  
AC AA26511;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 700.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene

CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AA25812-226825 represent  
CC human polymorphic sites described in the method of the invention  
SQ Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 558 GACATCCCTGGGAGGGA 577  
DB 1 GAGATCCCTGGCAAGGGA 20

RESULT 2571  
AA26572/c  
ID AA26572 standard; DNA; 21 BP.  
XX  
AC AA26572;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 761.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the

CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AA225812-226825 represent  
 CC human polymorphic sites described in the method of the invention

SQ Sequence 21 BP, 13 A, 1 C, 3 G, 4 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5744 TTTTCTCTATTCACCTGC 5763  
 21 TTTTCTCTATTCACCTGC 2

RESULT 2572  
 AA226485  
 ID AA226485 standard; DNA, 21 BP.  
 XX AA226485;  
 AC  
 XX  
 DT 30-NOV-1999 (first entry)  
 XX  
 DE Human polymorphic region 674.  
 XX  
 KM Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
 KM cell viability; loss of heterozygosity; precancerous condition; ASI;  
 KM allele specific inhibitor; somatic cell; diagnosis; prevention;  
 KM atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
 KM dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
 KM graft versus host disease; malignant cell removal; bone marrow; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9841648-A2.  
 XX  
 PD 24-SEP-1998.  
 XX  
 PF 19-MAR-1998; 98WO-US005419.  
 XX  
 PR 20-MAR-1997; 97US-0041057P.  
 XX  
 PA (VARI-) VARIAGENICS INC.  
 XX  
 PI Houseman D, Ledley PD, Stanton VP;  
 XX  
 DR WPI; 1998-521232/44.  
 XX  
 PT Identifying target genes for allele-specific drugs - used for diagnosis,  
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 PT dysplastic lesions, endometriosis or graft versus host disease.  
 XX  
 PS Disclosure; Fig 7; 605pp; English.

CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and

CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AA225812-226825 represent  
 CC human polymorphic sites described in the method of the invention

SQ Sequence 21 BP, 16 A, 0 C, 5 G, 0 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4020 AAAAAGAGGAAAAACAAA 4039  
 1 AAGAGAGAGGAAAAAAA 20

RESULT 2573  
 AA220460  
 ID AA220460 standard; DNA, 21 BP.  
 XX AA220460;  
 AC  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Forward PCR primer for microsatellite marker Bmag323.  
 XX  
 KM PCR primer; microsatellite marker; barley; chromosome 7 marker; cereal;  
 KM fermentability; group 5 chromosome; ethyl carbanate production; Bmag313;  
 KM wort fermentation; Triticaceae; Bmag36; epi-heterodendrin production;  
 KM diagnosis; ss.  
 XX  
 OS Synthetic.  
 OS Hordeum vulgare.  
 XX  
 PN WO9946404-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 01-MAR-1999; 99WO-GB000602.  
 XX  
 PR 10-MAR-1998; 98GB-00005087.  
 XX  
 PA (SCCR-) SCOTTISH CROP RES INST.  
 XX  
 PI Thomas WTB, Swanson JS, Powell W, Waugh R, Ramsey LD;  
 XX  
 DR WPI; 1999-551424/46.  
 XX  
 PT Screening cereals for fermentability, especially useful in barley.  
 XX  
 PS Claim 25; Page 23; 49pp; English.

CC This sequence represents a PCR primer for a barley chromosome 7  
 CC microsatellite marker, and can be used in the method of the invention.  
 CC The method is for screening cereal for fermentability, comprising  
 CC analysing cereal genomic DNA to determine which allele(s) of a gene/gene  
 CC complex affecting fermentability at a locus close to the centromere on  
 CC homologous Triticaceae group 5 chromosome (barley chromosome 7) is/are  
 CC present. The invention also relates to a method for screening cereal for  
 CC ethyl carbanate production on wort fermentation and distillation,  
 CC comprising analysing barley genomic DNA to determine which allele(s) of  
 CC the locus, designated eph on the short arm of homologous Triticaceae group  
 CC 1 chromosome (barley chromosome 5) is/are present. The method and  
 CC primers are useful for determining fermentability and/or epi-heterodendrin  
 CC production in cereals, especially barley. Current methods for determining  
 CC fermentability are difficult to apply within barley breeding programs.  
 CC Prior art methods using molecular markers have difficulty in detecting  
 CC levels of allelic variation

SQ Sequence 21 BP, 7 A, 5 C, 3 G, 6 T, 0 U, 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1720 TTCCGCACTCTCAAGACAC 1739

Db 2 TTGTGACATCTCAAGAACAC 21

RESULT 2574

AAK00040/c

ID AAX00040 standard; DNA; 21 BP.

XX AAX00040;

XX 16-MAR-1999 (first entry)

XX aGFP PCR antisense primer.

XX Neuroepithelial stem cell; lineage restricted intermediate precursor;

XX oligodendrocyte; astrocyte; self-renewal; neuron; differentiation; CNS;

XX neutral crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS;

XX central nervous system; glial cell; PCR primer; amplification; ss.

XX Synthetic.

XX Homo sapiens.

XX MO9850526-A1.

XX 12-NOV-1998.

XX 07-MAY-1998; 98MO-US009630.

XX 07-MAY-1997; 97US-00852744.

XX 06-MAY-1998; 98US-00073881.

XX (UTAH) UNIV UTAH RES FOUND.

XX Rao MS, Mayer-Proschel M, Mujtaba T;

XX WPI; 1999-070093/06.

XX Mammalian neuroepithelial stem cells and glial restricted precursor - can

XX self-renew and differentiate into central nervous system cells, used for

XX generating various types of cells.

XX Example 26; Page 59; 78pp; English.

XX The present invention describes an isolated, pure population of mammalian

XX neuroepithelial stem cells, which are capable of self-renewal in adherent

XX feeder-cell-independent (NFICI) culture medium and differentiation to

XX central nervous system (CNS) neuronal or glial cells and to neuronal

XX crest stem cells. Also described is an isolated population of mammalian

XX CNS glial-restricted precursor (GRP) cells which can self-renew in the

XX APF1 culture medium and can differentiate to CNS glial cells but not to

XX CNS neuronal cells. The stem cells can be used to generate a population

XX of mammalian motor neurons by incubating the stem cells in a medium

XX promoting cell proliferation and neuronal differentiation. The medium

XX comprises laminin-coated plates and NEP medium lacking chick embryo

XX extract. The stem cells can also produce neural crest stem cells by

XX inducing the cells to differentiate in vitro. The inducing step comprises

XX withdrawing a mitogen (preferably fibroblast growth factor; FGF) and

XX chick embryo extract. Inducing can also comprise adding a dorsalizing

XX agent to the cells, preferably a bone morphogenetic protein (BMP) such as

XX BMP-2, -4 or -7. The stem cells can be used to produce cells of the

XX peripheral nervous system, by inducing the stem cells to differentiate in

XX vitro to neural crest stem cells, and inducing these cells to

XX differentiate. AAX00029 to AAX00054 represent PCR primers which are used

XX in an example from the present invention to amplify different FGF and

XX FGFR genes

XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3683 GCCAGAAAGCCAGCTATT 3702

Db 21 GCCAGAAAGCCAGCTATT 2

RESULT 2575

AAZ95022

ID AAZ95022 standard; DNA; 21 BP.

XX AAZ95022;

XX 15-AUG-2000 (first entry)

XX Prostate cancer diagnostic marker Proll1 forward PCR primer.

XX Prostate cancer; cancer specific gene; CSG; expressed sequence tag; EST;

XX diagnosis; monitoring; staging; imaging; therapy; metastasis; marker;

XX human; Proll1; PCR primer; ss.

XX Homo sapiens.

XX WO200023111-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99MO-US024331.

XX 19-OCT-1998; 98US-0104737P.

XX (DIAD-) DIADEXUS LLC.

XX Salceda S, Recipon H, Cafferkey R;

XX WPI; 2000-339531/29.

XX Diagnosing, staging and monitoring the presence and metastases of

XX prostate cancer especially useful for treating prostate cancer comprises

XX measuring changes in cancer specific gene levels.

XX Example 2; Page 23; 74pp; English.

XX The present sequence is that of the forward primer used in the real-time

XX quantitative PCR amplification of cancer specific gene Proll1 (see

XX AAZ95002 and AAZ95003). Overexpression of Proll1 was found in 5 of 16

XX primary prostate cancer samples examined, indicative of it being a

XX diagnostic marker for prostate cancer. The invention provides ESTs and

XX full-length cDNAs for CSGs (see AAZ94998-295017). The CSGs,

XX polypeptides encoded by them, and antibodies that specifically bind CSG

XX are used in claimed methods for detecting, diagnosing, monitoring,

XX staging, imaging and treating prostate cancer

XX Sequence 21 BP; 5 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15.2; DB 1; Length 21;

XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;

XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX OY 5181 CTGCATGTTCTCCACTTGA 5200

XX Db 2 CTGCATGTTCTCCACTTGA 21

XX RESULT 2576

XX AAA46283

XX ID AAA46283 standard; DNA; 21 BP.

XX AAA46283;

XX 04-SEP-2000 (first entry)



```
PD 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 1715; 2745pp; English.
XX
XX AA65654 to AA69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA69579 to AA77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 21 BP; 0 A; 8 C; 1 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5707 CCTTTCCTCTCTCTCTT 5726
XX |||||
XX 1 CCTTTCCTCTCTCTCTCT 20
XX
XX Db
XX
XX RESULT 2579
XX AA276810
XX ID AA276810 standard; DNA; 21 BP.
XX
XX AA276810;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:11166.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX
XX Homo sapiens.
XX
XX MO9954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
```

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XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 2611; 2745pp; English.
XX
XX AA65654 to AA69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AA69579 to AA77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 21 BP; 6 A; 5 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 1.8e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4635 CAACCTCAGTGTGGAATTTC 4654
XX |||||
XX 2 CAACCTCAGTGTATATTTC 21
XX
XX Db
XX
XX RESULT 2580
XX AAC60966/c
XX ID AAC60966 standard; DNA; 21 BP.
XX
XX AAC60966;
XX
XX 13-FEB-2001 (first entry)
XX
XX Tumour necrosis factor beta short tandem repeat primer SEQ ID NO:26.
XX
XX Short tandem repeat; primer; STR; susceptibility; HIV; infection; AIDS;
XX detection; polymorphism; interleukin 10 promoter; IL-10;
XX chromosome position 6p21.3; tumour necrosis factor beta; ss.
XX
XX Homo sapiens.
XX
XX WO200061811-A2.
XX
XX 19-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009355.
XX
XX 09-APR-1999; 99US-0128521P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Smith MW, Shin HD, O'Brien SJ;
XX
XX WPI; 2000-687051/67.
XX
XX Predicting susceptibility to HIV infection or progression useful for
XX selection of therapeutic treatment for persons infected with HIV virus,
XX comprises detecting polymorphism in human interleukin-10 promoter.
XX
XX Example 1; Page 12; 40pp; English.
```

CC The present invention describes a method for predicting susceptibility to  
CC HIV infection or HIV progression in a subject. The method involves  
CC detecting a polymorphism in a human Interleukin-10 (IL-10) promoter,  
CC where the presence of the polymorphism indicates susceptibility to HIV  
CC infection or HIV progression. The method provides prognostic information  
CC to persons infected with HIV virus and is useful to help select  
CC treatments (such as administration of IL-10 or gene therapy with IL-10).  
CC The presence of polymorphism is useful as predictor that very aggressive  
CC treatment could substantially eradicate the virus from the infected  
CC person. The method is useful for the generation of normograms or other  
CC predictive algorithms that can be used, in association with allele  
CC status, to prognose probable survival or years to development of AIDS  
CC following HIV seroconversion. It indicates that increased expression of  
CC the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression  
CC and enables a variety of new therapeutic interventions in the treatment  
CC of HIV disease. The present sequence represents a short tandem repeat  
CC (STR) primer which is used in an example from the present invention  
XX  
SQ Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5179 CTTGCAAGTTCTCCACTTG 5198  
Db 21 CTTGCAAGTTCTCCACTG 2

RESULT 2581  
AAC80269/c  
ID AAC80269 standard; DNA; 21 BP.  
AC AAC80269;  
XX  
XX 03-MAY-2001 (first entry)  
DT  
XX  
DE Reverse primer #97 used for amplification of HLA-A exon 3.  
XX  
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX W0200061795-A2.  
XX  
XX 19-OCT-2000.  
PD  
XX  
XX 05-APR-2000; 2000WO-EP002998.  
PF  
XX  
XX 09-APR-1999; 99EP-00870068.  
PR  
XX 11-JUN-1999; 99US-0138614P.  
XX  
XX (INNO-) INNOGENETICS NV.  
XX  
XX De Canck I, Rombout A, Rosseau R;  
XX  
XX WPI; 2000-647426/62.  
DR  
XX  
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4  
XX of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined  
XX primer sets, useful for subtyping or typing of HLA Class I alleles.  
XX  
XX Claim 4; Page 40; 128pp; English.  
XX  
XX The present invention relates to a method for the locus-specific,  
XX separate amplification of exon 2, exon 3, and/or exon 4 of human  
XX leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful  
XX for subtyping or typing of HLA Class I alleles. The present sequence is  
XX an amplification primer used in the method  
XX  
SQ Sequence 21 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 1 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5151 GGGAGGAGGACTTCTCTGG 5170  
Db 21 GGGAGGAGGACTTCTCTGG 2

RESULT 2582  
AAF95320/c  
ID AAF95320 standard; DNA; 21 BP.  
AC AAF95320;  
XX  
XX 06-JUN-2001 (first entry)  
DT  
XX  
DE Human gene single nucleotide polymorphism #81.  
XX  
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
XX polymorphism; vascular disease; coronary artery disease; forensics;  
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
XX pulmonary embolism; paternity test; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH  
FT Variation replace(11,A)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
XX W0200118250-A2.  
XX  
XX 15-MAR-2001.  
PD  
XX  
XX 07-SEP-2000; 2000WO-US024503.  
PF  
XX  
XX 10-SEP-1999; 99US-0153357P.  
PR  
XX 26-JUL-2000; 2000US-0220947P.  
XX  
XX 16-AUG-2000; 2000US-0225724P.  
XX  
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;  
XX  
XX WPI; 2001-226749/23.  
DR  
XX  
XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
XX applications such as forensics, paternity testing, medicine, genetic  
XX analysis and phenotype correlations to diseases such as diabetes and  
XX atherosclerosis.  
XX  
XX Example; Page 52; 242pp; English.  
XX  
XX The present invention provides a method of diagnosing a vascular disease  
XX in an individual, involving determining the sequence at various  
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
XX genes. The sequences at a number of polymorphic sites are also provided  
XX in the specification. In particular, the method can be used in the  
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart  
XX disease, stroke, peripheral vascular diseases, venous thromboembolism  
XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
XX useful in forensics, paternity testing, genetic analysis and phenotype  
XX correlations to diseases. The present sequence is an example of one of  
XX the human gene SNPs shown in the specification  
XX  
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



```
OY 4761 ATCCGCGCTGTAGAGTTAG 4780
DB 21 ATCCGCGCTGTAGAGTTAG 2

RESULT 2583
AAF95430/c
ID AAF95430 standard; DNA; 21 BP.
AC AAF95430;
XX
XX
XX 06-JUN-2001 (first entry)
DT
DE Human gene single nucleotide polymorphism #191.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Variation replace(11,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 61; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX
XX Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;
XX

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7408 AACATCAGCAGCAGCAGCAG 7427
DB 20 AACATCAGCAGCAGCAGCAG 1
```

```
RESULT 2584
AAF96888/c
ID AAF96888 standard; DNA; 21 BP.
XX
XX AAF96888;
XX
XX 06-JUN-2001 (first entry)
DT
DE Human gene single nucleotide polymorphism #1649.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Variation replace(11,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 159; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX
XX Sequence 21 BP; 0 A; 13 C; 7 G; 1 T; 0 U; 0 Other;
XX

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 64 GGCCTGCGGGCGGCGGCGC 83
DB 21 GGCCTGCGGGCGGCGGCGC 2

RESULT 2585
AAH22257
ID AAH22257 standard; DNA; 21 BP.
```

AC	AAH22257;
XX	
DT	21-AUG-2001 (first entry)
DE	Placental growth factor forward PCR primer SEQ ID NO:3.
XX	
KW	Human; differentially expressed gene; angiogenesis; diagnosis;
KW	angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KW	vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KW	rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KW	neovascularisation; restenosis; hypertension; aneurysm; angina;
KW	myocardial infarction; chronic heart condition; osteoporosis; PCR primer;
KX	hybridisation; probe; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200132926-A2.
PD	
XX	10-MAY-2001.
PF	
XX	01-NOV-2000; 2000MO-US030051.
PR	
XX	01-NOV-1999; 99US-0162699P.
PR	13-APR-2000; 2000US-0196802P.
XX	
XX	31-OCT-2000; 2000US-00703350.
PA	(CUBA-) CUBAGEN CORP.
PA	(GETH ) GENENTECH INC.
PI	Mehraban F, Gerltzen M, Rastelli L;
DR	WPI: 2001-291056/30.
XX	
PT	Differentially expressed genes involved in angiogenesis, useful for
PT	treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT	subsequent to balloon angioplasty.
XX	
PS	Example 19; Page 147; 182pp; English.
XX	
CC	The present invention describes differentially expressed genes involved
CC	in angiogenesis (1), and the polypeptides that encode them. (1) have
CC	cardiovascular activity, and can be used in the modulation of
CC	angiogenesis. The nucleic acids and polypeptides may be used in the
CC	prevention, diagnosis and treatment of diseases associated with
CC	inappropriate angiogenesis. The polypeptides may also be used as antigens
CC	in the production of antibodies against them and in assays to identify
CC	modulators of their expression and activity. The antibodies and
CC	antagonists may also be used to down regulate expression and activity and
CC	modulate angiogenesis. The antibodies may also be used as diagnostic
CC	agents for detecting the presence of the polypeptides in samples.
CC	Disorders that may be prevented, diagnosed and/or treated by the above
CC	methods include, for example vascular tumors, proliferative tumore,
CC	proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC	atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC	associated with neovascularisation, restenosis subsequent to balloon
CC	angioplasty, scar tissue over production, peripheral vascular disease,
CC	hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's
CC	phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC	lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC	reperfusion injury, angina, myocardial infarctions, chronic heart
CC	conditions, heart failure such as congestive heart failure, age-related
CC	macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC	to AAB99325 represent sequence used in the exemplification of the present
CC	invention
XX	
XX	
SQ	Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
Query Match	0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Prd: No.1.8e+03;
Matches 17; Conservative	0; Mismatches 3; Indels 0; Gaps 0

Query Match	0.2%	Score 15.2	DB 1	Length 21
Best Local Similarity	85.0%	Pred. No. 1.8e+03		
Matches 17	Conservative 0	Mismatches 3	Indels 0	Gaps 0
DB	7412	TCAGCAGCAGCAGCAGC	7431	
	21	TCGCCAAGCAGCAGCAGC	2	

RESULT 2587  
AAH62143/C  
ID AAH62143 standard; DNA; 21 BP.  
XX

RESULT 2586  
AAH62597/C  
ID AAH62597 standard; DNA; 21 BP.  
XX  
AC  
XX  
AAH62597;  
XX  
12-SEP-2001 (first entry)  
XX  
CHRNA7 polymorphism containing DNA fragment #498.  
XX  
Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
XX  
heart disease; paternity testing; forensic science; ds.  
XX  
Homo sapiens.  
XX  
Key Location/Qualifiers  
FH replace(11,A)  
FT Variation /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
XX  
WO200138576-A2.  
XX  
31-MAY-2001.  
XX  
17-NOV-2000; 2000WO-US031639.  
XX  
PF 24-NOV-1999; 99US-0167334P.  
XX  
PR (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
PA Cargill M, Ireland JS, Lander ES;  
XX  
PI WPI; 2001-367705/38.  
XX  
DR  
XX  
XX  
New nucleic acid segments of the human genome, particularly from genes  
PT including polymorphic sites, for phenotype correlation, forensics,  
PT paternity testing, medicine and genetic analysis.  
XX  
PS Claim 1; Page 69; 80pp; English.  
XX  
XX  
DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
CC contain single nucleotide polymorphisms (SNPs). A method is included in  
CC the invention for analysing a nucleic acid sample, which consists of  
CC determining the base occupying any one of the polymorphic sites given in  
CC the SNP containing sequences. The nucleotide sequences can be used in the  
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
CC diseases, diseases of the cardiovascular system, and infection by  
CC microorganisms. The oligonucleotides are also useful in the manufacture  
CC of a medicament for the treatment or prophylaxis of the diseases, and as  
CC a pharmaceutical. SNP containing oligonucleotides are useful in  
CC applications such as phenotype correlation, forensics, paternity testing,  
CC medicine and genetic analysis  
CC  
SQ Sequence 21 BP; 1 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

AC	AAH62143;
XX	
DT	12-SEP-2001 (first entry)
XX	
DE	Solute carrier family 3 A1 polymorphism containing DNA fragment #44.
XX	
KM	Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX	
KW	heart disease; paternity testing; forensic science; de.
OS	
Homo sapiens.	
Key	Location/Qualifiers
Variation	replace(11,C)
FT	/tag= A
FT	/standard_name= "single nucleotide polymorphism"
PN	WO200138576-A2.
PD	
31-MAY-2001.	
PF	17-NOV-2000; 2000WO-US031639.
PR	
24-NOV-1999;	99US-0167334P.
PA	(MHED ) WHITEHEAD INST BIOMEDICAL RES.
PI	Cargill M, Ireland JS, Lander ES;
DR	WPI; 2001-367705/38.
PT	New nucleic acid segments of the human genome, particularly from genes
PT	including polymorphic sites,for phenotype correlation, forensics,
PT	paternity testing, medicine and genetic analysis.
PS	Claim 1; Page 32; 80pp; English.
CC	DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC	contain single nucleotide polymorphisms (SNPs). A method is included in
CC	the invention for analyzing a nucleic acid sample, which consists of
CC	determining the base occupying any one of the polymorphic sites given in
CC	the SNP containing sequences. The nucleotide sequences can be used in the
CC	diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC	diseases, diseases of the cardiovascular system, and infection by
CC	microorganisms. The oligonucleotides are also useful in the manufacture
CC	of a medicament for the treatment or prophylaxis of the diseases, and as
CC	a pharmaceutical. SNP containing oligonucleotides are useful in
CC	applications such as phenotype correlation, forensics, paternity testing,
CC	medicine and genetic analysis
SQ	Sequence 21 BP; 4 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
Query Match	0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity	85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative	0; Mismatches 3; Indels 0; Gaps 0
Oy	1580 CCCAATAAACAGTGTGCAGAA 1599                         Db 20 CCCAGAAAACAGTCTGACA 1
RESULT 2588	
AAH91825	
ID	AAH91825 standard; DNA; 21 BP.
XX	
AC	AAH91825;
XX	
DT	09-OCT-2001 (first entry)
XX	
DE	Human inflammatory bowel disease associated polymorphic site #900.
XX	
KM	Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW	chromosome 5q31-33; forensic test; gene therapy; de.

XX	Homo_sapiens.	
OS		Location/Qualifiers
XX	Key	11
FH	misc_feature	/tag= a
FT		/note= "SNP, optionally T or A at this position"
FT		
XX		
PN	WO200142511-A2.	
XX		
PD	14-JUN-2001.	
XX		
PF	11-DEC-2000; 2000WO-US033632.	
XX		
PR	10-DEC-1999; 99US-0170257P.	
XX		
PR	10-APR-2000; 2000US-0196046P.	
XX		
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES.	
XX		
PI	(ELTI-) ELTIPSIS BIOTHERAPEUTICS CORP.	
XX		
DR	Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;	
XX		
WPI:	2001-367874/38.	
XX		
PT	Testing for the presence of polymorphisms associated with inflammatory	
XX		
PS	bowel disease, using a hybridization assay.	
XX		
CC	Claim 1; Page 76; 463pp; English.	
XX		
CC	The present invention describes a method for detecting the presence of	
XX		
CC	polymorphisms associated with inflammatory bowel diseases such as	
XX		
CC	ulcerative colitis and Crohn's disease. The methods can be used to detect	
XX		
CC	the presence of genetic polymorphisms associated with inflammatory bowel	
XX		
CC	disease and correlating their occurrence with disease states. They may be	
XX		
CC	used in this way for phenotypic correlations, forensics, paternity	
XX		
CC	testing, medicine and genetic analysis. The present sequence is a	
XX		
CC	polymorphic site described in the exemplification of the invention	
XX		
SQ	Sequence 21 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 1 Other;	
	Query Match 0.2%; Score 15.2; DB 1; Length 21;	
	Best Local Similarity 81.0%; Pred. NO. 1.8e+03;	
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.	
OY	4463 CTTTCTTTTTTTTTTTTTTTT 4483                   1 CTCTTCATCNTTTTTTTTTT 21	
Db		
	RESULT 2589	
	AAF87033	
ID	AAF87033 standard; DNA; 21 BP.	
XX		
AC	AAF87033;	
XX		
DT	18-SEP-2001 (first entry)	
XX		
DE	Anchored 3' oligo drl2 primer.	
XX		
KM	Sequencing primer; definitive ectoderm equivalent cell; DEB cell;	
XX		
KM	cell preparation; early primitive ectoderm-like cell; EPL cell; human;	
XX		
KM	cell therapy; gene therapy; neuroectoderm cell; organ transplant;	
XX		
KM	neurodegenerative disease; Parkinson's disease; Alzheimer's disease;	
XX		
KM	stroke; spinal cord injury; therapy; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200151610-A1.	
XX		
PD	19-JUL-2001.	
XX		
PF	12-JAN-2001; 2001WO-AU0000029.	
XX		

PR 14-JAN-2000; 2000AU-00005098.  
 PR 20-APR-2000; 2000AU-00007045.  
 PR 27-APR-2000; 2000AU-00007143.  
 XX  
 XX (BRES-) BRESAGEN LTD.  
 PA (LONG/) LONG C L O.  
 XX  
 PI Long CLO, Rathjen PD, Rathjen J;  
 XX  
 DR WPI; 2001-432907/46.  
 XX  
 PT Preparing (M1) definitive ectoderm equivalent (DEE) cells in vitro for  
 PT treatment of Parkinson's and Alzheimers comprises culturing early  
 PT primitive ectoderm-like cells in conditioned medium.  
 XX  
 PS Example; Page 37; 116pp; English.  
 XX  
 CC This sequence represents a sequencing primer used within the scope of the  
 CC invention. The invention relates to a method for preparing definitive  
 CC ectoderm equivalent (DEE) cells in vitro comprising providing: (a) early  
 CC primitive ectoderm-like (EPL) cells; and (b) a conditioned medium or  
 CC extract exhibiting neural inducing properties and culturing the EPL cells  
 CC for a time to permit controlled differentiation to DEE cells. The DEE  
 CC cells, or their differentiated or partially differentiated progeny are  
 CC useful in human cell therapy or transgenic animal production and for use  
 CC in human or animal gene therapy. The method is useful for preparing DEE  
 CC cells in vitro. It can also be used for selectively producing  
 CC neuroectoderm cells or surface ectoderm cells from DEE cells. The method  
 CC can also be used to produce genetically modified DEE cells. It is also  
 CC useful for preparing tissues or organ for transplant. The cells are  
 CC useful for treating and curing neurodegenerative diseases such as  
 CC Parkinson's disease and Alzheimer's disease and pathological conditions  
 CC such as stroke and spinal cord injury by replacing or assisting the  
 CC function of normal disease tissues. They are also useful for the  
 CC treatment of corneal disorders. The methods are useful for producing  
 CC cells as a source for reprogramming and for use in pharmaceutical or  
 CC toxicological screening  
 XX  
 SQ Sequence 21 BP; 4 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4458 ATGACCTTTTCTTTTCTTTT 4477  
 DB 1 ATGAACTCTTTTCTTTTCTTTT 20  
 RESULT 2590  
 ABK51835/c  
 ID ABK51835 standard; DNA; 21 BP.  
 XX  
 AC ABK51835;  
 XX  
 DT 30-JUN-2002 (first entry)  
 XX  
 DE DNA probe #1 for human UGT8 gene.  
 XX  
 KM Human; enzyme classification; enzyme quantitative determination;  
 KM glucuronic acid conjugation; UDP-glucuronosyltransferase; UGT8; probe;  
 KM ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN JP2002085066-A.  
 XX  
 PD 26-MAR-2002.  
 XX  
 PF 07-SEP-2000; 2000JP-00272228.  
 XX  
 PR 07-SEP-2000; 2000JP-00272228.  
 XX

PA (SAKA ) OTSUKA SEIYAKU KOGYO KK.  
 XX  
 DR WPI; 2002-378271/41.  
 XX  
 PT Determination of enzymes participating in glucuronic acid conjugation in  
 PT human being, comprises use of oligonucleotide probes.  
 XX  
 PS Claim 8; Page 13; 13pp; Japanese.  
 XX  
 CC The present invention relates to a method for classification and  
 CC quantitative determination of enzymes participating in glucuronic acid  
 CC conjugation. The method involves the use of oligonucleotide probes  
 CC hybridizing to regions of the human UDP-glucuronosyltransferase (UGT)  
 CC genes (e.g. UGT1, UGT1A7, UGT1A10, UGT2A1, UGT2B7, UGT2B10,  
 CC UGT2B11, UGT2B15, UGT2B17, UGT8), and the DDOST gene. The method and  
 CC probes are useful for the genetic determination of enzymes participating  
 CC in glucuronic acid conjugation with catalysed UGT. The method is both  
 CC rapid and accurate. ABK51813-ABK51836 represent oligonucleotide probes  
 CC useful for human UGT or DDOST genes  
 XX  
 SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7250 TGGATGGGAAATGCTCTG 7269  
 DB 20 TAGATGGGCGGATGCTCTG 1  
 RESULT 2591  
 ABK8538/c  
 ID ABK8538 standard; DNA; 21 BP.  
 XX  
 AC ABK8538;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Human cholecystokinin associated PCR primer P2.  
 XX  
 KM Panic disorder; polymorphism; human cholecystokinin; upper stream; CCK;  
 KM PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 PN JP2002171990-A.  
 XX  
 PD 18-JUN-2002.  
 XX  
 PF 08-DEC-2000; 2000JP-00375090.  
 XX  
 PR 08-DEC-2000; 2000JP-00375090.  
 XX  
 PA (RIKA ) RIKAGAKU KENKYUSHO.  
 XX  
 DR WPI; 2002-569886/61.  
 XX  
 PT Diagnosis and identification of panic disorder caused by polymorphism of  
 PT upper stream region of human cholecystokinin gene.  
 XX  
 PS Claim 6; Page 6; 13pp; Japanese.  
 XX  
 CC The invention describes a method of diagnosing a panic disorder with a  
 CC polymorphism of the upper stream region of human cholecystokinin (CCK)  
 CC gene. This sequence represents a human cholecystokinin gene associated  
 CC PCR primer  
 XX  
 SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 21;  
 Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6914 TACTGACTTAGAGCCTCTGG 6933  
DB 20 TACTGAATTAGAGCCTCTGG 1

RESULT 2592  
ABK16848/c  
ID ABK16848 standard; DNA; 21 BP.  
XX  
XX ABK16848;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Human protein refolding PCR primer #71.  
XX  
XX Protein refolding; growth hormone supergene family; human; mouse; ss;  
XX  
XX therapeutic half-life; PCR primer; anti-angiogenesis factor.  
XX  
XX Homo sapiens.  
XX  
XX Synthetic.  
XX  
XX WO200187925-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 16-MAY-2001; 2001WO-US016088.  
XX  
XX 16-MAY-2000; 2000US-0204617P.  
XX  
XX (BOLD-) BOLDER BIOTECHNOLOGY INC.  
XX  
XX Rosendahl MS, Cox GN, Doherty DH;  
XX  
XX WPI; 2002-089843/12.  
XX  
XX Making and refolding insoluble or aggregated proteins having free  
XX  
XX cysteine by exposing host cell expressing protein to cysteine blocking  
XX  
XX agent, and exposing to cysteine reactive group to increase their  
XX  
XX effectiveness.  
XX  
XX Example 14; Page 52; 110pp; English.

CC The invention relates to a host cell, made to express an insoluble or  
CC aggregated protein having free cysteines residues. The cell is then lysed  
CC by chemical, enzymatic or physical agents and solubilised by exposing it  
CC to a denaturing agent, a reducing agent and a cysteine blocking agent,  
CC and is refolded into a biologically active form by reducing the  
CC concentrations of denaturing and reducing agents. The protein may belong  
CC to the growth hormone supergene family or may be an anti-angiogenesis  
CC factor. The method is useful for preparing a refolded, soluble form of an  
CC insoluble or aggregated protein. The proteins of the invention can act as  
CC delivery vehicles for enhancement of the circulatory half-life of the  
CC therapeutics that are attached or for directing delivery of a specific  
CC target within the body. Sequences ABK16774-ABK16852 represent PCR primers  
CC used in synthesis of the proteins  
XX  
XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6435 ATTAGCTTAAGCAGCAGTGT 6454  
DB 21 ATTATCTTCAGCAGCAGTGT 2

RESULT 2593  
ABZ31311  
ID ABZ31311 standard; DNA; 21 BP.  
XX  
XX ABZ31311;

XX 30-JAN-2003 (first entry)  
XX  
XX Candida albicans GRACE strain PCR primer SEQ ID NO 5530.  
XX  
XX  
XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;  
XX  
XX signal transduction; DNA replication; cell division; growth;  
XX  
XX proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.  
XX  
XX Candida albicans.  
XX  
XX WO200253728-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 26-DEC-2001; 2001WO-US049486.  
XX  
XX 29-DEC-2000; 2000US-0259128P.  
XX  
XX 20-FEB-2001; 2001US-0079202A.  
XX  
XX 22-AUG-2001; 2001US-0314050P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;  
XX  
XX WPI; 2002-566694/60.  
XX  
XX Constructing strains for identifying gene products as effective targets  
XX  
XX for therapeutic intervention, by inactivating in the strain one allele of  
XX  
XX a gene and placing other allele of the gene under conditional expression.  
XX  
XX Claim 36; SEQ ID NO 5530; 167bp + Sequence Listing; English.

CC The invention relates to constructing (M1) a strain of diploid fungal  
CC cells in which both alleles of a gene are modified, comprising modifying  
CC one allele by insertion or replacement by a cassette having an  
CC expressible selectable marker and modifying other allele by  
CC recombination, of a promoter replacement fragment with a heterologous  
CC promoter, so that expression of the second allele is regulated by the  
CC promoter. (M1) is useful for constructing a strain of diploid fungal  
CC cells in which both alleles of a gene are modified. The diploid fungal  
CC cells having both alleles modified are useful for identifying a gene that  
CC is essential to the survival or growth of a fungus, a gene that  
CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
CC that contributes to the resistance of a diploid fungus to an antifungal  
CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
CC and for identifying a therapeutic agent for treatment of a mammalian  
CC disease. (M1) is useful for identifying a compound which modulates the  
CC activity of a gene product, preferably enzymatic activity, carbon  
CC compound catabolism, biosynthetic, transporter, transcriptional,  
CC translational, signal transduction, DNA replication and cell division  
CC activity. The method is useful for identifying a compound having the  
CC ability to inhibit growth or proliferation of C. albicans cells and for  
CC treating infection by C. albicans. The present sequence is that of a PCR  
CC primer used in the method of the invention. Note: The sequence data for  
CC this patent is not represented in the printed specification but is based  
CC on sequence information supplied to Derwent by the European Patent Office  
XX  
XX Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5695 CTGTTTGCTTCCTTTTC 5714  
DB 2 CTCTTTGGCTGCTTTTC 21

RESULT 2594  
ABS98398/c  
ID ABS98398 standard; DNA; 21 BP.  
XX  
XX ABS98398;

AC ABS98398;  
XX  
XX 23-DEC-2002 (first entry)  
XX  
XX Human multidrug resistance associated protein 3 polymorphic sequence #20.  
DE  
KM Human; db; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;  
KM cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTP;  
KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;  
KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KM epoxide hydrolase 2; EPXH2; 5-lipoxygenase activating protein; FLAP;  
KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
KM NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;  
KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPAR;  
KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KM multidrug resistance associated protein 3; cancer; prostate;  
KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
KM altered drug metabolism; cardiovascular function; colorectal tumour;  
KM central nervous system; pulmonary; immunological; SNP;  
KM single nucleotide polymorphism.  
XX  
XX Homo sapiens.  
XX  
XX W0200257410-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044838.  
XX  
XX 28-NOV-2000; 2000US-00724389.  
XX  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
XX  
XX WPI; 2002-698522/75.  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes  
XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers  
XX for locating, identifying and characterizing the genes responsible for  
XX disorder-related traits.  
XX  
XX Example 24; Page 152; 714pp; English.  
XX  
XX This invention relates to the sequence of an isolated nucleic acid  
XX molecule comprising at least one base variation from that of a known  
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
XX (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
XX inhibitor (DBI), epoxide hydrolase 2 (EPXH2), 5-lipoxygenase activating  
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
XX transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl  
XX transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
XX sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
XX transferase (UGT2B15), urokinase receptor (uPAR), multidrug resistance 1  
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
XX (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic  
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
XX The polymorphisms in the human genes cited in the invention are useful as  
XX genetic linkage markers for locating and characterizing the genes that  
XX are responsible for specific traits within the genome and eventually  
XX identifying the genes responsible for a variety of disorder-related  
XX traits as a result of their e.g., overexpression, constitutive  
XX expression, mutation or underexpression, which may be used in diagnosing  
XX and/or treating the disorders. The nucleic acid molecules comprising the  
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,  
XX ARNT, EPXH2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug

CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
CC used to screen for altered cardiovascular function. In COX2 for altered  
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
CC nervous system function, in FLAP and NNMT for altered pulmonary,  
CC immunological or haematological function, in KLK2 for altered serine  
CC protease activity in the prostate, in LTF for altered immunological or  
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
CC peripheral nervous system function. The present sequence represents a  
CC polymorphic DNA sequence of the invention  
XX  
XX Sequence 21 BP; 3 A; 10 C; 2 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 562 ATCCCTGGGAGGAGGAGG 581  
Db 20 ATCCTTGGGAGGAGGAGG 1  
RESULT 2595  
ABK94358/c  
ID ABK94358 standard; DNA; 21 BP.  
XX  
XX ABK94358;  
XX  
XX 27-AUG-2002 (first entry)  
XX  
XX Endothelin converting enzyme 1 (ECE-1) SNP detection primer #146.  
DE  
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;  
XX EDNR; signaling system; cardiovascular disease; coronary heart disease;  
XX hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;  
XX diabetes; familial hypercholesterolaemia; forensic marker;  
XX transgenic animal; solid support; cardiovascular regulator; SNP;  
XX single nucleotide polymorphism; PCR; primer; ss.  
XX  
XX Synthetic.  
XX  
XX W0200224747-A2.  
XX  
XX 28-MAR-2002.  
XX  
XX 31-AUG-2001; 2001WO-EP010087.  
XX  
XX 19-SEP-2000; 2000EP-00120123.  
XX  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX  
XX Brinkmann U, Hoffmeyer S;  
XX  
XX WPI; 2002-435060/46.  
XX  
XX Novel polymolecule of the endothelin/endothelin converting  
XX enzyme/receptor of endothelin and endothelin converting enzyme signaling  
XX system associated with cardiovascular disease, useful for treating the  
XX disease.  
XX  
XX Example 6; Page 67; 190pp; English.  
XX  
XX The invention describes a polymolecule (I) of the endothelin  
XX (EDN) endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
XX signaling system which is associated with a cardiovascular disease. (I),  
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
XX or (II) is useful for producing cells capable of expressing a molecular  
XX variant polypeptide which is associated with a cardiovascular disease.  
XX (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
XX molecular variant gene comprising (I) is useful for identifying and  
XX obtaining a pro-drug or drug capable of modulating the activity of a  
XX molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolemia. The gene or a polynucleotide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP; 4 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

688 GCCCTGATGTGGCCAG 707  
20 GCCCTGATGTGGCCAG 1

RESULT 2596  
ABK94357  
ID ABK94357 standard; DNA; 21 BP.  
AC ABK94357;  
DT 27-AUG-2002 (first entry)  
XX Endothelin converting enzyme 1 (ECE-1) SNP detection primer #145.  
DE Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;  
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;  
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;  
KW diabetes; familial hypercholesterolemia; forensic marker;  
KW transgenic animal; solid support; cardiovascular regulator; SNP;  
KW single nucleotide polymorphism; PCR; primer; ss.  
XX Synthetic.  
OS  
XX WO200224747-A2.  
PN 28-MAR-2002.  
PD 31-AUG-2001; 2001WO-EP010087.  
PP 19-SEP-2000; 2000EP-00120123.  
PR (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
PA Brinkmann U, Hoffmeyer S;  
XX Brinkmann U, Hoffmeyer S;  
XX WPI; 2002-435060/46.  
DR Novel polynucleotide of the endothelin/endothelin converting  
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
PT system associated with cardiovascular disease, useful for treating the  
PT disease.  
XX Example 6; Page 67; 190pp; English.  
PS The invention describes a polynucleotide (I) of the endothelin  
XX (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
XX signaling system which is associated with a cardiovascular disease. (I),  
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
XX or (II) is useful for producing cells capable of expressing a molecular  
XX variant polypeptide which is associated with a cardiovascular disease.  
XX (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

molecular variant gene comprising (I) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polynucleotides encoding them are useful for preparation of a pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolemia. The gene or a polynucleotide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for creating a transgenic animal and in creation of a solid support comprising polynucleotides, genes, vectors, polypeptides, antibodies or host cells of the invention. This sequence represents a PCR primer used to identify single nucleotide polymorphisms in DNA encoding cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

Sequence 21 BP; 3 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

688 GCCCTGATGTGGCCAG 707  
2 GCCCTGATGTGGCCAG 1

RESULT 2597  
ABK94084  
ID ABK94084 standard; DNA; 21 BP.  
AC ABK94084;  
DT 27-AUG-2002 (first entry)  
XX Endothelin-1 (EDN-1) SNP detection PCR primer #28.  
DE Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;  
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;  
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;  
KW diabetes; familial hypercholesterolemia; forensic marker;  
KW transgenic animal; solid support; cardiovascular regulator; SNP;  
KW single nucleotide polymorphism; PCR; primer; ss.  
XX Synthetic.  
OS  
XX WO200224747-A2.  
PN 28-MAR-2002.  
PD 31-AUG-2001; 2001WO-EP010087.  
PP 19-SEP-2000; 2000EP-00120123.  
PR (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
PA Brinkmann U, Hoffmeyer S;  
XX Brinkmann U, Hoffmeyer S;  
XX WPI; 2002-435060/46.  
DR Novel polynucleotide of the endothelin/endothelin converting  
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
PT system associated with cardiovascular disease, useful for treating the  
PT disease.  
XX Example 6; Page 55; 190pp; English.  
PS The invention describes a polynucleotide (I) of the endothelin  
XX (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
XX signaling system which is associated with a cardiovascular disease. (I),  
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (ii) is useful for producing cells capable of expressing a molecular  
CC variant polypeptide which is associated with a cardiovascular disease.  
CC (ii), (iii), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
CC molecular variant gene comprising (i) is useful for identifying and  
CC obtaining a pro-drug or drug capable of modulating the activity of a  
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
CC or its gene product, or for identifying and obtaining an inhibitor of the  
CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
CC signaling system or its gene product. The isolated proteins and  
CC polynucleotides encoding them are useful for preparation of a  
CC pharmaceutical composition for treating a cardiovascular disease such as  
CC coronary heart disease, hypertension, atherosclerosis, or related to  
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial  
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the  
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for  
CC creating a transgenic animal and in creation of a solid support  
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or  
CC host cells of the invention. This sequence represents a PCR primer used  
CC to identify single nucleotide polymorphisms in DNA encoding  
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway  
XX  
SQ Sequence 21 BP; 3 A; 3 C; 2 G; 12 T; 0 U; 1 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3722 TCCTCATTCATTGAGCTTTT 3742  
Db 1 TCCTGATTANTGATCTTTT 21  
RESULT 2598  
ABK94083/c  
ID ABR94083 standard; DNA; 21 BP.  
XX  
XX ABR94083;  
DT 27-AUG-2002 (first entry)  
XX  
XX Endothelin-1 (EDN-1) SNP detection PCR primer #27.  
DE  
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;  
KM EDNR; signaling system; cardiovascular disease; coronary heart disease;  
KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;  
KM diabetes; familial hypercholesterolaemia; forensic marker;  
KM transgenic animal; solid support; cardiovascular regulator; SNP;  
KM single nucleotide polymorphism; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO200224747-A2.  
FN  
XX  
XX 28-MAR-2002.  
PD  
XX 31-AUG-2001; 2001WO-EP010087.  
PF  
XX 19-SEP-2000; 2000EP-00120123.  
PR  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
PA  
XX Brinkmann U, Hoffmeyer S;  
PI  
XX WPI; 2002-435060/46.  
DR  
XX  
XX Novel polynucleotide of the endothelin/endothelin converting  
PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
PT system associated with cardiovascular disease, useful for treating the  
PT disease.  
XX  
XX Example 6; Page 55; 190pp; English.  
PS  
XX The invention describes a polynucleotide (i) of the endothelin  
CC

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
CC signaling system which is associated with a cardiovascular disease. (i),  
CC the gene encoding EDN, ECE or EDNR (ii) or a vector (iii) expressing (i)  
CC or (ii) is useful for producing cells capable of expressing a molecular  
CC variant polypeptide which is associated with a cardiovascular disease.  
CC (ii), (iii), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
CC molecular variant gene comprising (i) is useful for identifying and  
CC obtaining a pro-drug or drug capable of modulating the activity of a  
CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
CC or its gene product, or for identifying and obtaining an inhibitor of the  
CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
CC signaling system or its gene product. The isolated proteins and  
CC polynucleotides encoding them are useful for preparation of a  
CC pharmaceutical composition for treating a cardiovascular disease such as  
CC coronary heart disease, hypertension, atherosclerosis, or related to  
CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial  
CC hypercholesterolaemia. The gene or a polynucleotide fragment of the  
CC EDN/ECE/EDNR signaling system are useful as forensic markers, for  
CC creating a transgenic animal and in creation of a solid support  
CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or  
CC host cells of the invention. This sequence represents a PCR primer used  
CC to identify single nucleotide polymorphisms in DNA encoding  
CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway  
CC  
XX  
SQ Sequence 21 BP; 12 A; 2 C; 3 G; 3 T; 0 U; 1 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3722 TCCTCATTCATTGAGCTTTT 3742  
Db 21 TCCTGATTANTGATCTTTT 1  
RESULT 2599  
ABV74830/c  
ID ABV74830 standard; DNA; 21 BP.  
XX  
XX ABV74830;  
AC  
XX 28-MAR-2003 (first entry)  
DT  
XX  
XX Murine OAS gene isoform L1 PCR primer SEQ ID 13.  
DE  
XX Virucide; hepatotropic; antiinflammatory; antiviral; OAS; murine;  
KM 2'-5'-oligoadenylate synthase; Flavivirus infection; PCR; primer; ss.  
KM  
XX Mus sp.  
OS  
XX  
XX WO200281741-A2.  
FN  
XX  
XX 17-OCT-2002.  
PD  
XX 04-APR-2002; 2002WO-FR001169.  
PF  
XX 04-APR-2001; 2001FR-00004598.  
PR  
XX (INSP) INST PASTEUR.  
PA  
XX (CNRS) CNRS CENT NAT RECH SCI.  
PI  
XX Guenet J, Mashimo T, Simon-Chazottes D, Montagueletti X;  
PI Frenkel M, Despres P, Deubel V, Bonhomme F, Lucas M;  
XX WPI; 2003-058566/05.  
DR  
XX  
XX Identifying stimulators of oligoadenylate synthase family genes, useful  
PT as antiviral agents against Flavivirus, also mutated genes responsible  
PT for sensitivity to virus.  
XX  
XX Claim 16; Page 80; 93pp; French.  
PS  
XX The present invention relates to a method for identifying compounds (i)  
CC



CC that can stimulate a gene of the OAS (2'-5'-oligoadenylate synthase)  
CC family. The method comprises: (a) inducing expression of the OAS gene in  
CC a culture of cells from a non-human mammal (P1vR/P1vR or P1vR/P1vR);  
CC indicating resistance or sensitivity to Flavivirus infection); (b)  
CC treating cells with test compound; and (c) measuring activity of OAS gene  
CC relative to a control. (1) are potentially useful as antiviral agents for  
CC treating infections by Flaviviruses (e.g. hepatitis C; dengue; yellow  
CC fever and various forms of encephalitis). Genomic OAS DNA and derived  
CC cDNA, also the encoded proteins, are useful: (a) for treating Flavivirus  
CC infection; (b) in screening for anti-Flavivirus agents, and (c) for  
CC evaluating sensitivity of subjects to Flavivirus infection and their  
CC likely response to interferon treatment, e.g. to identify patients at  
CC risk of developing severe forms of such infections. The present sequence  
CC is a PCR primer for murine OAS, which was used in an example from the  
CC invention  
CC  
SQ Sequence 21 BP; 4 A; 1 C; 9 G; 7 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1866 CAGACCTCAGCTCAGACTC 1885  
DB 20 CAGACCTCAGCTCAGACTC 1  
RESULT 2600  
ADC78764  
ID ADC78764 standard; DNA; 21 BP.  
XX  
AC ADC78764;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Mouse BORIS identification PCR primer SEQ ID NO:44.  
XX  
KW human; brother of regulator of imprinted site; BORIS; cytoskeletal;  
KW gene therapy; cancer; ss; PCR primer.  
XX  
OS Synthetic.  
OS Homo sapiens.  
OS Mus sp.  
XX  
FN WO2003072799-A2.  
XX  
PD 04-SEP-2003.  
XX  
PP 21-FEB-2003; 2003WO-US005186.  
XX  
PR 22-FEB-2002; 2002US-035889P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Lobanenko VV, Loukinov DI, Morse HC;  
XX  
DR WPI; 2003-721780/68.  
XX  
XX  
PT New nucleic acid molecule encoding a human or non-human brother of  
PT regulator of imprinted sites (BORIS), useful for preparing a composition  
PT for treating or preventing cancer.  
XX  
XX  
PS Example 1; SEQ ID NO 44; 71bp; English.  
XX  
XX  
CC The present invention describes the human brother of regulator of  
CC imprinted sites (BORIS) protein. Also described: (1) a vector comprising  
CC an isolated nucleic acid encoding BORIS; (2) a cell comprising the vector  
CC; (3) an isolated polypeptide molecule comprising a sequence encoding the  
CC human BORIS or its fragment comprising at least 307 or 21 contiguous  
CC amino acids, either one of which is optionally glycosylated, amidated,  
CC carboxylated, phosphorylated, esterified, N-acetylated or converted into an  
CC acid addition salt and/or optionally dimerised or polymerised; (4) a cell  
CC line that produces a monoclonal antibody that is specific for a region of

CC the isolated polypeptide, where the region comprises any region that is  
CC recognisable by the monoclonal antibody other than one spanning a zinc  
CC finger region; (5) diagnosing cancer or predisposition to cancer in a  
CC male or female mammal; (6) predicting a predisposition to cancer in an  
CC offspring of a male mammal; (7) prognosticating cancer in a mammal; (8)  
CC assessing the effectiveness of treatment of cancer in a mammal; (9)  
CC preventing or treating cancer that is due to the presence of BORIS  
CC nucleic acid or polypeptide; and (10) a composition comprising an  
CC inhibitor of BORIS and a carrier. BORIS has cytoskeletal activity, and can  
CC be used in gene therapy. A nucleic acid encoding BORIS can be used for  
CC preparing a composition for treating or preventing cancer. The present  
CC sequence represents a PCR primer corresponding to human BORIS and murine  
CC CtrF used to identify murine BORIS, which is used in an example from the  
CC present invention.  
CC  
SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7358 TTGTGAATATATCCAGCAG 7377  
DB 1 TTGTGAGTTATGCCAGCAG 20  
RESULT 2601  
ADD56481/C  
ID ADD56481 standard; DNA; 21 BP.  
XX  
AC ADD56481;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human gene expression analysis multiplex Start-PCR primer #1.  
XX  
KW Gene expression; multiplex standardised reverse transcriptase-PCR;  
KW Start-PCR; high density oligonucleotide array; cDNA array;  
KW small biological sample; fine needle aspirate biopsy;  
KW laser captured microdissected material; human; primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN US2003186246-A1.  
XX  
PD 02-OCT-2003.  
XX  
PP 28-MAR-2002; 2002US-00109349.  
XX  
PR 28-MAR-2002; 2002US-00109349.  
XX  
PA (WILL/) WILLEY J C.  
XX  
PA (CRAW/) CRAWFORD E L.  
XX  
PI Willey JC, Crawford EL;  
XX  
DR WPI; 2003-811730/76.  
XX  
XX  
PT Direct comparison of numerical gene expression values between samples of  
PT genes comprises using multiplex standardized reverse transcription-  
PT polymerase chain reaction.  
XX  
XX  
PS Example 1; SEQ ID NO 1; 59bp; English.  
XX  
XX  
CC The present invention relates to a method for the direct comparison of  
CC numerical gene expression values between samples of genes. The method  
CC comprises amplifying cDNA in the presence of a competitive template  
CC mixture and primer pairs for several genes and then amplifying aliquots  
CC of the PCR products using a primer pair specific for each gene. The  
CC method of amplification is by multiplex standardised reverse  
CC transcriptase-polymerase chain reaction (Start-PCR). High density  
CC oligonucleotide or cDNA arrays are used to measure PCR products following  
CC quantitative Start-PCR. The method is useful for the assessment of gene

expression in small biological samples such as fine needle aspirate biopsies, and laser captured microdissected materials. The method allows for the standardised measurement of hundreds of genes from the same sample, which in prior art, could only be assessed for one gene. The present sequence represents a multiplex Start-PCR primer which can be used in the method of the present invention.

Sequence 21 BP; 4 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6802 CAGATTGGGAGGAGTATT 6821  
DB 20 CAGAAATGGGAGGAGATATT 1

RESULT 2602

ADD90708  
ID ADD90708 standard; DNA; 21 BP.

AC ADD90708;

DT 29-JAN-2004 (first entry)

XX Mouse beta-actin PCR primer SEQ ID NO:18.

XX allergic disease; SOCS3; allergy; mouse; beta-actin; PCR primer; ss.

XX Synthetic.

OS Mus sp.

XX MO2003072778-A1.

XX 04-SEP-2003.

XX 23-JAN-2003; 2003WO-JP000600.

XX 27-FEB-2002; 2002JP-00052310.

XX (GENO-) GENOX RES INC.

XX (NIGE-) JAPAN GEN AGENCY NATION.

XX Nagata N, Oshida T, Sugita Y, Kubo M, Saito H;

XX WPI; 2003-671871/63.

XX Detecting allergic disease using SOCS3 as a marker for dermatitis.

XX Example 7; SEQ ID NO 18; 80pp; Japanese.

CC The present invention describes a method for detecting an allergic disease using SOCS3 as a marker. The method comprises determining the level of expression of the marker gene in the sample and comparing it with that of a healthy individual. Also described: (1) a reagent for detecting allergies; (2) method for screening for treatments for allergies; and (3) a kit for screening for treatments for allergies used for detecting the presence of allergies and for screening for treatment. The present sequence represents a PCR primer for mouse beta-actin, which is used in an example from the present invention.

XX Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 527 CCATTGGCAACGACGGGTC 546  
DB 2 CTATTGGCAACGACGGGTC 21

RESULT 2603

AAQ27806  
ID AAQ27806 standard; DNA; 22 BP.

AC AAQ27806;

DT 25-MAR-2003 (revised)

DT 28-JAN-1993 (first entry)

XX APP exon 17 primer 4.

XX Beta-amyloid protein; amyloid precursor protein; isoform; ss.

XX Synthetic.

XX WO9213069-A1.

XX 06-AUG-1992.

XX 21-JAN-1992; 92WO-GB000123.

XX 21-JAN-1991; 91GB-00001307.

XX 28-AUG-1991; 91GB-00018445.

XX (UNLO ) IMPERIAL COLLEGE SCI TECHN MED.

XX Hardy JA, Chartier-Harlin MC, Goate AM, Owen MJ, Mullan MJ;

XX WPI; 1992-284654/34.

XX Polynucleotide probe comprising nucleic acid encoding codon 717 mutant -

XX of human App770, useful for determining genetic pre-disposition to

XX Alzheimer's disease.

XX Disclosure, Page 31; 127pp; English.

CC The sequences given in AAQ27805-7 are primers which are complementary to intronic sequences within the amyloid precursor protein gene (APP). They were used to amplify exon 17. APP encodes various isoforms which are precursors of beta-amyloid protein. The beta-amyloid protein is an approx. 4KD protein (39-42 amino acids) which is an internal cleavage product from APP. There are five distinct isoforms of APP containing 563, 695, 714, 751 and 770 amino acids. These are generated by alternative splicing of primary transcripts of APP which is located on human chromosome 21. The APP isoforms are glycosylated transmembrane proteins. (updated on 25-MAR-2003 to correct PN field.) (updated on 25-MAR-2003 to correct PI field.)

XX Sequence 22 BP; 8 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5617 TTACCCAGCTTCAGGAG 5636  
DB 2 TAACCCAGCATCATGGAAG 21

RESULT 2604

AAQ78894  
ID AAQ78894 standard; DNA; 22 BP.

AC AAQ78894;

DT 25-MAR-2003 (revised)

DT 27-JUL-1995 (first entry)

XX Synthetic EcoRI-BglII fragment from plasmid p7,582-S.

XX Hepatitis B virus pres2 gene; vaccine; ds.

XX Synthetic.



PT correct. DNA and nucleic acid constructs for inactivating the transferase  
 PT gene; for eliminating hyperacute region in human transplants.  
 XX  
 PS Example 6; Page 58; 184pp; English.  
 CC The primers given in AAQ93081-86 are based on conserved regions of mouse  
 CC and cattle alpha-GalT genes and were used to isolate porcine alpha-1,3-  
 CC GalT cDNA (AAQ93077) by PCR amplification. (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 XX  
 SQ Sequence 22 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 2 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4459 TGGACCTTTTCTTTTCTTTT 4478  
 DB 1 TTGAATCTTTTCTTTTCTTTT 20

RESULT 2607  
 AAT78987/C  
 ID AAT78987 standard; DNA; 22 BP.  
 XX  
 AC AAT78987;  
 XX  
 DT 13-JUN-1998 (first entry)  
 XX  
 DE Mouse Huntington's disease gene Intron 2 5' donor site.  
 XX  
 KM Huntington's disease; animal model; transgenic animal; mouse; therapy;  
 KM drug screening; Hdh gene; ss.  
 XX  
 OS Mus musculus.  
 OS  
 PN CA2178022-A.  
 XX  
 PD 02-DEC-1996.  
 XX  
 PF 03-JUN-1996; 96CA-02178022.  
 XX  
 PR 01-JUN-1995; 95US-00457273.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Hayden M, Lin B, Nasir J;  
 XX  
 DR WPI; 1997-298677/28.  
 XX  
 PT Mouse Huntington's Disease gene - useful for generating transgenic mice  
 PT as a model of Huntington's Disease.  
 XX  
 PS Disclosure; Page 60; 69pp; English.  
 CC This oligonucleotide comprises the 5' donor site of intron 2 of the mouse  
 CC Huntington's disease (HD) gene (see also AAT78974). The splice site  
 CC sequences for the first 5 exons of the mouse and human HD genes were  
 CC compared (see AAT78985-T79002). Targeted disruption of the murine HD  
 CC gene, e.g. at exon 5, can be used to examine the function of the HD gene  
 CC and its role in development. Transgenic mice can be used as models of HD  
 XX  
 SQ Sequence 22 BP; 10 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5474 TTTTGTAAAGATATT 5493  
 DB 22 TTTTGTAAAGCAATT 3

RESULT 2608  
 AAX78249/C  
 ID AAX78249 standard; DNA; 22 BP.  
 XX  
 AC AAX78249;  
 XX  
 DT 24-AUG-1999 (first entry)  
 XX  
 DE Human cyclin T1 PCR primer 1.  
 XX  
 KM Cyclin T1; cyclin K; human; TAT protein; transcriptional coactivator;  
 KM human immunodeficiency virus; HIV; Tat-associated kinase; TAK; TEFB;  
 KM Transcription elongation factor subunit b; TAK/TEFB complex; cis-acting;  
 KM transactivation response element; TAR; divalent cation metal; modulator;  
 KM treatment; infection; immunogen; tissue localization; diagnosis;  
 KM transgenic animal; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 OS Homo sapiens.  
 XX  
 PN WO9929730-A1.  
 XX  
 PD 17-JUN-1999.  
 XX  
 PF 11-DEC-1998; 98WO-US026470.  
 XX  
 PR 11-DEC-1997; 97US-0069341P.  
 PR 30-JUL-1998; 98US-00126980.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Jones KA, Wei P, Garber M, Fang S;  
 XX  
 DR WPI; 1999-394960/33.  
 XX  
 PT Cyclin T1, a transcriptional co-activator that interacts with Tat  
 PT protein.  
 XX  
 PS Example 7; Page 103; 107pp; English.

XX  
 CC This invention describes a novel human transcriptional co-activator,  
 CC designated cyclin T1 (also known as cyclin K), which interacts with the  
 CC human immunodeficiency virus (HIV) Tat protein. Cyclin T1 is capable of  
 CC participating as a constituent of the Tat-associated kinase  
 CC (TAK); Transcription elongation factor subunit b (TEFB) complex. The  
 CC polypeptide modulates Tat transactivation by enhancing the affinity of  
 CC the Tat protein with the cis-acting transactivation response element  
 CC (TAR) RNA. Compounds identified by methods of the invention that disrupt  
 CC the association of divalent cation metal(s) with cyclin T1 and/or Tat  
 CC protein are useful for the modulation of Tat transactivation in  
 CC biological systems. Cyclin T1, or antibodies specific for it, can be used  
 CC to treat a subject infected with HIV. Antibodies against cyclin T1 can be  
 CC used as immunogens and also for studying tissue localization of protein  
 CC and complexes, for purification of inhibitors and are useful in  
 CC diagnostic applications. The probes and primers are useful for  
 CC identification and amplification of the cyclin T1 DNA. The transgenic  
 CC animals are useful for elucidating the physiological and behavioural  
 CC roles of HIV infection  
 XX  
 SQ Sequence 22 BP; 10 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5695 CTGTTTGCTTCCTTTTCC 5714  
 DB 20 CTGTTTGCTCAGCCTTTTC 1

RESULT 2609  
 AAV99612  
 ID AAV99612 standard; DNA; 22 BP.

```

XX AAV99612;
AC
XX 29-MAR-1999 (first entry)
DT
XX Maize c1p gene primer c1p#3.
DE
XX Promoter; nuclear encoded plastid RNA polymerase; NEP; c1p; chloroplast;
KW
XX transgenic plant; maize; PCR; primer; ss.
XX
OS Synthetic.
OS Zea mays.
XX
XX W09655595-A1.
PN
XX 10-DEC-1998.
PD
XX
XX 03-JUN-1998; 98WO-US011437.
PF
XX
XX 03-JUN-1997; 97US-0048376P.
PR
XX 12-SEP-1997; 97US-0058670P.
RR
XX (RUT) UNIV RUTGERS STATE NEW JERSEY.
PA
XX
XX Maliga P, Silhavy D, Sritaman P;
PI
XX WPI; 1999-070262/06.
PR
XX Isolated nuclear-encoded plastid RNA polymerase promoter sequences -
PT useful for expressing exogenous protein in plant plastids such as
PT chloroplasts.
XX
XX Example 1; Page 17; 79pp; English.
PS
XX This is the nucleotide sequence of maize c1p gene primer c1p#3. The 5'
CC nucleotide of the primer corresponds to nucleotide 70549 of the
CC complementary strand of the maize plastid genome sequence. The primer was
CC designed to add a XhoI restriction site downstream of an amplified c1p
CC fragment following PCR amplification. The PCR product was cloned into
CC vector pBSKS+ and used to generate protecting RNA for use in in vitro
CC capping experiments. The invention provides isolated rpoB, acpB, c1p and
CC 16S rDNA NEP and PEP promoter elements (see AAV99569-99) useful for
CC producing exogenous proteins of interest in plant plastids
XX
XX Sequence 22 BP; 7 A; 1 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY
3342 GAATCCAGTTGTAGAGA 3361
DB 3 GAATTCGTGTGTAGAGA 22

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```

XX 05-AUG-1998; 98WO-US016211.
PF
XX
XX 05-AUG-1997; 97US-00906494.
PR
XX (UYMA-) UNIV MASSACHUSETTS.
PA
XX
XX Stern S;
PI
XX
XX WPI; 1999-167451/14.
DR
XX
XX Nucleic acid isolation, quantification and structural probing - using new
PT hybridisation-based and ligation-dependent methods.
PT
XX
XX Example 8; Fig 9B; 71pp; English.
PS
XX
XX The specification describes a method for isolating a target nucleic acid
CC fragment from a mixture of nucleic acid fragments. The method comprises
CC removing a non-target fragment by hybridising it to an immobilised
CC "subtraction" oligonucleotide that is complementary to a sequence present
CC in the non-target fragment but absent in the target fragment, repeating
CC this step until a known sequence in the target nucleic acid is unique and
CC then selecting the target fragment by hybridizing to a complementary
CC immobilised "selection" oligonucleotide. The method can be used in
CC structure probing experiments to determine whether a given nucleotide is
CC modified by a modifying agent, or whether a compound alters reactivity of
CC a nucleotide in a test nucleic acid toward a modifying agent. The present
CC sequence represents a cDNA transcript resulting from reverse
CC transcription of the test RNA (AAZ26474)
XX
XX Sequence 22 BP; 8 A; 2 C; 11 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY
5702 GCCTTCCTTTCTCTCTC 5721
DB 21 GCCTTCCTTCCTCTCTC 2

```

```

RESULT 2610
AAZ26493/C
ID AAZ26493 standard; cDNA; 22 BP.
AC
XX
XX AAZ26493;
AC
XX
XX 26-MAY-1999 (first entry)
DT
XX
XX cDNA transcript resulting from reverse transcription of the test RNA.
DE
XX
XX Isolation; nucleic acid; subtraction oligonucleotide;
KW
XX selection oligonucleotide; structure probing; ss.
XX
XX Synthetic.
XX
XX W09907890-A1.
PN
XX
XX 18-FEB-1999.
PD

```

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RESULT 2611
AAZ32687
ID AAZ32687 standard; DNA; 22 BP.
AC
XX
XX AAZ32687;
AC
XX
XX 21-JAN-2000 (first entry)
DT
XX
XX Human APP exon 17-specific PCR primer APP-17B.
DE
XX
XX APP; amyloid precursor protein; Alzheimer's disease; transfection;
KW transgenic animal; animal model; disease; transgene; co-lipofection;
KW yeast artificial chromosome; YAC; lipid; cationic; selectable; exon; PCR;
KW primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
OS
XX
XX US5981175-A.
PN
XX
XX 09-NOV-1999.
PD
XX
XX 25-JAN-1994; 94US-00187161.
PF
XX
XX 07-JAN-1993; 93US-00001493.
PR
XX 18-JUN-1993; 93US-00079444.
RR
XX (GENP-) GENPHARM INT INC.
PA
XX
XX Kay RM, Choi T, Loring JF;
PI
XX
XX WPI; 1999-633306/54.
DR

```

XX Production of transfected mammalian cells by co-lipofection with multiple  
PT DNA species, useful for the production of transgenic animals for use as  
PT disease models.  
XX  
PS Example 2; Col 20; 29pp; English.  
XX  
CC This sequence represents human APP (amyloid precursor protein) exon 17-  
CC specific PCR primer APP-17B, used with PCR primer APP-17A (AA232686) to  
CC amplify exon 17 of the human APP gene in murine embryonic stem cells  
CC transfected via a novel method with a YAC (Yeast artificial chromosome)  
CC containing the human APP gene. The novel method of transfection produces  
CC a selectable co-lipofected mammalian cell incorporating multiple  
CC heterologous DNA species. It comprises forming a co-lipofection complex  
CC comprising a cationic lipid, a first polynucleotide larger than 50 kb,  
CC and an unlinked second polynucleotide comprising a selectable marker gene  
CC expression cassette, and transfecting mammalian cells with it. Both  
CC heterologous nucleotides are integrated into the genome, forming  
CC selectable co-lipofected mammalian cells which contain incorporated  
CC multiple heterologous DNA species. The method can be used for  
CC transferring large segments of DNA, such as large YAC clones, into  
CC mammalian cells such as embryonic stem cells. The methods can be used for  
CC producing mammalian cells which express APP which can be used to produce  
CC transgenic animals as models for Alzheimer's disease. The methods can  
CC also be used for producing transgenic animals as models for autoimmunity  
XX  
SQ Sequence 22 BP; 8 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5617 TTACCCAGCTTCAAGGAG 5636  
DB 2 TAACCCAGCATCATGAG 21  
XX  
RESULT 2612  
AA237259 ID AA237259 standard; DNA; 22 BP.  
XX  
AC AA237259;  
XX  
DT 28-JAN-2000 (first entry)  
XX  
DE PCR primer for AV37 antigen coding sequence.  
XX  
KW AV37 antigen; monoclonal antibody; hybridoma AV37; vaccine; avian tumour;  
KW oncogenic avian virus; Marek's disease virus; avian leucosis virus;  
KW Rous-associated virus; reticuloendotheliosis virus; therapy; PCR primer;  
KW 88.  
XX  
OS Synthetic.  
OS Gallus sp.  
XX  
PM WO9955860-A1.  
XX  
PD 04-NOV-1999.  
XX  
PF 22-APR-1999; 99WO-GB001238.  
XX  
PR 29-APR-1998; 98GB-00009070.  
XX  
PA (ANIM-) INST ANIMAL HEALTH LTD.  
XX  
PI Burgess SC, Davison TF, Rose LJM;  
XX  
DR WPI; 2000-013437/01.  
XX  
PT New polypeptide, useful as a vaccine and to generate monoclonal  
PT antibodies.  
PS Claim 31; Page 39; 63pp; English.

XX This sequence is a PCR primer for DNA encoding the AV37 antigen protein  
CC of the invention. The protein is recognised by a monoclonal antibody  
CC (MAb) secreted by the hybridoma AV37 deposited at the European Collection  
CC of Cell Cultures (ECACC) accession number 98030304. The polypeptide can  
CC be used to isolate a MAb, produce a hybridoma producing the MAb, and in a  
CC composition for use as a vaccine. The vaccine can be used against  
CC oncogenic avian viruses, including Marek's disease virus, avian leucosis  
CC virus, Rous-associated virus and reticuloendotheliosis virus. The vector  
CC can be used to create avian tumours  
XX  
SQ Sequence 22 BP; 2 A; 11 C; 0 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5734 TTCTTTCCTTCTTCTTCA 5753  
DB 2 TTCTTTCCTTCTTCTTCA 21  
XX  
RESULT 2613  
AAC61082 ID AAC61082 standard; DNA; 22 BP.  
XX  
AC AAC61082;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
DE Primer BEK311 used in isolation of cDNA encoding nurse cell receptor.  
XX  
KW Mouse; nurse cell receptor; detection; DiGeorge's syndrome; primer; 88.  
XX  
OS Synthetic.  
OS JP2000236882-A.  
XX  
PN 05-SEP-2000.  
XX  
PD 24-FEB-1999; 99JP-00046603.  
XX  
PR 24-FEB-1999; 99JP-00046603.  
XX  
PA (SHIO) SHIONOGI & CO LTD.  
XX  
DR WPI; 2000-597089/57.  
XX  
PT A mouse nurse cell receptor gene.  
XX  
PS Claim 9; Page 7; 27pp; Japanese.  
XX  
CC This invention relates to a mouse nurse cell receptor. The invention  
CC includes DNA and protein sequences for the receptor (AAC61078 and  
CC AA85616). Also included in the invention is an antibody specific for the  
CC murine nurse cell receptor. DNA encoding the receptor can be used to  
CC detect DiGeorge's syndrome. The present sequence represents a primer used  
CC in the isolation and characterisation of the receptor of the invention  
XX  
SQ Sequence 22 BP; 7 A; 7 C; 7 G; 1 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7405 AGCAACATCAGCAGCAGCAG 7424  
DB 1 AGCAACATCAGCAGCAGCAG 20  
XX  
RESULT 2614  
AAA39764 ID AAA39764 standard; DNA; 22 BP.

```

XX AC AAA39764;
XX XX
XX DT 15-SEP-2003 (revised)
XX DT 18-SEP-2000 (first entry)
XX DE H. polymorpha TP81 DNA primer F9.
XX XX
XX KM Trehalose-6-phosphate synthase; TP81; heat shock inducible; promoter;
XX KM yeast; primer; ss.
XX OS Pichia angusta.
XX PN CH690127-A5.
XX PD 15-MAY-2000.
XX PF 11-FEB-1999; 99CH-00000279.
XX PR 11-FEB-1999; 99CH-00000279.
XX PA (RHEI-) RHEINBIOTECH GES NEUE BIOTECHNOLOGISCHE.
XX PI Ivano R, De Virgilio C;
XX DR WPI; 2000-329626/29.
XX PT Heat-inducible promoter from Hansenula polymorpha, useful for controlling
XX PT expression of foreign genes in yeast, contains no general stress response
XX PT elements.
XX PS Example 3; Page 12; 19pp; German.
XX XX
XX CC This invention describes a novel heat-inducible promoter (I). (I) is used
XX CC to express foreign genes in fungi, particularly yeast and specifically
XX CC Hansenula polymorpha, especially proteins that require glycosylation and
XX CC can not be expressed in bacteria. (I) is active even at high temperature,
XX CC allowing yeast to be cultured at higher than normal temperatures with
XX CC reduced contamination by other microorganisms and reduced need for
XX CC expensive cooling. (I) is selectively activated by heat (it contains no
XX CC general stress-responsive elements), so permits expression of foreign
XX CC genes to be suppressed during selected stages of growth, resulting in
XX CC less injury to cells and biomass. This sequence represents a primer used
XX CC in the isolation of the trehalose-6-phosphate synthase TP81 gene from
XX CC Hansenula polymorpha. (Updated on 15-SEP-2003 to standardise OS field)
XX SQ Sequence 22 BP; 2 A; 3 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7190 GTGTGACTACTCTGTGTTTC 7209
DB 3 GTGTGACTACTCTGTGTTTC 22

RESULT 2615
AAZ94181/c
ID AAZ94181 standard; DNA; 22 BP.
XX AC AAZ94181;
XX DT 19-JUN-2000 (first entry)
XX DE Human GABAB-R1a PCR primer.
XX KM GABAB receptor 2; GABAB-R2; human; bladder disorder;
XX KM gastrointestinal disorder; central nervous system disorder;
XX KM lung disorder; spasticity; epilepsy; Alzheimer's disease; pain;
XX KM affective disorder; feeding disorder; diagnosis; gene therapy;
XX KM G-protein coupled receptor; GABA; gamma-aminobutyric acid;
XX KM signal transduction; PCR primer; GABAB-R1a; ss.

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XX OS Homo sapiens.
XX PN WO200014222-A2.
XX PD 16-MAR-2000.
XX PF 03-SEP-1999; 99WO-GB002918.
XX PR 07-SEP-1998; 98GB-00019420.
XX PR 09-OCT-1998; 98US-0103670P.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Barnes AA, Wise A, Marshall FH, Frazer NJ, White JHM, Foord SM;
XX DR WPI; 2000-256974/22.
XX PT GABA-B receptor subtypes useful for identifying modulators of GABA-B
XX PT receptor activity that may be used for preventing and treating diseases
XX PT including Alzheimer's disease, epilepsy and spasticity.
XX PS Disclosure; Page 29; 67pp; English.
XX CC The present sequence is that of a primer used in a PCR-RACE in order to
XX CC generate a 800 bp fragment of GABAB receptor GABAB-R1a cDNA. The
XX CC invention relates to novel GABAB subtypes GABAB-R1c and GABAB-R2 (see
XX CC AA79202). It also relates to variants of the receptors, nucleotide
XX CC sequences (see AAZ94168) encoding the receptors, vectors, stable cell
XX CC lines, antibodies, screening methods, methods of receptor production, and
XX CC methods of treatment or prophylaxis of a disorder that is responsive to
XX CC modulation of GABAB receptor activity. The disorder is especially a
XX CC central nervous system disorder, a gastrointestinal disorder, a lung
XX CC disorder or a bladder disorder, especially spasticity, epilepsy,
XX CC Alzheimer's disease, pain or an affective or feeding disorder (claimed)
XX SQ Sequence 22 BP; 3 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7417 AGCAGCAGCAGCAGCAGCAGC 7436
DB 21 AGCAGCAGCAGCAGCAGCAGC 2

RESULT 2616
AAC81233
ID AAC81233 standard; DNA; 22 BP.
XX AC AAC81233;
XX DT 23-FEB-2001 (first entry)
XX DE Human tyrosine phosphatase HD-PTP exon 2. PCR primer, SEQ ID NO.11.
XX KM Human, histidine domain tyrosine phosphatase; HD-PTP;
XX KM chromosome 3p21.3; gene deletion; tumor suppressor; cytostatic;
XX KM lung cancer; tumour; gene therapy; diagnosis; recombinant production;
XX KM anticancer; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200063392-A1.
XX PD 26-OCT-2000.
XX PF 14-APR-2000; 2000WO-JP002455.
XX PR 16-APR-1999; 99JP-00108842.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

```

XX Shimizu K;  
PI WPI; 2000-672740/65.  
XX Human tyrosine phosphatase with oncostatic activity encoded by a gene  
PT frequently deleted in lung cancer, useful for treatment and diagnosis of  
PT tumors.  
XX Example 3; Page 119; 134pp; Japanese.  
XX The invention relates to a novel human tyrosine phosphatase, histidine  
CC domain-protein tyrosine phosphatase (HD-PTP; AAB29661) and to human HD-  
CC PTP nucleic acids (AAC81224, AAC81225, AAC81262, AAC81263). The HD-PTP  
CC gene is located on chromosome 3p21.3. This region is frequently found to  
CC be deleted in lung cancers, and is therefore thought to contain a tumour  
CC suppressor gene. The invention also relates to expression vectors and  
CC host cells containing human HD-PTP nucleic acids; the recombinant  
CC production of HD-PTP; anticancer drugs containing HD-PTP; gene therapy  
CC compositions containing DNA encoding HD-PTP; diagnostic reagents  
CC containing HD-PTP oligonucleotides; antibodies specific for HD-PTP; and  
CC an immunoassay method using HD-PTP-specific antibodies for use in cancer  
CC diagnosis and investigation. HD-PTP proteins, nucleic acids and  
CC antibodies may be used in the treatment, investigation and diagnosis of  
CC cancers, particularly those of the lung. The present sequence represents  
CC a human HD-PTP PCR primer used in an exemplification of the invention  
XX  
SQ Sequence 22 BP; 7 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2529 CACAGCAGATGAGCTCCAGA 2548  
DB 1 CACAGTAGATGACCTCCACA 20  
RESULT 2617  
AAC80270/c  
ID AAC80270 standard; DNA; 22 BP.  
XX AAC80270;  
AC 03-MAY-2001 (first entry)  
DT Reverse primer #98 used for amplification of HLA-A exon 3.  
XX  
DE Reverse primer #98 used for amplification of HLA-A exon 3.  
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.  
KM  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200061795-A2.  
PN 19-OCT-2000.  
PD  
XX 05-APR-2000; 2000WO-EP002398.  
PF  
XX 09-APR-1999; 99EP-00870068.  
PR 11-JUN-1999; 99US-0138614P.  
XX (INNO-) INNOGENETICS NV.  
PA  
XX De Canck I, Rombout A, Rossau R;  
PI WPI; 2000-647426/62.  
DR  
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4  
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined  
PT primer sets, useful for subtyping or typing of HLA Class I alleles.  
XX  
PS Claim 4; Page 40; 128pp; English.

XX The present invention relates to a method for the locus-specific,  
CC separate amplification of exon 2, exon 3, and/or exon 4 of human  
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful  
CC for subtyping or typing of HLA class I alleles. The present sequence is  
CC an amplification primer used in the method  
XX  
SQ Sequence 22 BP; 5 A; 9 C; 4 G; 3 T; 0 U; 1 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5151 GGGAGGGAGTTCTCCGGG 5170  
DB 22 GGGAGAGAAATCTCTCTGGG 3  
RESULT 2618  
AAH26873/c  
ID AAH26873 standard; DNA; 22 BP.  
XX AAH26873;  
AC 21-DEC-2001 (first entry)  
DT Human prostate specific gene clone sqpro030 reverse PCR primer.  
XX  
DE Human prostate cancer; diagnosis; therapy; imaging; vaccine; PCR primer;  
XX ss.  
KM Human; prostate cancer; diagnosis; therapy; imaging; vaccine; PCR primer;  
KM ss.  
XX Homo sapiens.  
OS  
XX WO200170095-A2.  
PN 27-SEP-2001.  
PD  
XX 23-MAR-2001; 2001WO-US009217.  
PF  
XX 23-MAR-2000; 2000US-0191511P.  
PR (DIAD-) DIADEXUS INC.  
XX  
PA All S, Recipon H, Hu P, Cafferty R;  
PI WPI; 2001-611439/70.  
DR  
XX Novel prostate cancer specific genes and polypeptides encoded by the  
XX genes, useful for detecting, diagnosing, monitoring, staging,  
PT prognosticating, imaging and treating prostate cancer.  
PT  
XX Example 2; Page 56; 83pp; English.  
PS  
XX The present sequence is that of primer sqpro030 reverse, which was used  
CC with primer sqpro030 forward (see AAH26872) for the PCR amplification of  
CC novel human prostate cancer specific gene (PSG) clone sqpro030 (see  
CC AAH26855). A semi-quantitative PCR was performed to determine relative  
CC expression patterns of sqpro030 in multiple samples. High expression was  
CC observed in healthy lung, with very little expression in healthy  
CC prostate, high levels of expression in liver and pancreatic carcinomas  
CC and moderate expression in prostate, kidney and ovarian carcinomas, and  
CC at moderate levels in 2 of 6 prostate cancer samples. The 25 PSG  
CC polynucleotides of the invention (see AAH26845-69) are diagnostic markers  
CC for prostate cancer. The polynucleotides, antisense oligonucleotides,  
CC host cells, PSG polypeptides, and antibodies immunospecific for the  
CC polypeptides are claimed. Also claimed are methods and tools for using  
CC the markers for diagnosing prostate cancer, diagnosing metastasis of  
CC prostate cancer, staging prostate cancer, monitoring prostate cancer,  
CC identifying potential therapeutic agents, imaging prostate cancer,  
CC treating prostate cancer (using an antibody), PSG polypeptide agonists  
CC and antagonists, and a vaccine comprising a PSG polypeptide or a vector  
CC expressing a PSG polypeptide, as well as a method of treating prostate  
CC cancer using the vaccine





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XX AAH28297;
AC 05-SEP-2001 (first entry)
DT 3' untranslated region sequence from neuronal cadherin gene.
DE mRNA protein complex; tumour development; cell aging; death.
KW ribonucleic profile; RNA-binding protein; ss.
KM Unidentified.
XX
XX NO200148480-A1.
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035583.
XX
XX 28-DEC-1999; 99US-0173338P.
XX
XX (KEENE/) KEENE J D.
XX Keene JD, Tenenbaum SA, Carson C;
XX WPI; 2001-425706/45.
XX
XX Partitioning endogenous mRNA-protein complexes in vivo, by contacting
XX sample comprising the complex with ligand that binds to a component of
XX the complex and separating complex by binding ligand with a binding
XX molecule.
XX
XX Example 6; Page 31; 49pp; English.
XX
XX The specification describes a method for partitioning endogenous cellular
XX mRNA-protein (mRNP) complexes. The method comprises contacting a
XX biological sample comprising mRNP complex with ligand that specifically
XX binds a component of mRNP complex, separating mRNP complex by binding the
XX ligand with a molecule specific for ligand, which is attached to the
XX solid support and then collecting the mRNP complex by removing the
XX complex from the support. The method is useful for in vivo partitioning
XX of cellular mRNA protein complexes in a biological sample. The method is
XX useful for determining the ribonucleic profile of a cell which has numerous
XX uses including monitoring of tumour development, state of growth or state
XX of development, perturbations of a biological system such as disease,
XX drug or toxin treatment and the state of cell aging or death,
XX distinguishing ribonucleic profiles among organisms, to discriminate
XX between transcriptional and post-transcriptional contributions to gene
XX expression and to track the movement of RNAs through RNP complexes,
XX including the interactions of combinations of proteins with RNAs in RNP
XX complexes. AAH28281-AAH28316 represent sequences derived from the 3'
XX untranslated region (UTR) of mRNA of various genes. The sequences contain
XX target sequences for RNA-binding proteins
XX
XX Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4020 AAAAAAGAGAAACAAA 4039
XX ||||| ||||| |||||
XX 22 AAAAAATACAGAAATAAAA 3
XX
XX RESULT 2622
XX ABL35693
XX ID ABL35693 standard; DNA; 22 BP.
XX
XX ABL35693;
XX
XX 04-APR-2002 (first entry)
XX
XX Immunostimulatory oligonucleotide SEQ ID NO: 619.

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XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX anti-inflammatory; antibacterial; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..22
XX /*tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX NO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JF, Flora M, Kliman DM;
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX
XX Example 11; Page 63; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 22 BP; 1 A; 3 C; 2 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5460 GTTCTTACTCTGATTTT 5479
XX ||||| ||||| |||||
XX 3 GTTGTACTCTTTT 22
XX
XX RESULT 2623
XX ABR97546
XX ID ABR97546 standard; DNA; 22 BP.
XX
XX ABR97546;
XX
XX 07-OCT-2002 (first entry)
XX
XX Human LCAT gene forward PCR primer #7.
XX
XX Lecithin-cholesterol acyltransferase; LCAT; Norum disease; gene therapy;
XX

```

KW fish-eye disease; atherosclerotic cardiovascular disease; forensic;  
 KW population diversity; anthropological lineage; paternity testing; human;  
 KW polymorphism; PCR; primer; ss.  
 XX Homo sapiens.  
 XX OS  
 XX MO200253575-A1.  
 XX  
 XX 11-JUL-2002.  
 PD  
 XX  
 XX 03-JAN-2001; 2001WO-US000092.  
 XX  
 XX 03-JAN-2001; 2001WO-US000092.  
 XX  
 XX (GENA-) GENA15555 PHARM INC.  
 XX  
 XX Chew A, Denton RR, Nandabalan K, Stephens JC;  
 XX WPI; 2002-557737/59.  
 XX  
 XX  
 XX Novel isolated polymorphic variant polynucleotide of lecithin-cholesterol  
 PT acyltransferase gene, useful for studying expression and biological  
 PT function of the gene, and for therapeutic, diagnostic or forensic  
 PT purposes.  
 XX  
 XX Example 1; Page 27; 72pp; English.  
 XX  
 XX The present invention relates to a new polynucleotide comprising a  
 CC nucleotide sequence which is a polymorphic variant of a reference  
 CC sequence for lecithin-cholesterol acyltransferase (LCAT). The invention  
 CC is useful for identifying an association between a trait (preferably a  
 CC clinical response to drug targeting LCAT) and at least one genotype or  
 CC haplotype of LCAT gene. The method of the invention has applicability in  
 CC developing diagnostic tests and therapeutic treatments for Norm disease,  
 CC fish-eye disease and atherosclerotic cardiovascular disease. The  
 CC haplotype and genotyping methods are useful for studying population  
 CC diversity, anthropological lineage, the significance of diversity and  
 CC lineage at the phenotypic level, paternity testing, forensic applications  
 CC and for identifying association between the LCAT genetic variation and a  
 CC trait such as level of drug response or susceptibility to disease. In  
 CC addition, the methods for identifying the LCAT haplotypes present in  
 CC individuals are useful in the development of drugs targeting LCAT. For  
 CC example, determining the frequency of individual LCAT haplotypes in a  
 CC population with a specific disease, e.g. Norm disease, will facilitate  
 CC the development of drugs targeting the LCAT isoform(s) that are most  
 CC frequent in that disease population. The present nucleic acid sequence  
 CC represents one of a collection (ABK97534-ABK97573) of PCR primers that  
 CC were used in the methods of the invention to detect polymorphisms in the  
 CC human LCAT gene  
 CC  
 XX  
 XX Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1849 CAGGTGAAGAACTGTCTCA 1868  
 Db 2 CTGTGTGAGAACTGTCTCA 21  
 RESULT 2624  
 ID ABR40406 standard; DNA; 22 BP.  
 XX ABR40406;  
 AC  
 XX 15-JUL-2002 (first entry)  
 XX  
 XX Probe for gene amplification analysis of human PRO7133.  
 DB  
 XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;

KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
 KW neuroprotective; probe; ss.  
 XX Homo sapiens.  
 XX OS  
 XX MO200153486-A1.  
 XX  
 XX 26-JUL-2001.  
 PD  
 XX  
 XX 11-FEB-2000; 2000WO-US003565.  
 XX  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 11-MAR-1999; 99US-0123972P.  
 XX 11-MAY-1999; 99US-0133459P.  
 XX 02-JUN-1999; 99WO-US012252.  
 XX 22-JUN-1999; 99US-0140650P.  
 XX 22-JUN-1999; 99US-0140653P.  
 XX 20-JUL-1999; 99US-0144758P.  
 XX 26-JUL-1999; 99US-0145698P.  
 XX 28-JUL-1999; 99US-0146222P.  
 XX 17-AUG-1999; 99US-0149395P.  
 XX 31-AUG-1999; 99US-0151689P.  
 XX 01-SEP-1999; 99WO-US020111.  
 XX 15-SEP-1999; 99WO-US021090.  
 XX 30-NOV-1999; 99WO-US028313.  
 XX 01-DEC-1999; 99WO-US028301.  
 XX 01-DEC-1999; 99WO-US028634.  
 XX 05-JAN-2000; 2000WO-US000219.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan MJ;  
 PT Masters SA, Pan J, Pitli RM, Roy MA, Smith V, Stone DM;  
 PT Watanabe CK, Wood WI;  
 XX WPI; 2002-205567/26.  
 XX  
 XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
 PT benign or malignant tumors, leukemias and lymphoid malignancies,  
 PT inflammatory, angiogenic and immunologic disorders.  
 XX  
 XX Example 26; Page 143; 302pp; English.  
 XX  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences  
 CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO  
 CC antibodies are useful for treating benign or malignant tumors (e.g.  
 CC renal, kidney, bladder, breast, etc), leukemias and lymphoid  
 CC malignancies, other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic, glandular, macropagal, stromal and blastocoele disorders,  
 CC inflammatory, immune and angiogenic disorders. The polynucleotide  
 CC sequences are also useful in gene therapy. The present sequence  
 CC represents a probe used in the methods of the present invention  
 CC  
 XX  
 XX Sequence 22 BP; 0 A; 11 C; 2 G; 9 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 6893 TGTCTCTCCCTTACTCTACTC 6912  
 Db 2 TGTCTCTCCCTTACTCTACTC 21  
 RESULT 2625  
 ID AAS16493/C standard; DNA; 22 BP.  
 XX AAS16493;  
 AC  
 XX 14-FEB-2002 (first entry)  
 XX

DE Marmoset Type II GnRH-R PCR primer S1.  
 XX  
 XX Marmoset; ss; type II gonadotrophin-releasing hormone receptor; GnRH-R;  
 KW contraceptive; neural development; sexual arousal; gene therapy;  
 KM transgenic animal; PCR primer; S1.  
 XX  
 OS Callithrix jacchus.  
 XX  
 PN W0200178796-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 17-APR-2001; 2001WO-GB001755.  
 XX  
 PR 15-APR-2000; 2000GB-00009269.  
 PR 17-JUN-2000; 2000GB-00014761.  
 PR 30-JUN-2000; 2000US-0215232P.  
 XX  
 PA (MEDIC-) MEDICAL RES COUNCIL.  
 XX  
 PI Millar RP, Lowe S, Conklin D;  
 XX  
 DR WPI; 2002-041317/05.  
 XX  
 PT New polypeptide, useful in gene therapy, as contraceptive or for  
 PT inhibiting endogenous Type II GnRH binding to its native receptor in  
 PT vivo, comprises Type II gonadotrophin-releasing hormone receptor and  
 PS polynucleotides encoding receptor.  
 XX  
 PS Example; Page 24; 92pp; English.  
 XX  
 CC The invention relates to an isolated functional Type II gonadotrophin-  
 CC releasing hormone receptor (Type II GnRH-R), or a peptide comprising at  
 CC least a portion of exon I of Type II GnRH-R, nucleic acids encoding the  
 CC receptor, an expression vector comprising the nucleic acid, a host cell  
 CC transformed with the vector, a transgenic animal having the construct  
 CC stably integrated into its genome, an antibody able to bind specifically  
 CC to Type II GnRH-R. The Type II GnRH-R is useful in gene therapy. The Type  
 CC II GnRH-R is particularly useful for inhibiting endogenous Type II GnRH  
 CC binding to its native receptor in vivo or as a contraceptive. The  
 CC receptor may also have roles in neural development and sexual arousal.  
 CC The present sequence is a PCR primer used to isolate a nucleic acid  
 CC encoding marmoset type II GnRH-R  
 CC  
 SQ Sequence 22 BP; 6 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1976 CAGTGATTTCTCTGGAGCA 1995  
 Db 22 CAGTGATTTCTCTGGAGCA 3  
 RESULT 2626  
 ABL55000/C  
 ID ABL55000 standard; DNA; 22 BP.  
 XX  
 AC ABL55000;  
 XX  
 DT 08-OCT-2002 (first entry)  
 XX  
 DE Human lymphoma-specific immunoglobulin PCR primer VH1L.  
 XX  
 KM Human; lymphoma; immunoglobulin; B-cell mediated pathology; cytostatic;  
 KM immunosuppressive; dermatological; antiinflammatory; neuroprotective;  
 KM antidiabetic; antithyroid; autoimmune disease; B-cell lymphoma; PCR;  
 KM primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PD Homo sapiens.  
 XX  
 PN W0200213862-A2.

XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US025204.  
 XX  
 PR 11-AUG-2000; 2000US-0224722P.  
 PR 11-AUG-2000; 2000US-0224723P.  
 PR 23-MAR-2001; 2001US-0279079P.  
 XX  
 PA (FAVR-) FAVRILE INC.  
 XX  
 PI Gold DP, Shopes RJ;  
 XX  
 DR WPI; 2002-280742/32.  
 XX  
 PT Composition for altering B-cell mediated pathology, has a chimeric  
 PT protein having portion of variable region of heavy chain or light chain  
 PT linked to portion constant region associated with patient B cell clone.  
 XX  
 PS Example 1; Page 43; 100pp; English.  
 XX  
 CC The sequence represents a PCR primer used in the invention to amplify  
 CC lymphoma-specific immunoglobulin heavy and light chains. The invention  
 CC relates to a novel composition for altering a B-cell mediated pathology  
 CC in a patient. The composition contains a chimeric protein comprising at  
 CC least a portion of a variable region of heavy chain or light chain (VH or  
 CC VL) linked to at least a portion of an immunoglobulin constant region,  
 CC where VH or VL region is associated with a B cell clone from the patient  
 CC having the B cell mediated pathology. The composition of the invention  
 CC has cytostatic, immunosuppressive, dermatological, antiinflammatory,  
 CC neuroprotective, antidiabetic, and antithyroid activity. The composition  
 CC is a vaccine useful for altering a B cell mediated pathology. This  
 CC includes B cell lymphoma e.g. non-Hodgkins lymphoma, refractory low grade  
 CC or follicular B-cell lymphoma; autoimmune disease e.g. multiple  
 CC sclerosis, systemic lupus erythematosus, anti-hu associated  
 CC paraneoplastic neurological syndrome, autoimmune hepatitis, Type I  
 CC diabetes, autoimmune thyroiditis and scleroderma. The pathology is  
 CC treated by administering the composition to the patient, preferably with  
 CC a cytokine e.g. granulocyte-macrophage-colony stimulating factor (GM-CSF)  
 CC or chemokine e.g. monocyte chemoattractant protein 3 (MCP 3)  
 CC  
 SQ Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7344 CCTGTCTCAGTCCATTGTGA 7363  
 Db 20 CCAAGTCCAGTCCATTGTGA 1  
 RESULT 2627  
 ABS67627  
 ID ABS67627 standard; DNA; 22 BP.  
 XX  
 AC ABS67627;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Mouse casein kinase-2 RT-PCR primer #1.  
 XX  
 KM ss; antisense therapy; casein kinase-2 alpha; cytostatic; antidiabetic;  
 KM antiinflammatory; diabetes; hyperproliferative disorder; cancer; PCR;  
 KM breast cancer; prostate cancer; liver cancer; infection; inflammation;  
 KM tumour; RT-PCR; reverse transcriptase PCR; primer; mouse.  
 XX  
 OS Mus musculus.  
 XX  
 PN W0200262818-A2.  
 XX  
 PD 15-AUG-2002.  
 XX

PF 31-JAN-2002; 2002WO-US002942.  
XX  
PR 08-FEB-2001; 2001US-00780172.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI McKay R, Freier SM, Wyatt JR;  
XX WPI; 2002-627521/67.  
DR  
XX  
XX New antisense oligonucleotides targeted to nucleic acid encoding casein  
PT kinase 2-alpha, useful in diagnostic and research applications, or for  
PT treating a disease or condition associated with expression of casein  
PT kinase 2-alpha.  
XX  
XX Example 13; Page 92; 166pp; English.  
PS  
XX  
XX The invention relates to a compound 8-50 nucleobases in length targeted  
CC to a nucleic acid molecule encoding casein kinase 2-alpha. The compound  
CC specifically hybridizes with and inhibits the expression of casein kinase  
CC 2-alpha, or specifically hybridizes with at least an 8-nucleobase portion  
CC of an active site on a nucleic acid molecule encoding casein kinase 2-  
CC alpha i.e. an antisense oligonucleotide. Also included are: (1) a  
CC composition comprising the compound and a carrier or diluent; (2)  
CC inhibiting the expression of casein kinase 2-alpha in cells or tissues by  
CC contacting the cells or tissues with the novel compound; and (3) treating  
CC an animal having a disease or condition associated with casein kinase 2-  
CC alpha by administering to the animal the compound cited above so that  
CC expression of casein kinase 2-alpha is inhibited. The antisense compounds  
CC are useful for modulating the expression of casein kinase 2-alpha and for  
CC treating diseases or conditions associated with expression of casein  
CC kinase 2-alpha, e.g. diabetes or hyperproliferative disorder,  
CC particularly cancer, such as breast cancer, prostate cancer, or liver  
CC cancer. The antisense compounds are also useful for diagnostics,  
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,  
CC inflammation or tumor formation, as research reagents and kits, and in  
CC distinguishing between functions of various members of a biological  
CC pathway. The present sequence is a reverse transcriptase (RT)-PCR primer  
CC used in an experiment to measure the levels of casein kinase-2 alpha mRNA  
XX  
SQ Sequence 22 BP; 8 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2408 CCACAGTGCACCAACATC 2427  
DB 2 CCACAGTGCACCAACATC 21  
RESULT 2628  
ABL45313  
ID ABL45313 standard; DNA; 22 BP.  
XX  
XX ABL45313;  
XX  
XX 11-APR-2002 (first entry)  
XX  
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:2357.  
DE Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
XX PCR primer; ss.  
XX Homo sapiens.  
XX OS  
XX JP2001321190-A.  
XX PN  
XX 20-NOV-2001.  
PD  
XX 12-MAR-2001; 2001JP-00068285.  
PF  
XX 10-MAR-2000; 2000JP-00066716.  
PR

XX  
XX (RIKA) RIKAGAKU KENKYUSHO.  
PA (GENO-) GENOTEX YG.  
XX  
XX WPI; 2002-144136/19.  
DR  
XX  
XX Arraying genome clones.  
PT  
XX  
PS Claim 4; Page 51; 528pp; Japanese.  
XX  
XX The present invention describes a method of arraying genome clones. The  
CC method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each well of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
XX  
SQ Sequence 22 BP; 6 A; 2 C; 8 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 5265 AATGTCATAGGAGGAGGT 5284  
DB 3 AATGTCATAGGAGGAGGT 22  
RESULT 2629  
ABQ80518  
ID ABQ80518 standard; DNA; 22 BP.  
XX  
XX ABQ80518;  
XX  
XX 31-OCT-2002 (first entry)  
XX  
XX HBP17 reverse PCR primer.  
DE  
XX  
XX PCR; primer; allergic disease; allergy; NB-1; E48 antigen; c-fos;  
XX involucrin; BENE; HBP17; fibronectin; Id1; ss.  
XX  
XX Synthetic.  
XX OS  
XX JP2002191398-A.  
XX PN  
XX 09-JUL-2002.  
PD  
XX 26-DEC-2000; 2000JP-00396167.  
PF  
XX 26-DEC-2000; 2000JP-00396167.  
PR  
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.  
XX  
XX WPI; 2002-594354/64.  
DR  
XX  
XX Inspection of allergic diseases, and a reagent for the inspection of  
PT allergic diseases.  
XX

PS Example 2; Page 13; 31pp; Japanese.

XX The present invention relates to a method for the inspection of allergic  
 CC diseases. The method involves measuring the expression level of a gene  
 CC selected from the group consisting of NB-1, E48 antigen, c-fos,  
 CC involucrin, BDNF, HSP70, fibronectin and Id1 in a biopsy sample, and  
 CC comparing it with the expression level of the gene in a biopsy sample of  
 CC a healthy person. The present primer was used in an example from the  
 CC invention

XX Sequence 22 BP; 2 A; 6 C; 5 G; 9 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3849 GCCTCTTTCTCTTATTC 3868  
 |||||  
 Db 3 GCCTGCTTTCTCTTATTC 22

RESULT 2630  
 ABS52976/c  
 ID ABS52976 standard; DNA; 22 BP.

XX ABS52976;  
 AC  
 XX 29-NOV-2002 (first entry)  
 DT  
 XX Human IGE receptor sequencing primer #13.  
 DE  
 XX Human; IGE receptor; Receptor; alpha; HSA; human serum albumin;  
 KW anti-allergic; dermatological; anti-inflammatory; antiasthmatic; ss;  
 KW IGE binding domain; systemic allergy; IGE-receptor-mediated disorder;  
 KW atopic dermatitis; atopic asthma; chronic urticaria; primer.

XX Homo sapiens.  
 OS  
 XX US6423512-B1.  
 PN  
 XX 23-JUL-2002.  
 PD  
 XX 21-JUL-1997; 97US-00897956.  
 PE  
 XX 26-JUL-1996; 96US-0022689P.  
 PR  
 XX (NOVS ) NOVARTIS AG.  
 PA  
 XX Digan ME, Lake P, Gram H;  
 PI  
 XX WPI; 2002-672940/72.  
 DR

XX New fusion IGE-binding polypeptide, useful for the prevention and  
 PT treatment of systemic allergy and/or other IGE-receptor-mediated  
 PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.

XX Disclosure; Fig 7; 49pp; English.

PS The invention relates to a new fusion polypeptide or its pharmaceutically  
 CC acceptable salt comprises at least one IGE-binding domain fused to at  
 CC least one human serum albumin (HSA) component, where the IGE-binding  
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein  
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus  
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined  
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a  
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell  
 CC transformed with the polynucleotide; (4) a method of preparing the fusion  
 CC protein comprising transforming a host cell with a vector comprising a  
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion  
 CC polypeptide in the cell, and recovering the fusion polypeptide from the  
 CC host cell, optionally in the form of its salt; and (5) a vector for  
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of  
 CC formula (I), (II), (III), (IV), or (V) or its salts (R<sub>1</sub>-L-R<sub>2</sub> (I), R<sub>2</sub>-

CC L-R<sub>1</sub> (II), R<sub>1</sub>-L-R<sub>2</sub>-L-R<sub>1</sub> (III), R<sub>1</sub>-L-R<sub>1</sub>-L-R<sub>2</sub> (IV), R<sub>2</sub>-L-R<sub>1</sub>-L-R<sub>1</sub>  
 CC (V) where R<sub>1</sub> = the polypeptide (a) or its truncation at the carboxy  
 CC terminus by 1-12 amino acids and R<sub>2</sub> = a polypeptide selected from the  
 CC sequence defined by residues Asp25-Leu609 the human HSA sequence  
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10  
 CC amino acids and L = independently a chemical bond, where the vector is  
 CC PMWT3-Rla-HAS-1(a). The compositions and methods of the present invention  
 CC are useful for the prevention and treatment of systemic allergy and other  
 CC IGE-receptor-mediated disorders such as atopic dermatitis, atopic asthma  
 CC and chronic urticaria. The IGE-binding polypeptide have a more prolonged  
 CC effective serum life, more improved clinical utility in the treatment of  
 CC allergy, as well as improved activity in a more efficient and cost-  
 CC effective manner. The present sequence is a sequencing primer for the IGE  
 CC receptor cDNA

XX Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3704 CATTGAGGATTCCTTC 3723  
 |||||  
 Db 20 CATTGCTGAGACTGCTTC 1

RESULT 2631  
 ABS71631  
 ID ABS71631 standard; DNA; 22 BP.

XX ABS71631;  
 AC  
 XX 28-NOV-2002 (first entry)  
 DT  
 XX T cell receptor (TCR) variable alpha (AV) peptide RT-PCR primer #9.  
 DE  
 XX T cell receptor; TCR; receptor; variable alpha peptide; AV peptide; TCRV;  
 KW T cell variable gene; T cell regulatory activity; autoimmune disease;  
 KW multiple sclerosis; human; reverse transcriptase; RT-PCR; primer; ss.

XX Homo sapiens.  
 OS  
 XX US2002107388-A1.  
 PN  
 XX 08-AUG-2002.  
 PD  
 XX 10-MAY-2001; 2001US-00853830.  
 PE  
 XX 12-MAY-2000; 2000US-0203984P.  
 PR  
 XX (VAND/) VANDENBARK A A.  
 PA  
 XX Vandenbark AA;  
 PI  
 XX WPI; 2002-697882/75.  
 DR

XX Identifying a T cell receptor variable gene expressed by target T cells  
 PT in an individual is useful to identify disease-associated T cells for  
 PT design of individualized therapies, particularly for autoimmune disease.

XX Example 2; Page 11; 20pp; English.

PS The invention relates to a method for identifying a T cell receptor  
 CC variable (TCRV) gene expressed by target T cells in an individual.  
 CC comprising determining expression of TCRV genes by activated T cells from  
 CC the individual and determining regulatory activity elicited in response  
 CC to TCRV peptides from the individual. A preferentially expressed TCRV  
 CC gene whose TCRV peptide elicits low T cell regulatory activity is  
 CC identified as a variable gene expressed by target T cells. The method is  
 CC used to identify disease-associated T cells in an individual so that  
 CC individualised therapies can be designed to prevent or treat the disease,  
 CC particularly an autoimmune disease, especially multiple sclerosis. This  
 CC sequence represents a reverse transcriptase PCR (RT-PCR) primer used in

CC analysis of expression of DNA encoding TCR variable alpha (AV) peptides  
 XX Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6195 GAGATGAGAGATTTGAA 6214  
 DB 1 GTGATGAGAGATTTGAA 20

RESULT 2632

AA167914  
 ID AA167914 standard; DNA; 22 BP.

AC AA167914;

DT 13-MAR-2002 (first entry)

DE Human MFO-110 cDNA cloning primer 01.

XX Zinc finger protein; MFO-110; developmental disorder; neurodegenerative;  
 KW psychiatric; vascular disease; angiogenesis; cancer; PCR primer; ss.

OS Homo sapiens.

PN WO200185765-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-EP005372.

PR 12-MAY-2000; 2000EP-00110089.

PA (MERCK) MERCK PATENT GMBH.

P1 Rodas Gubern B, Messegue Peypoch R, Masa Alvarez M;  
 P1 Rosell Vives E;

DR WPI; 2002-055583/07.

XX Identification of a new human C2H2-type zinc finger protein, MFO-110, which  
 PT may be useful in the treatment and diagnosis of disease such as  
 PT developmental disorders, neurodegenerative disease, vascular disease and  
 PT cancer.

PS Example 1; Page 62; 63pp; English.

XX The invention provides new human C2H2-type zinc finger proteins, MFO-110.  
 CC The MFO-110 polypeptides can be expressed by standard recombinant  
 CC methodology. The MFO-110 polypeptides and polynucleotides can be used in  
 CC diagnostic assays for detection of abnormally decreased or increased  
 CC levels of polypeptide or mRNA expression. This may be used for diagnosing  
 CC or determining susceptibility of a subject to diseases that include  
 CC developmental disorders, neurodegenerative disease, brain stroke,  
 CC psychiatric disorders such as schizophrenia, cardiac and vascular  
 CC disease, angiogenesis and cancer especially lymphomas. The polypeptides  
 CC may be used to identify membrane bound or soluble receptors and may be  
 CC used to identify agonists and antagonists which compete with receptor  
 CC binding. The polynucleotides may be used as diagnostic reagents through  
 CC detecting mutations in the associated gene, for chromosome localization  
 CC studies and tissue expression studies. Sequences AA167914-17 represent  
 CC primers for the PCR amplification and cloning of human MFO-110 cDNA

SO Sequence 22 BP; 4 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6670 CATTGGGAGACATTCTATT 6689

DB 2 CATTGGGAGACATTCTATT 21

RESULT 2633

ABK55618/c  
 ID ABK55618 standard; DNA; 22 BP.

AC ABK55618;

DT 18-JUN-2002 (first entry)

DE Human NOV3a RT-PCR primer #1.

XX Human; ss; primer; NOVX; gene therapy; cardiomyopathy; atherosclerosis;  
 KW diabetes; cell signal processing; metabolic pathway modulation;  
 KW inflammation; autoimmune disorder; scleroderma; transplantation; allergy;  
 KW systemic lupus erythematosus; haemophilia; Alzheimer's disease;  
 KW graft versus host disease; Leisch-Nyhan syndrome; periodontitis;  
 KW pancreatitis; musculoskeletal disorder; Parkinson's disease;  
 KW Huntington's disease; behavioural disorder; pain; obesity; wound healing;  
 KW neurodegenerative disorder; neuropsychiatric disorder; hypertension;  
 KW growth disorder; reproductive disorder; lung disease;  
 KW reverse transcriptase PCR.

OS Homo sapiens.

PN WO200216600-A2.

PD 28-FEB-2002.

PF 27-AUG-2001; 2001WO-US026518.

PR 25-AUG-2000; 2000US-0227800P.

PR 25-AUG-2000; 2000US-0228205P.

PR 25-AUG-2000; 2000US-0228324P.

PR 30-AUG-2000; 2000US-0228987P.

PR 30-AUG-2000; 2000US-0229185P.

PR 01-SEP-2000; 2000US-0229780P.

PR 01-SEP-2000; 2000US-0229848P.

PR 01-SEP-2000; 2000US-0229850P.

PR 22-JAN-2001; 2001US-0263337P.

PR 31-JAN-2001; 2001US-0265518P.

PR 15-MAR-2001; 2001US-0276451P.

PR 27-MAR-2001; 2001US-0279196P.

PR 24-AUG-2001; 2001US-00939398.

PA (CURA-) CURAGEN CORP.

P1 Gerlach V, MacDougall JR, Smithson G, Stone DJ, Ellerman K,  
 P1 Spytek KA, Zernusen BD, Raetelli L, Verney CAM, Patirajan M,  
 P1 Tcherev VT, Padigaru M, Taupier RJ;

DR WPI; 2002-292064/33.

XX New isolated cytoplasmic, nuclear, membrane bound and secreted  
 PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune  
 PT disorders, hemophilia, Leisch-Nyhan syndrome, pancreatitis,  
 PT musculoskeletal disorders.

PS Example 2; Page 207; 245pp; English.

XX The invention relates to an isolated cytoplasmic, nuclear, membrane bound  
 CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,  
 CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a  
 CC mature form, or a variant of the mature form of NOVX. Also included are a  
 CC polynucleotide encoding NOVX (or its complement), a vector comprising the  
 CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,  
 CC determining the presence of NOVX in a sample using the antibody,  
 CC determining the presence of NOVX polynucleotide in a sample using a probe  
 CC which binds to NOVX polynucleotide, identifying a an agent which binds to  
 CC NOVX (including modulators of NOVX), NOVX, the polynucleotide and the  
 CC antibody are useful for diagnosing, treating or preventing a NOVX-

CC associated disorder selected from cardiomyopathy, atherosclerosis, diabetes, a disorder related to cell signal processing and metabolic pathway modulation, inflammation, autoimmune disorders, scleroderma, transplacental, allergies, systemic lupus erythematosus, haemophilia, CC graft versus host disease, Alzheimer's disease, stroke, Leisch-Nyhan CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders, CC Parkinson's disease, Huntington's disease, behavioural disorders, pain, CC neurodegenerative and neuropsychiatric disorders, hypertension, wound healing, obesity, growth and reproductive disorders, lung diseases and CC many other diseases and disorders listed in the specification. NOVX, the CC polynucleotide and the antibody are useful in screening assays, detection CC assays (e.g., chromosomal mapping, tissue typing, forensic biology), CC predictive medicine (e.g., diagnostic assays, prognostic assays, CC monitoring clinical trials and pharmacogenomic), and in methods of CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to CC screen for potential agonist and antagonist compounds, and as bait CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is CC useful for producing non-human transgenic animals. The antibody is useful CC for isolating, and purifying NOVX and to monitor protein levels in tissue CC as part of a clinical testing procedure. The present sequence is an RT CC (reverse transcriptase)-PCR primer used to quantitate mRNA encoding a CC NOVX protein

XX  
SQ Sequence 22 BP; 8 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.24; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7080 CTGAGTCCTTGCTGTGTA 7039  
DB 22 CTGATCCCGTGTGTGTA 3

RESULT 2634  
ACD19520/c  
ID ACD19520 standard; DNA; 22 BP.  
XX  
AC ACD19520;  
XX  
DT 25-AUG-2003 (first entry)  
XX  
DE Novel human protein associated PCR primer #19.

XX  
KW Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW metabolic-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection; PCR; primer; ss.

XX  
OS Homo sapiens.  
XX  
PN WO2003023002-A2.  
XX  
PD 20-MAR-2003.  
XX  
PP 09-SEP-2002; 2002WO-US028539.  
XX  
PR 07-SEP-2001; 2001US-0318120P.  
PR 07-SEP-2001; 2001US-0318130P.  
PR 10-SEP-2001; 2001US-0318430P.  
PR 17-SEP-2001; 2001US-0322636P.  
PR 17-SEP-2001; 2001US-0322781P.  
PR 17-SEP-2001; 2001US-0322816P.  
PR 17-SEP-2001; 2001US-0322817P.

PR 19-SEP-2001; 2001US-0323519P.  
PR 20-SEP-2001; 2001US-0323631P.  
PR 20-SEP-2001; 2001US-0323636P.  
PR 25-SEP-2001; 2001US-0324699P.  
PR 25-SEP-2001; 2001US-0325091P.  
PR 26-SEP-2001; 2001US-0324990P.  
PR 17-APR-2002; 2002US-0373212P.  
PR 06-SEP-2002; 2002US-00236177.

XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Spytek KA, Paturajan M, Gorman L, Li L, Anderson DM, Zhong M;  
PI Gerlich VL, Verne CM, Ellerman K, Bergs C, Rothenberg ME, Guo X;  
PI Shimkova RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsebrook JP;  
PI Lepley DM, Edinger SR, Burgess CE;  
DR WPI; 2003-313242/30.

XX  
XX  
PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
PT and polynucleotides, useful in gene therapy, e.g. for treating or  
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
PT stroke or infections.

XX  
PS Example 92; Page 494; 586pp; English.

XX  
CC The invention describes a new isolated polypeptide (NOVX). The NOVX  
CC polypeptide, nucleic acid and antibody are useful as therapeutics.  
CC particularly in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease, which includes a pathology associated  
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene  
CC therapy for treating the disease or condition. In particular, the NOVX  
CC polypeptide or polynucleotide is useful for treating endocrine/  
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous  
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,  
CC asthma, inflammatory bowel disease, rheumatoid arthritis or  
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,  
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver  
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),  
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).  
CC These are also useful in developing powerful assay system for functional  
CC analysis of various human disorders, as well as in diagnostic  
CC applications, and for monitoring the effects of drugs during clinical  
CC trials. This sequence represents a primer used to isolate DNA encoding  
CC novel human NOV proteins

XX  
SQ Sequence 22 BP; 13 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.24; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3921 CTTTGCTTCTTTCTTCC 3940  
DB 22 CTTTGCTTCTTTCTTCC 3

RESULT 2635  
ACF03609  
ID ACF03609 standard; DNA; 22 BP.  
XX  
AC ACF03609;  
XX  
DT 15-SEP-2003 (first entry)  
XX  
DE Human NOV6 forward PCR primer SEQ ID NO:179.

XX  
KW Human; NOVX; cytosolic; cardiac; anti-inflammatory; immunosuppressive;  
KW anti-allergic; haemostatic; anti-HIV; antidiabetic; antileukosclerotic;  
KW anorectic; antisthmatic; nephrotropic; antirheumatic; hepatotropic;  
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;



KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;  
KW vulnerability; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;  
KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;  
KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;  
KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;  
KW Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;  
KW muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX MO200294870-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 02-NOV-2001; 2001WO-US051580.  
XX  
XX 02-NOV-2000; 2000US-0245291P.  
XX 02-NOV-2000; 2000US-0245317P.  
XX 07-NOV-2000; 2000US-0245562P.  
XX 08-NOV-2000; 2000US-0246871P.  
XX 26-JAN-2001; 2001US-0264389P.  
XX 26-JAN-2001; 2001US-0264423P.  
XX 29-JAN-2001; 2001US-0264799P.  
XX  
XX (CUBA-) CUBAGEN CORP.  
XX  
XX Grose WM, MacDougall JR, Smitheon G, Millet I, Stone DJ;  
XX Gunther E, Ellerman K, Alsbrook JP, Lepley DM, Burgess CE;  
XX Spletke KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L;  
XX Guo X, Fernandes ER, Vernet CM, Tchernev VT, Casman SJ, Shenoy S;  
XX Mishra V, Putrak K, Baumgartner JC, Colman SD;  
XX WPI; 2003-140359/13.  
XX  
XX New NOXV polypeptide useful for preventing or treating NOXV-associated  
XX disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and  
XX PT in chromosome mapping, tissue typing or pharmacogenomics.  
XX  
XX Example 2; Page 260; 346pp; English.  
XX  
XX AC03547 to AC03570 encode the human NOXV proteins (1) given in ABR57412  
XX CC to ABR57435. (1) have cytostatic, cardiant, antiinflammatory, nootropic,  
XX CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,  
XX CC antiatherosclerotic, anorectic, antiasthmatic, nephrotropic, virocidic,  
XX CC antiparasitic, hepatotropic, neuroprotective, antibacterial, relaxant,  
XX CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,  
XX CC vulnerability, angiogenic and antiangiogenic activities, and can be used in  
XX CC gene therapy and vaccines. The NOXV polypeptides and their antibodies can  
XX CC be used to determine the presence or absence of (1) in a sample. The NOXV  
XX CC polypeptides, polynucleotides encoding them, and antibodies against them,  
XX CC are useful in manufacturing a medicament for treating or preventing a  
XX CC syndrome associated with a NOXV-associated disorder such as hypertension,  
XX CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,  
XX CC autoimmune disorders, allergies, blood disorders, obesity, acquired  
XX CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) nephropathy,  
XX CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,  
XX CC infections (e.g. bacterial, viral, parasitic), stroke, muscular  
XX CC dystrophy, epilepsy, and other wasting disorders associated with chronic  
XX CC diseases. AC03571 to AC03644 represent PCR primers and probes for NOXV  
XX CC sequence, which are used in an example from the present invention  
XX  
XX Sequence 22 BP; 8 A; 8 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;  
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2636  
AC058206/C  
ID ACC58206 standard; DNA, 22 BP.  
XX  
XX AC058206;  
XX  
XX 11-AUG-2003 (first entry)  
XX  
XX PCR primer used in human FCGR2A-131H/R genotyping.  
XX  
XX  
XX Human; FCGR2A; Fc gammaRIIa; receptor; antibody;  
XX KW single nucleotide polymorphism; SNP; lymphoma; PCR; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO2003035904-A2.  
XX  
XX 01-MAY-2003.  
XX  
XX 11-OCT-2002; 2002WO-EP011397.  
XX  
XX 19-OCT-2001; 2001EP-00402718.  
XX  
XX (UYLI-) UNIT LITTLE CENT HOSPITALIER REGIONAL.  
XX PA (INNA-) INNATE PHARMA.  
XX  
XX Watier H, Cartton G, Colombat P;  
XX  
XX WPI; 2003-482053/45.  
XX  
XX Assessing the response of a subject having a tumor to a therapeutic  
XX PT antibody e.g., rituximab treatment, or selecting patients for therapeutic  
XX PT antibody treatment, comprises determining the FCGR3A158 genotype of the  
XX PT subject.  
XX  
XX Disclosure; Page 15; 53pp; English.  
XX  
XX The present sequence is that of a PCR primer used in human FCGR2A  
XX CC genotyping. Genotyping of FCGR2A-131H/R was performed in order to  
XX CC determine any correlation between genotype and response to therapeutic  
XX CC antibody treatment in non-Hodgkin's lymphoma (NHL) patients. The present  
XX CC (sense) primer was modified to create a BstUI site in case of R allele,  
XX CC and the antisense primer (see AC058207) was modified to create a BstUI  
XX CC site that served as an internal control. PCR amplification of genomic DNA  
XX CC was performed. Amplified DNA was digested with BstUI and separated by  
XX CC electrophoresis, staining with ethidium bromide. The FCGR2A-131H and -  
XX CC 131R alleles were visualized as a 337 bp and 316 bp DNA fragment,  
XX CC respectively. There was no correlation between FCGR2A-131H/R genotype and  
XX CC response to treatment. In contrast, FCGR3A-158V/F genotyping revealed a  
XX CC correlation with antibody treatment response in NHL patients  
XX  
XX Sequence 22 BP; 8 A; 6 C; 4 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 15.2; DB 1; Length 22;  
XX Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6005 GAGGGTTCTGGCATTTTCC 6024  
DB 20 GAGGAATTTCTGGGATTTTCC 1

RESULT 2637  
AC057219  
ID AC057219 standard; DNA, 22 BP.  
XX  
XX AC057219;  
XX  
XX 16-OCT-2003 (first entry)  
XX  
XX Human LAMB3 forward PCR primer SEQ ID NO:19.  
XX  
XX Human; mouse; skin structure; skin; laminin 5 chain gene; LAMB3; LAMB3;

KW LAMC2; extracellular matrix component; matrix metalloproteinase; MMP-1;  
 KW MMP-2; MMP-3; MMP-9; TIMP-1; TIMP-2; TIMP-3; collagen; PCR primer; ss.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX JP2002330792-A.  
 XX PD 19-NOV-2002.  
 XX PF 15-JAN-2002; 2002JP-00006797.  
 XX PR 15-JAN-2001; 2001JP-00006952.  
 XX PA (SHIS ) SHISEIDO CO LTD.  
 XX DR WPI; 2003-407328/39.  
 XX PT A method and a kit for determination of expression of mRNA or cDNA of a  
 PT protein participating in the maintenance of skin structure.  
 XX PS Claim 1; Page 2; 34pp; Japanese.  
 CC The present invention describes a method and a kit for determining the  
 CC expression of mRNA or cDNA of a protein participating in the maintenance  
 CC of skin structure. The method is quantitative, simple and accurate in the  
 CC determination of extracellular matrix components of laminin 5 chain genes  
 CC LAMB3, LAMB3 and LAMC2, matrix metalloproteinases MMP-1, MMP-2, MMP-3 and  
 CC MMP-9, VII collagen, type I collagen alpha 1 chain, type I collagen alpha  
 CC 2 chain, type III collagen alpha 1 chain, type IV collagen alpha 1 chain,  
 CC type IV collagen alpha 2 chain, TIMP-1, TIMP-2 and TIMP-3. ACF57201 to  
 CC ACF57290 represent PCR primers and probes used in the method of the  
 CC invention  
 XX SQ Sequence 22 BP; 6 A; 3 C; 10 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4513 CAGGACTGGAGAGCGTGTG 4532  
 DB 3 CAGGACTGGAGAGCGTGTG 22  
 RESULT 2638  
 ADB81310/c  
 ID ADB81310 standard; DNA; 22 BP.  
 XX AC ADB81310;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE PCR primer 9 used to amplify F8 scFv antibody to generate anti-ligands.  
 XX KW ss; PCR; primer; F8 scFv; antibody; anti-ligand library;  
 KW site directed mutagenesis.  
 XX OS Unidentified.  
 XX OS WO2003064648-A1.  
 XX PD 07-AUG-2003.  
 XX PF 30-JAN-2003; 2003WO-EP000982.  
 XX PR 31-JAN-2002; 2002GB-00002206.  
 XX PA (BIOI-) BIOINVENT INT AB.  
 XX PI Ohlin M;  
 XX WPI; 2003-627612/59.

XX Making a library of anti-ligands having a cavity binding site for a  
 PT ligand, useful in screening for a ligand.  
 PS Example 1; Page 16; 65pp; English.  
 CC This invention relates to a novel method of generating anti-ligand  
 CC libraries that have a cavity binding site. The method comprises providing  
 CC several novel anti-ligands having a cavity for binding a first ligand,  
 CC and differing from the first anti-ligand in that one or more of the amino  
 CC acid residues which make up the ligand binding surface of the cavity are  
 CC varied. Diversification of the first anti-ligand is achieved by site  
 CC directed mutagenesis, such that one or more of the amino acids that form  
 CC the cavity binding surface are replaced by those having similar but  
 CC different physicochemical properties. Preferably the anti-ligand is an  
 CC antibody, or fragment thereof, where amino acid replacements are derived  
 CC from a natural CDR (complementarity determining region) that makes up the  
 CC cavity and which binds to the ligand - an antigen. Specific anti-ligands  
 CC from such a library can be used as a starting point for further evolution  
 CC in order to improve their binding characteristics or to better correlate  
 CC the final use. This oligonucleotide is PCR primer 9 used to amplify the  
 CC F8 scFv antibody fragment in order to generate the anti-ligand library of  
 CC the invention.  
 XX SQ Sequence 22 BP; 6 A; 7 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1984 TTCTGGGAGCAGATGTTAC 2003  
 DB 21 TTCTGGGAGCAGCTGTATAC 2  
 RESULT 2639  
 ADC10255  
 ID ADC10255 standard; DNA; 22 BP.  
 XX AC ADC10255;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Human NOXV polypeptide gene forward primer SEQ ID NO: 277.  
 XX KW ss; primer; cytosstatic; antidiabetic; anorectic; cerebroprotective;  
 KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;  
 KW thymimetic; NOXV; pathology; cancer; diabetes; obesity;  
 KW endocrine disorder; CNS disorder; inflammatory disorder;  
 KW chromosome mapping; tissue typing; predictive medicine.  
 XX OS Homo sapiens.  
 XX OS WO2003000842-A2.  
 XX PD 03-JAN-2003.  
 XX PF 04-JUN-2002; 2002WO-US017443.  
 XX PR 04-JUN-2001; 2001US-0295607P.  
 XX PR 04-JUN-2001; 2001US-029561P.  
 XX PR 06-JUN-2001; 2001US-0296404P.  
 XX PR 06-JUN-2001; 2001US-0296418P.  
 XX PR 07-JUN-2001; 2001US-0296575P.  
 XX PR 11-JUN-2001; 2001US-0297414P.  
 XX PR 12-JUN-2001; 2001US-0295573P.  
 XX PR 12-JUN-2001; 2001US-0297567P.  
 XX PR 14-JUN-2001; 2001US-0298285P.  
 XX PR 15-JUN-2001; 2001US-0298528P.  
 XX PR 18-JUN-2001; 2001US-0299133P.  
 XX PR 19-JUN-2001; 2001US-0299230P.  
 XX PR 21-JUN-2001; 2001US-0299949P.  
 XX PR 22-JUN-2001; 2001US-0300177P.

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PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358565P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359644P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI DiIppio VA, Edinger SR, Eissen A, Ellerman K, Gangoli EW;
PI Gerlach VA, Gorman L, Guo X, Hermann JT, Hjal T, Ji W, Kekuda R;
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Miller I;
PI Ort T, Padigaru M, Paturajan M, Pena CE, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsbrook JP;
PI Bugees CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
XX
PT New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Example B; SEQ ID NO 277; 772pp; English.
XX
CC The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to a primer used to
CC amplify and isolate the coding sequence for one of the polypeptides of
CC the invention.
XX
SQ Sequence 22 BP; 0 A; 7 C; 2 G; 13 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 5733 CTTCCTTCCTTCCTTCCTTCCT 5752
DB 1 CTGCTTTGCGCTTCCTTCCT 20
XX
RESULT 2640
ADE76823/c
ID ADE76823 standard; DNA; 22 BP.
XX
AC ADE76823;
XX
DT 29-JAN-2004 (first entry)

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XX
XX Pfisteria shumwayae-specific PCR primer Seq ID4.
DE
XX
XX water-borne organism; algal bloom; ship ballast; dinoflagellate;
KW Pfisteria; Gymnodinium; Chattonella; Alexandrium; Aureococcus;
KW zebra mussel; Dreissena; PCR; primer; ss.
XX
OS Pfisteria shumwayae.
XX
XX MO2003053855-A2.
XX
XX 03-JUN-2003.
XX
XX 25-OCT-2002; 2002MO-US034123.
XX
XX 30-OCT-2001; 2001US-0131335P.
XX
XX 10-JUN-2002; 2002US-0394654P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Cary SC, Coyne KJ;
XX
XX WPI; 2003-618038/58.
XX
XX
XX Identifying water-borne organisms associated with harmful algal bloom
XX comprises fractionating an aliquot of water, isolating DNA from
XX fractions, amplifying DNA, contacting amplicon obtained with probe, and
XX detecting amplicon.
XX
XX Claim 17; SEQ ID NO 4; 36pp; English.
XX
XX This invention relates to a novel method of identifying water-borne
XX organisms associated with harmful algal bloom. The method comprises
XX isolating DNA from an aliquot of water by size to yield several fractions,
XX isolating DNA from the fractions, amplifying DNA by high throughput, real
XX time PCR comprising forward and reverse genus-specific primer to yield
XX amplified DNA amplicon, contacting the amplicon with a species-specific
XX labelled probe, and detecting the amplicon. The method is useful for
XX identifying water-borne organisms associated with harmful algal bloom or
XX transported in the ballast of a ship, where the water-borne organisms are
XX dinoflagellates selected from Pfisteria, Gymnodinium, Chattonella,
XX Alexandrium and Aureococcus, or is a zebra mussel (Dreissena). The
XX present sequence is that of a species-specific PCR primer which may be
XX used in the method of the invention.
XX
SQ Sequence 22 BP; 7 A; 3 C; 6 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2545 CAGATCCTGACGTACACGCT 2564
DB 20 CAGATTCTGACCTATACGCT 1
XX
RESULT 2641
ADE15462
ID ADE15462 standard; DNA; 22 BP.
XX
AC ADE15462;
XX
XX 29-JAN-2004 (first entry)
XX
XX T cell receptor variable region alpha, RT PCR primer #9.
XX
XX Human; T cell receptor variable region alpha; TCRV alpha;
XX cytokine response; CD4+ T cell; CD25+ T cell; autoimmune disease;
XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX type 1 diabetes; non-obese diabetes; myaschemia gravis; Grave's disease;
XX Hashimoto's thyroiditis; PCR; primer; ss; RT-PCR;
XX reverse transcriptase PCR.
XX

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OS Homo sapiens.  
 XX US2003190665-A1.  
 PN 09-OCT-2003.  
 PD 14-MAY-2003; 2003US-00438729.  
 PF 12-MAY-2000; 2000US-0203984P.  
 PR 10-MAY-2001; 2001US-00853830.  
 XX (USOR-) UNIV OREGON HEALTH SCI.  
 PA (USGO) US DEPT VETERANS AFFAIRS.  
 XX Vanderbark AA;  
 PI WPI; 2003-864176/80.  
 DR WPI; 2003-864176/80.  
 XX Identifying T cell receptor variable peptides useful for treating  
 PT autoimmune disease including multiple sclerosis, rheumatoid arthritis,  
 PT lupus, diabetes, myasthenia gravis, Grave's disease, Hashimoto's  
 PT thyroiditis and psoriasis.  
 PS Example 1; SEQ ID NO 125; 68pp; English.  
 XX The invention relates to identifying a T cell receptor (TCR) variable (V)  
 CC peptide useful as a therapeutic agent in a subject with a disorder,  
 CC comprising screening TCR V beta and/or TCR V alpha peptides to select a  
 CC TCR V peptide that produces altered expression of a cytokine in response  
 CC to the peptide by T cells from the subject, and determining a regulatory  
 CC activity of CD4+CD25+ T cells isolated from the subject in response to  
 CC the peptide. Also included are monitoring the efficacy of a TCR V peptide  
 CC for treatment of a subject (comprising exposing CD4+ T cells from the  
 CC subject to the peptide and determining a T cell regulatory activity of  
 CC CD4+CD25+ T isolated from the subject, where induction or regulatory  
 CC activity indicates the efficacy of the peptide for treatment of the  
 CC subject), selecting a therapy for a subject (comprising: identifying a  
 CC TCR V gene expressed by target T cells in the subject for screening for  
 CC expression of a TCR V gene by activated T cells from the subject and  
 CC determining expression of a cytokine elicited in response to one or more  
 CC TCR V peptides corresponding to the TCR V gene by T cells from the  
 CC subject, thereby identifying a TCR V gene expressed by target T cells)  
 CC and identifying a TCR V peptide corresponding to the TCR V gene that  
 CC elicits T cell regulatory activity by a T cell isolated from the subject.  
 CC The method is useful for identifying a T cell receptor (TCR) variable (V)  
 CC peptide useful as a therapeutic agent in a subject with a disorder. The  
 CC peptide is used to treat an autoimmune disease, particularly multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus, type I  
 CC diabetes, non-obese diabetes, myasthenia gravis, Grave's disease,  
 CC Hashimoto's thyroiditis or psoriasis. The present sequence is a TCR V  
 CC alpha reverse transcriptase (RT)-PCR primer used to measure TCR gene  
 CC expression levels, in the method of the invention.  
 XX Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 22;  
 Best Local Similarity 85.0%; Pred. No. 1.9e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 6195 GAGGATGAGGAGGATTTGAA 6214  
 DB 1 GTGATGAGGAGGATGCGA 20  
 RESULT 2642  
 AAT05666/C  
 ID AAT05666 standard; DNA; 23 BP.  
 AC AAT05666;  
 XX 20-JUN-1996 (first entry)  
 DT PCR primer for nucleic acid encoding TNF microsatellite.  
 DE

XX Tumour necrosis factor; TNF; microsatellite; Crohn's disease; allele;  
 KM inflammatory bowel disease; diagnosis; therapeutic; ulcerative colitis;  
 KW ss.  
 OS Synthetic.  
 XX WO9531575-A1.  
 PN 23-NOV-1995.  
 PD 17-MAY-1995; 95WO-US006107.  
 PF 17-MAY-1994; 94US-00245297.  
 PR (CEDA-) CEDARS SINAI MEDICAL CENT.  
 PA Plevy SE, Rotter JI, Targan SR, Toyoda H, Yang H;  
 PI WPI; 1996-010959/01.  
 DR Screening for Crohn's disease - by detecting nucleic acid encoding  
 PT particular tumour necrosis factor micro-satellite allele(s).  
 PS Claim 10; Page 32; 43pp; English.  
 XX AAT05661-T05670 are PCR primers used for the detection of a nucleic acid  
 CC encoding tumour necrosis factor (TNF) microsatellite alleles a to e.  
 CC These alleles are associated with Crohn's disease (CD). The presence of  
 CC nucleic acid encoding 3 or more of the alleles in a subject is indicative  
 CC of CD. The primers provide a reliable method of screening for CD and are  
 CC useful for distinguishing between CD and ulcerative colitis patients. The  
 CC presence of a nucleic acid carrying 3 or more of the alleles a2, b1, c2,  
 CC d4 and e1 indicates a CD patient and in ulcerative colitis patients  
 CC alleles a2, b1 and c2 are absent  
 XX Sequence 23 BP; 8 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5179 CTCGATGTTCTCCACTTG 5198  
 DB 21 CTCGAGGTTCTCCCATG 2  
 RESULT 2643  
 AAT63128/C  
 ID AAT63128 standard; DNA; 23 BP.  
 AC AAT63128;  
 XX 22-JUN-1997 (first entry)  
 DT Glutathione S-transferase promoter PCR primer A12.  
 DE Promoter; glutathione S-transferase; herbicide safener; gene switch;  
 KM transcription factor; transgenic plant; maize; primer; PCR;  
 KW polymerase chain reaction; ss.  
 OS Synthetic.  
 XX WO9711189-A2.  
 PN 27-MAR-1997.  
 PD 30-AUG-1996; 96WO-GB002116.  
 PF 22-SEP-1995; 95GB-00019404.  
 PR 22-SEP-1995; 95GB-00019406.  
 XX (ZENB) ZENECA LTD.  
 PA

XX Jenson I, Greenland AJ, Bevan M, Sheppard H;  
XX  
XX WPI; 1997-202896/18.  
XX  
XX Chemically inducible promoter from the glutathione S-transferase gene -  
XX provides inducible gene expression in plants, esp. with herbicide  
XX bateners as inducer.  
XX  
XX Disclosure; Page 12; 49pp; English.  
XX  
XX Preliminary deletion analysis of the maize glutathione S-transferase 27  
XX kDa subunit gene promoter region (see also AAT63125) suggested that  
XX element(s) conferring inducibility lay within 900 bp immediately upstream  
XX of the transcription start point (TSP). A series of fine deletion  
XX constructs were made by fusing 200 bp deleted fragments of this 900 bp  
XX region to a beta-glucuronidase marker gene. PCR primer A12 (AAT63128) was  
XX designed to correspond to a PstI site adjacent to the TSP. It was used in  
XX combination with primers A13, A14, A15 and A16 (AAT63129-32) in PCR  
XX experiments to generate fragments of 217, 378, 570 and 760 bp,  
XX respectively. Transient transformation assays indicated that the  
XX inducible element(s) lay between -217 and -318 upstream of the TSP  
XX  
SQ Sequence 23 BP; 3 A; 7 C; 5 G; 8 T; 0 U; 0 Other;  
Query Match .0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 7411 ATCAGCAGCAGCAGCAGCAG 7430  
DB 23 ATAACTAGCAGCTGCAGCAG 4  
RESULT 2644  
AAV57842/c  
ID AAV57842 standard; DNA; 23 BP.  
XX  
XX AAV57842;  
XX  
XX 18-NOV-1998 (first entry)  
XX  
XX Human chromosome 18 PCR primer F for D18S996.  
XX  
XX Manic-depressive illness; susceptibility; genotype; diagnosis;  
XX chromosomal marker; polymorphic marker; chromosome 18; human;  
XX myo-inositol monophosphatase protein; IMP-18p; PCR primer; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX WO9818963-A1.  
XX  
XX 07-MAY-1998.  
XX  
XX 28-OCT-1997; 97WO-US019381.  
XX  
XX 28-OCT-1996; 96US-0029278P.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Decera-Wadleigh SD, Gershon ES, Badner JA, Goldin LR;  
XX Berretini WH, Yoshikawa T, Sanders AR, Esterling LE;  
XX  
XX WPI; 1998-272247/24.  
XX  
XX New isolated IMP 18p myo-inositol monophosphatase - used to develop  
XX products for determining susceptibility to manic depressive illness and  
XX as targets for preventive and therapeutic treatments.  
XX  
XX Disclosure; Page 3; 118pp; English.  
XX  
XX A method has been developed for determining a genotype associated with

CC increased susceptibility to manic-depressive (MD) illness. The method  
CC comprises determining the genotype of an affected individual with at  
CC least one polymorphic marker localised within the chromosomal region  
CC defined by and including markers D18S843 and D18S869 and determining the  
CC genotype associated with increased susceptibility to MD disorder. The  
CC method can be used for determining susceptibility to MD illness including  
CC bipolar disorder, genetic counselling of individuals from families  
CC affected with MD illness, and aid in the differential diagnosis of MD  
CC illness from other psychiatric pathologies. Products from the present  
CC invention can also be used to obtain modulators of IMP 18p myo-inositol  
CC monophosphatase protein activity and as targets for preventive and  
CC therapeutic treatments. The present sequence represents a PCR primer from  
CC Table 1 in the present invention (see AAV57798 to AAV57877)  
XX  
SQ Sequence 23 BP; 6 A; 3 C; 4 G; 10 T; 0 U; 0 Other;  
Query Match .0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 7108 GAAATAATGAATTAATTCTTCC 7127  
DB 23 GAAATAATGAATTAATGCTTCC 4  
RESULT 2645  
AAV64634/c  
ID AAV64634 standard; DNA; 23 BP.  
XX  
XX AAV64634;  
XX  
XX 09-FEB-1999 (first entry)  
XX  
XX PCR primer for amplification of tumour necrosis factor locus c.  
XX  
XX Tumour necrosis factor; TNF; microsatellite allele; Crohn's disease;  
XX clinical subtype; anti-TNF cytokine therapy; PCR primer; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX WO9847004-A1.  
XX  
XX 22-OCT-1998.  
XX  
XX 08-APR-1998; 98WO-US006991.  
XX  
XX 11-APR-1997; 97US-00837056.  
XX  
XX 12-MAY-1997; 97US-00855825.  
XX  
XX (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX (PROM-) PROMETHEUS LAB INC.  
XX  
XX Plevy SE, Targan SR, Taylor K, Barry MJ;  
XX  
XX WPI; 1998-583296/49.  
XX  
XX Diagnosis of Crohn's disease subtypes - by detecting serological and  
XX genetic markers for identifying subtypes having characteristic  
XX responsiveness to anti-TNF cytokine therapy.  
XX  
XX Claim 37; Page 76; 117pp; English.  
XX  
XX PCR primers AAV64633-34 are used in PCR analysis of tumour necrosis  
XX factor (TNF) microsatellite alleles to identify TNF locus c. The  
XX specification describes a method for detecting the presence or absence of  
XX at least two TNF microsatellite alleles selected from TNFA10, TNFB4,  
XX TNFC1, TNFD3 and TNPE3 in a patient with Crohn's disease, where the  
XX presence of an allelic combination comprising at least two of the alleles  
XX indicates a clinical subtype of Crohn's disease having an inferior  
XX clinical response to anti-TNF cytokine therapy. The methods and the  
XX products can be used for diagnosing clinical subtypes of Crohn's disease,  
XX that affect the gastrointestinal tract and produce similar symptoms, with



KW Mouse; carcinoma cell; IMC-HAL; cancer; metastasis; CMAP; inhibitor;  
 KW cancer metastasis associated protein; PCR primer; ss.  
 OS Synthetic.  
 OS Mus musculus.  
 XX MO9845431-A1.  
 XX PD 15-OCT-1998.  
 XX PF 07-APR-1998; 98WO-JP001592.  
 XX PR 08-APR-1997; 97JP-00105333.  
 XX PA (BANY ) BANYU PHARM CO LTD.  
 XX PI Morita M, Arakawa H, Ohta M;  
 XX WPI; 1999-080732/07.  
 XX DR  
 XX PT Protein associated with cancer metastasis and gene encoding it - useful  
 XX for screening for potential inhibitors of cancer metastasis.  
 XX PS Example 2; Page 20; 74pp; Japanese.  
 CC The present invention provides gene sequences associated with cancer  
 CC metastasis which are isolated from mouse IMC carcinoma cells by detection  
 CC of their higher expression in IMC-HM cell lines than in IMC-IM cell lines  
 CC using differential display of the mRNA in these cells. The gene sequences  
 CC can be used for the screening of potential inhibitors of cancer  
 CC metastasis by either: bringing into contact with the cancer metastasis  
 CC associated protein (CMAP) and determining the degree of binding; or  
 CC creating a transformant cell line which expresses CMAP and measuring the  
 CC degree of expression of CMAP using an antibody recognising the protein,  
 CC either in the presence or absence of the potential inhibitor. IMC-HM  
 CC cells transformed with antisense CMAP DNA show a lowered ability to  
 CC metastasise. The present sequence represents a PCR primer used in an  
 CC example from the present invention  
 CC  
 XX Sequence 23 BP; 5 A; 9 C; 3 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3222 TGGGAGGAGGAGGATT 3241  
 Db 23 TGGGAGGAGGAGGAGTATT 4  
 RESULT 2649  
 AAA13773/c  
 ID AAA13773 standard; DNA; 23 BP.  
 XX  
 AC AAA13773;  
 XX  
 DT 26-JUL-2000 (first entry)  
 XX  
 DE Deleted GST promoter sequence PCR primer #2.  
 XX  
 KW Maize; glutathione-S-transferase; GST; promoter; plant; tuber; potato;  
 KW expression; sprouting inhibition; storage; PCR primer; ss.  
 XX  
 OS Zea mays.  
 OS WO200018930-A1.  
 XX PN  
 XX PD 06-APR-2000.  
 XX PF 13-SEP-1999; 99WO-GB003021.  
 XX PR 25-SEP-1998; 98GB-00020970.  
 XX

PA (ZENEC ) ZENEGA LTD.  
 XX  
 PI Robertson NM, Paine JM, Jepson I;  
 XX WPI; 2000-293164/25.  
 XX  
 PT Constitutively expressing a target gene in a storage organ or stem of a  
 PT plant comprises transfecting the plant with a gene promoter region for  
 PT the 27 kD subunit of glutathione-S-transferase operably linked to a  
 PT target sequence.  
 XX  
 XX Example 1; Page 15; 53pp; English.  
 CC A method has been developed of constitutively expressing a target gene in  
 CC a storage organ or stem of a plant by using the gene promoter region (1)  
 CC for the 27 kD subunit of the glutathione-S-transferase (GST), isoform II,  
 CC or its deleted fragment which retains the activity of (1), operably  
 CC linked to and controlling a target sequence. The present invention also  
 CC describes: (1) a DNA construct comprising (1) operably linked to and  
 CC controlling a target gene sequence; (2) potato plant germ plasma  
 CC comprising the DNA construct of (1); (3) a potato plant, potato seed or  
 CC potato plant cell comprising a DNA construct of (1); and (4) a method for  
 CC preventing or inhibiting sprouting in a potato tuber comprising causing  
 CC the tuber to express a target sequence under the control of (1). The  
 CC method is used for constitutively expressing a target gene in a storage  
 CC organ or stem of a plant in order to prevent or inhibit sprouting of  
 CC tubers. The method obviates the use of chemicals and their associated  
 CC costs for inhibiting sprouting in potatoes. The present sequence  
 CC represents a PCR primer used in the generation of the specifically  
 CC claimed deleted GST promoter sequence comprising 693 bases  
 CC  
 XX Sequence 23 BP; 3 A; 7 C; 5 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7411 ATCAGCAGCAGCAGCAGCAG 7430  
 Db 23 ATTAGTAGCAGCTGCAGCAG 4  
 RESULT 2650  
 AAA59333/c  
 ID AAA59333 standard; DNA; 23 BP.  
 XX  
 AC AAA59333;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE PCR primer used to amplify the cDNA sequence of I-2 resistance gene.  
 XX  
 KW Regulatory activity; transcription; I-2 resistance gene; tomato;  
 KW egg plant; potato; melon; tobacco; Arabidopsis; plant pathogen; fungi;  
 KW tissue-specific; PCR primer; ss.  
 XX  
 OS Fusarium oxysporum.  
 OS EPI024196-A1.  
 XX PN  
 XX PD 02-AUG-2000.  
 XX PF 29-JAN-1999; 99EP-00400212.  
 XX PR 29-JAN-1999; 99EP-00400212.  
 XX PA (KEYG-) KEYGENE NV.  
 XX  
 PI Haring MA, Cornelissen BJC, Mes JJ, Simons AFM;  
 XX WPI; 2000-516034/47.  
 XX  
 PT New I-2 resistance gene tissue-specific regulatory sequence useful in

PT plant resistance mechanisms against plant pathogens such as fungi.  
 XX  
 PS Disclosure; Page 7; 47pp; English.  
 XX  
 CC PCR primers AAA59333-34 were used to amplify cDNA encoding an I-2  
 CC resistance protein. The specification describes nucleotide sequences  
 CC which have a regulatory activity on the transcription of the I-2  
 CC resistance gene in plant host cells. The transgenic plants, especially  
 CC tomato, egg plant, potato, melon, tobacco and Arabidopsis, are capable of  
 CC expressing a gene mediating resistance to a plant pathogen, such as  
 CC fungi, in a tissue-specific manner. The plant is capable of preventing  
 CC infection by a plant pathogen, such as fungi. Inserting the regulatory  
 CC activity polynucleotide into plant cell genomes is useful for providing  
 CC plants with reduced susceptibility to plant pathogens, especially for  
 CC protecting plants in cultivation  
 XX  
 SQ Sequence 23 BP; 2 A; 12 C; 1 G; 8 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0;  
 Qy 6989 GAATGAGGTGGGAAAGGAG 7008  
 Db 21 GAGTGAGGTGAGAAAGGAG 2  
 RESULT 2651  
 AAC80271/c  
 ID AAC80271 standard; DNA; 23 BP.  
 XX  
 AC AAC80271;  
 XX  
 DT 03-MAY-2001 (first entry)  
 XX  
 DE Reverse primer #99 used for amplification of HLA-A exon 3.  
 XX  
 KM HLA-A; HLA-B; HLA-C; typing; primer; human; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0200061795-A2.  
 PD 19-OCT-2000.  
 XX  
 PF 05-APR-2000; 2000WO-EP002398.  
 XX  
 PR 09-APR-1999; 99EP-00870068.  
 PR 11-JUN-1999; 99US-0138614P.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI De Canck I, Rombout A, Rousseau R;  
 XX  
 DR WPI; 2000-647426/62.  
 XX  
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4  
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined  
 PT primer sets, useful for subtyping or typing of HLA Class I alleles.  
 XX  
 PS Claim 4; Page 40; 128pp; English.  
 XX  
 CC The present invention relates to a method for the locus-specific,  
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human  
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful  
 CC for subtyping or typing of HLA class I alleles. The present sequence is  
 CC an amplification primer used in the method  
 XX  
 SQ Sequence 23 BP; 6 A; 9 C; 4 G; 3 T; 0 U; 1 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03;  
 Matches 17; Conservative 0; Mismatches 0;  
 Qy 6989 GAATGAGGTGGGAAAGGAG 7008  
 Db 21 GAGTGAGGTGAGAAAGGAG 2

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 5151 GGGAGGAGCTTCTCTGGG 5170  
 Db 23 GGGAGAGAMTCTCTCTGGG 4  
 RESULT 2652  
 AAH19012/c  
 ID AAH19012 standard; DNA; 23 BP.  
 XX  
 AC AAH19012;  
 XX  
 DT 21-JUN-2001 (first entry)  
 XX  
 DE Forward primer used to amplify UCP3 gene exon 2.  
 XX  
 KM UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200118232-A2.  
 PD 15-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-US024784.  
 XX  
 PR 08-SEP-1999; 99US-0152789P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 PA (STEP/) STEPHENS J C.  
 XX  
 PI Chew A, Choi JY, Denton RR, Nandabalan K;  
 XX  
 DR WPI; 2001-218562/22.  
 XX  
 DE Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton  
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,  
 PT useful for the design of drugs for treating obesity.  
 XX  
 PS Example 1; Page 33; 94pp; English.  
 XX  
 CC The present invention relates to the human uncoupling protein 3  
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The  
 CC polymorphisms are associated with obesity, especially diabetes mellitus  
 CC associated obesity. They polymorphisms may be identified and analysed to  
 CC determine whether an individual is susceptible to obesity and may be used  
 CC as the basis for targeted design of drugs to treat obesity. The present  
 CC sequence was used in the identification and amplification of UCP3  
 CC polymorphisms  
 XX  
 SQ Sequence 23 BP; 3 A; 11 C; 1 G; 8 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 3202 GAGGGGCTTGAAGAGTGGG 3221  
 Db 23 GAGGGGCTTGAAGAGGAG 4  
 RESULT 2653  
 AAF76321/c  
 ID AAF76321 standard; DNA; 23 BP.  
 XX  
 AC AAF76321;  
 XX  
 DT 05-JUN-2001 (first entry)  
 XX  
 DE Human TNF $\alpha$  microsatellite marker reverse PCR primer.  
 XX  
 KW Autoimmune disease; diagnosis; susceptibility; 2-2-4 haplotype;





```

PD 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US006466.
PF
XX 01-MAR-2000; 2000US-0186199P.
PR
XX (UYSF-) UNIV SOUTH FLORIDA.
PA
XX Dalton WS, Damiano JS;
XX
XX WPI, 2001-582112/65.
DR
XX
XX use of bisphosphonate compounds for inhibiting cell adhesion mediated
PT drug resistance and enhancing efficacy of chemotherapeutic and/or
PT radiation treatments.
PT
XX
XX Example 2; Page 32; 77pp; English.
PS
XX
XX This invention relates to the use of bisphosphonate compounds for
XX inhibiting cell adhesion mediated drug resistance and enhancing efficacy
XX of chemotherapy and/or radiation therapy in the treatment of cancer by
XX inhibiting integrin-mediated cell adhesion. Cell adhesion is required by
XX many normal processes but in some circumstances is undesirable, being
XX involved in many pathologies. Cancer cell interaction with the
XX extracellular matrix prevents apoptosis and can result in cell adhesion
XX mediated drug resistance. This nucleotide sequence represents a primer
XX used for human alpha4 integrin subunit specific reactions
XX
SQ Sequence 23 BP; 2 A; 9 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5729 CTGGCTTCCTTCCTTCCTTC 5748
Db 3 CTGGCTTCCTTCCTTCCTTC 22

RESULT 2656
AAC85127
ID AAC85127 standard; DNA; 23 BP.
XX
XX AAC85127;
AC
XX 08-MAY-2001 (first entry)
DT
XX
XX R. anaplastifer Ompa gene amplifying primer 4.
DE
XX
XX Ompa; outer membrane protein; avian; immunization; poultry; vaccine;
KM septicemia anserum exsudativa; antibacterial; PCR primer; ss.
XX
XX Riemerella anaplastifer.
OS
XX
XX WO200104317-A1.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 14-JUL-1999; 99WO-SG000075.
PF
XX
XX 14-JUL-1999; 99WO-SG000075.
PR
XX
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA
XX
XX Frey J, Sumathi S;
PI
XX
XX WPI; 2001-138355/14.
DR
XX
XX New Ompa gene of Riemerella anaplastifer for production of vaccines and
PT for diagnosing septicemia anserum exsudativa of avian species.
PT
XX
XX Disclosure; Page 12; 50pp; English.
PS
XX

```

CC	The invention relates to a Riemerella anatipestifer outer membrane
CC	protein OmpA. The OmpA protein can be expressed by standard recombinant
CC	methodology. An antibody (Ab) specific to the OmpA polypeptide is useful
CC	for diagnosing an infection by R.anatipestifer in an avian species. The
CC	OmpA gene and protein are useful for the preparation of vaccines and
CC	serodetective diagnostic assays. A vaccine composition comprising the
CC	OmpA gene, protein or Ab is useful for effective immunization of poultry
CC	against R. anatipestifer infection, especially septicemia anseum
CC	exudative. Sequences AAC85124-119 represent PCR primers used for
CC	amplifying the R. anatipestifer Ompa gene
XX	
SQ	Sequence 23 BP; 2 A; 5 C; 2 G; 14 T; 0 U; 0 Other;
Query Match	0.2%; Score 15.2; DB 1; Length 23;
Best Local Similarity	85.0%; Pred. No. 2e+03;
Matches 17; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	6459 GGATACCTTTTTCGCTT 6478 
Dn	4 GGATCCTTTCCTTTCCTT 23 
RESULT 2657	
ABST3976/C	
ID	ABST3976 standard; DNA; 23 BP.
XX	
AC	ABST3976;
XX	
DT	09-DEC-2002 (first entry)
XX	
DE	Interleukin-3 mutant-associated DNA sequence #1.
XX	
KM	Interleukin-3; Il-3; db; haematopoietic cell; haematopoietic disorder; acute myelogenous leukemia; ALL; bone marrow transplant; neutropenia; chromocytopenia; aplastic anaemia; Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia; myelodysplastic syndrome; myelofibrosis; viral infection; microbial infection; parasitic infection; stem cell; immune deficiency; immune disorder; rheumatoid arthritis; leukopenia.
KM	
KM	
XX	
OS	Unidentified.
XX	
FN	US6440407-B1.
PD	27-AUG-2002.
XX	
PF	09-DEC-1996; 96US-00764114.
XX	
PR	24-NOV-1992; 92US-00981044. PR 22-NOV-1993; 93WO-US011197. PR 06-APR-1995; 95US-00411795.
XX	
PA	(SEAR/) SEARLE G D.
XX	
PI	Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM; PI Klein BK, McKearn JP, Ollins PO, Paik K, Thomas JW; PI Klein BK, McKearn JP, Ollins PO, Paik K, Thomas JW; DR WPI; 2002-711523/77.
XX	
PX	Ex vivo expansion of stem cells e.g. hematopoietic stem cells for use in treating hematopoietic disorders, comprises culturing the cells in medium having human interleukin-3 mutant polypeptide and harvesting cultured cells.
XX	
PS	Disclosure; Col 21; 215pp; English.
CC	The invention relates to ex vivo expansion of stem cells, comprises
CC	culturing stem cells with a growth medium comprising a human interleukin-
CC	3 (Il-3) mutant polypeptide or a polypeptide comprising an N-terminal
CC	methionine residue, alanine residue or methionine-alanine di-peptide
CC	preceding the Il-3 sequence, and harvesting the cultured stem cells. Also
CC	include are enhancing the efficiency of the transduction of cultured stem
CC	cells by a heterologous gene, comprising: (a) culturing the stem cells



Query Match	0.2%	Score 15.2;	DB 1;	Length 23;
Best Local Similarity	85.0%	Pred. No. 2e+03;		
Matches 17; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

5476 TTTTGTAAAGATTAATTTT 5495

Db 23 TTTTGGGAAAGAAATTTT 4

RESULT 2660  
ABZ57960  
ID ABZ57960 standard; DNA; 23 BP.

AC ABZ57960;

DT 14-APR-2003 (first entry)

Human respiratory chemokine forward PCR primer.

KW G-protein coupled receptor; GPCR; receptor; chemokine; human;  
 KW antiasthmatic; antiinflammatory; antitussive; vaccine; PCR; primer; 88

OS Homo sapiens.

PN WO2003002604-A2.

PD 09-JAN-2003.

PF 25-JUN-2002; 2002WO-EP007021.

PR 26-JUN-2001; 2001US-0300944P.

PA (NOVS ) NOVARTIS AG.

PA (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH

PI Bhatia U, Jones CE, Bouhelal R, Seuwen K, Tenalllon L;

DR WPI; 2003-210243/20.

PT New polypeptide, useful for diagnosing or treating e.g., asthma, chronic obstructive pulmonary disease, emphysema, chronic bronchitis or acute respiratory distress syndrome.

PS Example 7; Page 44; 44pp; English.

CC The present sequence is a forward primer for a polynucleotide encoding a  
CC novel human G-protein coupled receptor (GPCR) that has been characterised  
CC as a respiratory chemokine receptor. RT-PCR was used to determine  
CC expression levels of the GPCR in different tissues. The receptor was  
CC expressed in respiratory tissues and tissues related to  
CC monocyte/macrophage migration/activation, airway remodeling, airway  
CC fibrosis, regulation of epithelial differentiation, regulation of mucus  
CC hypersecretion, regulation of mucociliary clearance, regulation of  
CC inflammation, modulation of neutrophil, T-cell and eosinophil migration  
CC and/or activation, and regulation of epithelial cell or mast cell  
CC activation. GPCR polypeptides (see AB558452-53) and polynucleotides (see  
CC AB57956-57) of the invention may be useful in treatment of asthma,  
CC chronic obstructive pulmonary disease, emphysema, chronic bronchitis,  
CC acute respiratory distress syndrome, cough and acute bronchitis, in  
CC diagnostic assays, and as vaccines

**Sequence 23 BP; 5 A; 7 C; 5 G; 6 T; 0 U; 0 Other;**

Query Match	0.2%	Score 15.2	DB 1	Length 23
Best Local Similarity	85.0%	Pred. No. 2e+03		
Best Match 17; Conservative		0; Mismatches 3;	Indels 0;	Gaps 0;

QY 1189 CTACAGTTGGCCAGGACA 1208

Db 3 CTTCACGTTGGCCATGAACA 22

```
RESULT 2661
ADC03090/c
ID ADC03090 standard; DNA; 23 BP.
```

AC ADC03090;

DT 18-DEC-2003 (first entry)

DE Ex vivo stem-cell expansion related polynucleotide #1.

KM cytosarcoma; antinaeemic; immunomodulator; immunostimulant;  
KM immunosuppressive; antiinflammatory; interleukin agonist 3;  
KM interleukin antagonist 3; gene therapy; ex vivo expansion of stem cell;  
KM modified human interleukin-3; cell proliferation;  
KM acute myelogenous leukaemia cell proliferation; TF-1 cell proliferation;  
KM methylcellulose assay; haematopoietic disorder; cancer;  
KM acute myelogenous leukaemia; B lymphoid cancer; leukopenia; neutropenia;  
KM aplastic anaemia; Chedak-Higashi's syndrome;  
KM systemic lupus erythematosus; myelodysplastic syndrome; myelofibrosis;  
KM bone marrow; blood cell activation; blood cell growth; ds.

OS Synthetic

PN US6479261-B1.

PD 12-NOV-2002.

PF 15-NOV-1995; 95US-00559390.

PR 24-NOV-1992; 92US-00981044.

PR 06-APR-1995; 95US-00411796.

PA ( PHAA ) PHARMACIA CORP.

PI Bauer SC, Abrams MA,

XX

XX

PT Selective ex vivo expansion of stem cells, useful for treating a patient  
PT having hematopoietic disorder, e.g. leukemia, neutropenia or aplastic  
PT anemia, comprises using recombinant human interleukin-3 variant or mutant  
PT proteins.

PS Example 1; SEQ ID NO 1; 288pp; English.

The invention describes selective ex vivo expansion of stem cells comprising separating stem cells from other cells, culturing the cells with modified human interleukin-3 polypeptide with at least 3 times greater cell proliferative activity than native human interleukin-3 in at least one assay selected from the group of acute myelogenous leukaemia cell proliferation, TF-1 cell proliferation, and methylcellulose assay, and harvesting the cultured cells. The method is useful for selective ex vivo expansion of stem cells. The recombinant human interleukin-3 variant or mutant proteins are useful for treating a patient having a haematopoietic disorder, such as cancer (e.g. acute myelogenous leukaemia or certain types of B lymphoid cancers), leukaemia, neutropenia, aplastic anaemia, Chediak-Higashi's syndrome, systemic lupus erythematosus, myelodysplastic syndrome, or myelofibrosis. The interleukin-3 mutants are also useful as antagonists for producing antibodies used in immunoassay and immunotherapy protocols, or for stimulating bone marrow and blood cell activation and growth before infusion into patients. This sequence represents an ex vivo stem cell expansion method associated polynucleotide.

**sq** Sequence 23 BP; 6 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match	0.2%	Score 15.2;	DB 1;	Length 23;
Best Local Similarity	85.0%;	Pred. No. 2e+03;		
Matches 17; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

3735 AGCTTTTAAAGATCACA 3754

Db 21 AGCTTATTTAAAGATCGCTA 2  
|||||  
RESULT 2662  
ADCC2390/c  
ID ADC02390 standard; DNA; 23 BP.  
XX  
AC ADC02390;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Ex vivo stem cell expansion related polynucleotide #1.  
XX  
KW antihaemic; immunomodulator; dermatological; antiinflammatory;  
KW immunosuppressive; cytostatic; haemostatic; antithrombotic; antiarthritic;  
KW osteopathic; gene therapy; cell therapy; ex vivo expansion; stem cell;  
KW human interleukin-3 mutant; htl-3 mutant; haematopoietic disorder;  
KW aplastic anaemia; Chediak-Higashi syndrome; systemic lupus erythematosus;  
KW leukaemia; myelodysplastic syndrome; myelofibrosis; neutropenia;  
KW thrombocytopenia; radiation; chemotherapy; bone marrow suppression;  
KW haematopoietic deficiency; azidothymidine; AZT; alkylating agent;  
KW chloramphenicol; rheumatoid arthritis; immune disorder; infection; de.  
XX  
OS Synthetic.  
XX  
PN US2003103936-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 04-MAR-2002; 2002US-00090182.  
XX  
PR 24-NOV-1992; 92US-00981044.  
PR 22-NOV-1993; 93WO-US011197.  
PR 06-APR-1995; 95US-00411795.  
PR 09-DEC-1996; 96US-00764114.  
XX  
PA (BAUER/) BAUER S. C.  
PA (ABRA/) ABRAMS M. A.  
PA (BRAFO/) BRAFORD-GOLDBERG S. R.  
PA (CAPA/) CAPARON M. H.  
PA (EAST/) EASTON M. M.  
PA (KLEI/) KLEIN B. K.  
PA (MCKE/) MCKEARN J. P.  
PA (OLIN/) OLINS P. O.  
PA (PAIK/) PAIK K.  
PA (THOM/) THOMAS J. W.  
XX  
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM,  
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;  
XX  
DR WPI; 2003-678181/64.  
XX  
PT Ex vivo expansion of stem cells (e.g. hematopoietic cells) for gene  
PT therapy, e.g. using expanded stem cells for treating thrombocytopenia, by  
PT culturing the cells in a growth medium containing a variant or mutant of  
PT human interleukin-3.  
XX  
PS Disclosure; SEQ ID NO 1; 242pp; English.  
XX  
CC The invention describes ex vivo expansion of stem cells comprising  
CC culturing the stem cells with a growth medium containing a human  
CC interleukin-3 (hIL-3) mutant polypeptide. The hIL-3 mutant polypeptide  
CC has a 133, 111, 133 or 111 amino acid sequence (designated hIL-3a, hIL-  
CC 3b, hIL-3c and hIL-3d, respectively), given in the specification. The  
CC method is useful for ex vivo expansion of stem cells for gene therapy.  
CC The expanded stem cells are useful for treating patients with a  
CC hematopoietic disorder e.g. aplastic anaemia, Chediak-Higashi syndrome,  
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome,  
CC myelofibrosis, neutropenia or thrombocytopenia. The method is  
CC particularly useful for ex vivo expansion of hematopoietic cells for use  
CC in: (a) restoring hematopoietic cells to normal amounts in those cases  
CC where the number of cells has been reduced due to diseases or to

CC therapeutic treatments (e.g. radiation or chemotherapy); (b) preventing  
CC or treating bone marrow suppression or haematopoietic deficiencies, which  
CC occur in patients treated with e.g. azidothymidine (AZT), alkylating  
CC agents or chloramphenicol; or (c) treating rheumatoid arthritis or other  
CC immune disorders resulting from viral, microbial or parasitic infection.  
CC This sequence represents an ex vivo stem cell expansion method associated  
CC polynucleotide.  
XX  
SQ Sequence 23 BP; 6 A; 4 C; 4 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3735 AGCTTTTAAAGATCAAA 3754  
Db 21 AGCTTATTTAAAGATCGCTA 2  
|||||  
RESULT 2663  
ADE27638/c  
ID ADE27638 standard; RNA; 23 BP.  
XX  
AC ADE27638;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:582.  
XX  
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;  
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;  
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;  
KW atherosclerosis; cancer; viral infection; drug screening;  
KW genetic engineering; pharmacogenomic; gene mapping; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003070885-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-US004317.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409283P.  
PR 20-SEP-2002; 2002US-0412304P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (RIBO-) RIBOCYME PHARM INC.  
XX  
PI Mcswigen J, Beigelman L, Thompson J;  
XX  
DR WPI; 2003-721687/68.  
XX  
PT New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of obesity or diabetes, downregulates expression of the  
PT stearoyl-CoA desaturase gene.  
XX  
PS Example 3; SEQ ID NO 582; 139pp; English.  
XX  
CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene  
CC by RNA interference. Also described: (1) modulating expression of SCD  
CC genes in cells, tissue explants or organisms by introduction of siNA;  
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and  
CC virucide activities. The siNAs can be used to modulate expression of SCD  
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
 CC They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents an SCD sRNA, which is  
 CC used in the exemplification of the present invention.  
 XX  
 SQ Sequence 23 BP; 7 A; 3 C; 9 G; 0 T; 4 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 23;  
 Best Local Similarity 85.0%; Pred. No. 2e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7230 TATCCCTCTCAAGTCCAGCA 7249  
 DB 22 TCTCCATCTCATGTCAGCA 3  
 RESULT 2664  
 AAF62506 standard; DNA; 24 BP.  
 XX  
 AC AAF62506;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Primer #5.  
 XX  
 KM Guanosine 5'-diphosphofucose; GDP-fucose;  
 KM Guanosine 5'-diphospho-4-keto-6-deoxymannose; GKDM; immunotherapy;  
 KM cardiovascular; infection; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EPI076096-A1.  
 XX  
 PD 14-FEB-2001.  
 XX  
 PF 10-AUG-2000; 2000EP-00117167.  
 XX  
 PR 10-AUG-1999; 99JP-00225889.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Koizumi S, Nagano H, Endo T, Tabata K, Ozaki A;  
 XX  
 DR WPI; 2001-193203/20.  
 XX  
 PT Producing guanosine 5'-diphosphofucose (GDP-fucose) useful as a substrate  
 PT of complex carbohydrates for immunotherapy comprises employing  
 PT microorganisms that convert guanosine 5' diphospho-4-keto-6-deoxymannose  
 PT to GDP-fucose.  
 XX  
 PS Example 2; Page 12; 19pp; English.  
 XX  
 CC The present invention relates to producing guanosine 5'-diphosphofucose  
 CC (GDP-fucose) by employing an enzyme source that is a culture broth of  
 CC microorganisms. GDP-fucose is useful as a synthetic substrate of complex  
 CC carbohydrates that are useful e.g. for immunotherapy for protection  
 CC against cardiovascular diseases, or infections by bacteria or viruses.  
 CC Guanosine 5'-diphospho-4-keto-6-deoxymannose (GKDM) is useful as an  
 CC intermediate for the production of GDP-fucose  
 XX  
 SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 24;  
 Best Local Similarity 85.0%; Pred. No. 2.1e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3109 AAGACTCATGCTTGACAGCT 3128  
 DB 5 AATTCATCTGTTGACAGCT 24

RESULT 2665  
 AAH46618 standard; DNA; 24 BP.  
 ID AAH46618  
 AC AAH46618;  
 XX  
 DT 17-SEP-2001 (first entry)  
 XX  
 DE Synthetic oligonucleotide #21.  
 XX  
 KM Helicobacter pylori; alpha-1,2-fucosyltransferase;  
 KM fucose-containing sugar production; Lewis antigen; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200146400-A1.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 20-DEC-2000; 2000WO-JP009033.  
 XX  
 PR 21-DEC-1999; 99JP-00362243.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Endo T, Koizumi S, Tabata K, Ozaki A;  
 XX  
 DR WPI; 2001-418061/44.  
 XX  
 PT Modified alpha-1,2-fucosyltransferase gene and its expression product for  
 PT efficient production of fucose-containing sugars such as Lewis antigen.  
 XX  
 PS Example 3; Page 63; 63pp; Japanese.  
 XX  
 CC The invention relates to DNA encoding a modified form of the alpha-1,2-  
 CC fucosyltransferase of Helicobacter pylori. The polycytosine sequence, the  
 CC AAAAAG sequence and/or the number of TAA repeats has been modified in  
 CC the DNA sequence. The modified gene is useful in the production of large  
 CC amounts of fucose-containing sugars, such as Lewis antigens for medicinal  
 CC use. The present sequence is an oligonucleotide provided in the  
 CC specification  
 XX  
 SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 24;  
 Best Local Similarity 85.0%; Pred. No. 2.1e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3109 AAGACTCATGCTTGACAGCT 3128  
 DB 5 AATTCATCTGTTGACAGCT 24  
 RESULT 2666  
 ABA03363 standard; DNA; 24 BP.  
 ID ABA03363  
 AC ABA03363;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE B alpha1,2-fucosyltransferase coding sequence related DNA #7.  
 XX  
 KM Alpha1,2-fucosyltransferase; fucose-containing carbohydrate; cytostatic;  
 KM virucide; antibacterial; microbial infection; anticancer; tumour marker;  
 KM primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200177313-A1.  
 XX  
 PD 18-OCT-2001.

```

XX 11-APR-2001; 2001WO-JP003109.
PP
XX
XX 11-APR-2000; 2000JP-00109148.
PR
XX
XX (KYOM ) KYOMA HAKKO KOGYO KK.
PA
XX
PI Endo T, Koizumi S;
XX
XX WPI; 2002-034238/04.
DR
XX
XX Expression of approximately 1.2 fucosyltransferase producing fucose-
PT containing complex carbohydrates as preventives or remedies of e.g.
PT microbial infections, comprises using a transformation procedure.
XX
XX Disclosure; Page 52; 56pp; Japanese.
PS
XX
XX The present invention relates to a method of producing a fucose-
CC containing complex carbohydrate, involving using a culture of a
CC transformant expressing a protein with Bacteroides-originated alpha1,2-
CC fucosyltransferase as enzyme source, receptor complex carbohydrate and
CC guanosine diphosphate fucose in an aqueous medium to transfer fucose to
CC the receptor complex carbohydrate to accumulate the product for
CC isolation. The resulting carbohydrates can be used as preventives or
CC remedies of microbial infections, as tumour markers and as anticancer
CC drugs. The present sequence is an oligonucleotide described in the
CC exemplification of the invention
XX
XX
SQ Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match          0.2%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3109 AAGACTCATGCTTGACAGCT 3128
Db      |||||
5 AATTCATCATGTTGACAGCT 24

RESULT 2667
AAF74926
ID AAF74926 standard; DNA; 27 BP.
XX
XX AAF74926;
AC
XX
XX 23-MAY-2001 (first entry)
DT
XX
XX CD40L poly-A tract sequence SEQ ID NO:23.
DE
XX
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200119844-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 13-SEP-2000; 2000WO-US024966.
PF
XX
XX 13-SEP-1999; 99US-0153625P.
PR
XX
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA
XX
XX Crow MK, Li Y;
PI
XX
XX WPI; 2001-244776/25.
DR
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX

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PS Example 1; Fig 3; 90pp; English.
XX
XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C (I) has antiarthritis,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
XX
SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          0.2%; Score 15.2; DB 1; Length 27;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4020 AAAAAAGAGAGAAAAACAAA 4039
Db      |||||
1 AAAAAAAAAAAAAAAAACAAAA 20

RESULT 2668
AAF74932
ID AAF74932 standard; DNA; 27 BP.
XX
XX AAF74932;
AC
XX
XX 23-MAY-2001 (first entry)
DT
XX
XX CD40L poly-A tract sequence SEQ ID NO:29.
DE
XX
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200119844-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 13-SEP-2000; 2000WO-US024966.
PF
XX
XX 13-SEP-1999; 99US-0153625P.
PR
XX
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA
XX
XX Crow MK, Li Y;
PI
XX
XX WPI; 2001-244776/25.
DR
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
XX Example 1; Fig 3; 90pp; English.
PS
XX
XX The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritis,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX

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SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 27;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4020 AAAAAAGAGAAAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAACAAA 20  
 RESULT 2669  
 AAF74931  
 ID AAF74931 standard; DNA, 27 BP.  
 AC AAF74931;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE CD40L poly-A tract sequence SEQ ID NO:28.  
 XX  
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;  
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200119844-A1.  
 PD 22-MAR-2001.  
 PF 13-SEP-2000; 2000WO-US024966.  
 PS  
 XX 13-SEP-1999; 99US-0153625P.  
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
 XX  
 PI Crow MK, Li Y;  
 DR WPI; 2001-244776/25.  
 XX  
 PT New altered CD40L promoter for use in the study, diagnosis and treatment  
 of a variety of inflammatory disorders and autoimmune diseases, such as  
 PT rheumatoid arthritis.  
 XX  
 PS Example 1; Fig 3; 90pp; English.  
 XX  
 CC The present invention describes an isolated, purified nucleic acid, which  
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
 CC residues 331-455 of the sequence comprising 455 nucleotides given in  
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
 CC to position -125) is replaced with C. (I) has antiarthritis.  
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
 CC be used in gene therapy. (I) is useful in the study, diagnosis and  
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
 CC which is used in an example from the present invention  
 CC  
 SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 27;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4020 AAAAAAGAGAAAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAACAAA 20  
 RESULT 2670  
 AAF74934  
 ID AAF74934 standard; DNA, 27 BP.

XX  
 AC AAF74934;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE CD40L poly-A tract sequence SEQ ID NO:31.  
 XX  
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;  
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200119844-A1.  
 PD 22-MAR-2001.  
 PF 13-SEP-2000; 2000WO-US024966.  
 PS  
 XX 13-SEP-1999; 99US-0153625P.  
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
 XX  
 PI Crow MK, Li Y;  
 DR WPI; 2001-244776/25.  
 XX  
 PT New altered CD40L promoter for use in the study, diagnosis and treatment  
 of a variety of inflammatory disorders and autoimmune diseases, such as  
 PT rheumatoid arthritis.  
 XX  
 PS Example 1; Fig 3; 90pp; English.  
 XX  
 CC The present invention describes an isolated, purified nucleic acid, which  
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
 CC residues 331-455 of the sequence comprising 455 nucleotides given in  
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
 CC to position -125) is replaced with C. (I) has antiarthritis.  
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
 CC be used in gene therapy. (I) is useful in the study, diagnosis and  
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
 CC which is used in an example from the present invention  
 CC  
 SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15.2; DB 1; Length 27;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4020 AAAAAAGAGAAAAACAAA 4039  
 Db 1 AAAAAAAAAAAAAACAAA 20  
 RESULT 2671  
 AAF74920  
 ID AAF74920 standard; DNA, 28 BP.  
 AC AAF74920;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE CD40L poly-A tract sequence SEQ ID NO:17.  
 XX  
 PA Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
 KM diagnosis; antiarthritis; antirheumatic; immunosuppressive;  
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200119844-A1.



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XX 22-MAR-2001.
PD
XX 13-SEP-2000; 2000WO-US024966.
PF
XX 13-SEP-1999; 99US-0153625P.
PR
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
PA
XX Crow MK, Li Y;
PI
XX WPI; 2001-244776/25.
DR
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
XX rheumatoid arthritis.
PS
XX Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic.
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 28;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 4020 AAAAAAGAGAAAAACAAA 4039
Db 2 AAAAAAAAAAAAAAAAAAAAAA 21
RESULT 2672
AAF74906
ID AAF74906 standard; DNA; 28 BP.
XX
XX AAF74906;
AC
XX 23-MAY-2001 (first entry)
DT
XX CD40L poly-A tract sequence SEQ ID NO:3.
DE
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
XX diagnosis; antiarthritic; antirheumatic; immunosuppressive;
XX antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX WO200119844-A1.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US024966.
XX
XX 13-SEP-1999; 99US-0153625P.
XX
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
XX Crow MK, Li Y;
XX
XX WPI; 2001-244776/25.
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT

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PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
XX Example 1; Fig 3; 90pp; English.
PS
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic.
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 15.2; DB 1; Length 28;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 4020 AAAAAAGAGAAAAACAAA 4039
Db 2 AAAAAAAAAAAAAAAAAAAAAA 21
RESULT 2673
AAF74916
ID AAF74916 standard; DNA; 28 BP.
XX
XX AAF74916;
AC
XX 23-MAY-2001 (first entry)
DT
XX CD40L poly-A tract sequence SEQ ID NO:13.
DE
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
XX diagnosis; antiarthritic; antirheumatic; immunosuppressive;
XX antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
XX Homo sapiens.
OS
XX WO200119844-A1.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-US024966.
XX
XX 13-SEP-1999; 99US-0153625P.
XX
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
XX Crow MK, Li Y;
XX
XX WPI; 2001-244776/25.
XX
XX New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
XX rheumatoid arthritis.
PS
XX Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic.
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
XX
XX which elevated expression of CD40L is a factor, e.g., rheumatoid

```

CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
 CC which is used in an example from the present invention  
 XX  
 XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 28;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4020 AAAAAAGAGAAAAA 4039  
 Db 2 AAAAAAAAAAAAAA 21

RESULT 2674  
 AAF74927  
 ID AAF74927 standard; DNA; 28 BP.

XX AAF74927;  
 AC  
 XX 23-MAY-2001 (first entry)  
 DT  
 XX CD40L poly-A tract sequence SEQ ID NO:24.

DE Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
 KM diagnosis; antirheumatic; antirheumatic; immunosuppressive;  
 KM antiinflammatory; inflammatory disease; autoimmune disease; ds.

XX Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

XX 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIIEF RUPTURED & CRIPPLED.

XX Crow MK, L1 Y;

XX WPI; 2001-244776/25.

PT New altered CD40L promoter for use in the study, diagnosis and treatment  
 PT of a variety of inflammatory disorders and autoimmune diseases, such as  
 PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
 CC residues 331-455 of the sequence comprising 455 nucleotides given in  
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
 CC to position -125) is replaced with C. (I) has antirheumatic,  
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
 CC be used in gene therapy. (I) is useful in the study, diagnosis and  
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
 CC which is used in an example from the present invention

XX Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 28;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4020 AAAAAAGAGAAAAA 4039  
 Db 2 AAAAAAAAAAAAAA 21

RESULT 2675  
 AAQ93201/c  
 ID AAQ93201 standard; DNA; 29 BP.

XX AAQ93201;

XX 24-FEB-1996 (first entry)

DE C. perfringens beta 1 toxin PCR primer BetatoxL.

XX Enterotoxin; beta 1 toxin; food poisoning; feces; contamination;  
 KM Clostridium perfringens; polymerase chain reaction; primer; PCR; ss.

XX Synthetic.

XX WO9517521-A2.

XX 29-JUN-1995.

XX 22-DEC-1994; 94WO-EP004292.

XX 22-DEC-1993; 93US-00172026.

XX (INSP ) INST PASTEUR.

XX (CNEVA-) CNEVA CENT NAT ETUD VETERINAIRES & ALIME.

XX Fach P, Guillou J, Popoff M;

XX WPI; 1995-240681/31.

PT New primers for amplification of Clostridium perfringens toxin genes -  
 PT and new beta 2 toxin gene, used to detect and quantify C. perfringens in  
 PT e.g. food and faecal samples.

PS Example 7; Page 28; 43pp; English.

XX The presence of beta 1 and beta 2 toxin genes was examined by PCR in a  
 CC series of type B and C Clostridium perfringens strains. For beta 2 gene  
 CC amplification, primers P319 and P320 (AAQ93199-200) were used; primers  
 CC BetatoxL and BetatoxR (AAQ93201-02) were used for the beta 1 gene. The 3  
 CC B strains examined possessed the beta 1 gene. Type C strains had either  
 CC the beta 2 gene, or the beta 1 gene, or both

XX Sequence 29 BP; 5 A; 0 C; 6 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 15.2; DB 1; Length 29;  
 Best Local Similarity 71.4%; Pred. No. 2.5e+03;  
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 7017 CTTACGAGGAAATAGMAACCTCC 7044  
 Db 29 CTTCAAAAAAAAAATTAATAAACCTCC 2

RESULT 2676  
 AAQ20018/c  
 ID AAQ20018 standard; DNA; 15 BP.

XX AAQ20018;

XX 01-APR-1992 (first entry)

DE Cross-linking agent 132 binds to HIV target DNA.

XX deoxyribonucleic acid; major groove; ethanoamino group;  
 KM aziridinylcytosine; cross-linking group; human immunodeficiency virus;  
 KM ss.

XX Synthetic.

OS Key Location/Qualifiers  
 XX modified\_base 2  
 FT /\*tag= a

```

FT      modified_base 4/mod_base= m5c
FT      /*tag= b
FT      /mod_base= m5c
FT      modified_base 6/*tag= c
FT      /mod_base= m5c
FT      modified_base 13/*tag= d
FT      /mod_base= m5c
FT      modified_base 15/*tag= e
FT      /mod_base= OTHER
FT      /note= "NA4-ethanocytosine"
XX
XX      W09118997-A.
XX
XX      12-DEC-1991.
XX
XX      25-MAY-1990; 90US-00529346.
XX
XX      25-MAY-1990; 90US-00529346.
XX      14-JAN-1991; 91US-00640654.
XX
XX      (GILE-) GILEAD SCIE INC.
XX
XX      Matteucci MD, Krawczyk S;
XX      WPI; 1992-007480/01.
XX
XX      New sequence-specific non-photo-activated crosslinking agents - bind to
XX      the major groove of duplex DNA and are esp. useful for treating latent
XX      infections e.g. HIV.
XX
XX      Example 4; Page 24; 42pp; English.
XX
XX      This sequence is designed to bind to the HIV target sequence 5'-
XX      AGAGAGAGAGAGAGAG-3' and to covalently cross-link to it via the NA4-
XX      ethanocytosine (aziridinyl) group. See also AAQ20009-Q20025
XX
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4017 GAGAGAGAGAGAGAGAG 4031
Db      15 GAGAGAGAGAGAGAGAG 1
XX
RESULT 2677
AAQ20017/C
ID      AAQ20017 standard; DNA; 15 BP.
XX
XX      AAQ20017;
XX
XX      01-APR-1992 (first entry)
XX
XX      Cross-linking agent 131 binds to HIV target DNA.
XX
XX      deoxyribonucleic acid; major groove; ethanocytosine group;
XX      aziridinylcytosine; cross-linking group; human immunodeficiency virus;
XX      ss.
XX
XX      Synthetic.
XX
XX      Key
XX      Location/Qualifiers
XX      modified_base 2/*tag= a
XX      /mod_base= m5c
XX      modified_base 4/*tag= b

```

```

FT      modified_base 6/mod_base= m5c
FT      /*tag= c
FT      /mod_base= m5c
FT      modified_base 13/*tag= d
FT      /mod_base= m5c
FT      modified_base 15/*tag= e
FT      /mod_base= m5c
XX
XX      W09118997-A.
XX
XX      12-DEC-1991.
XX
XX      25-MAY-1990; 90US-00529346.
XX
XX      25-MAY-1990; 90US-00529346.
XX      14-JAN-1991; 91US-00640654.
XX
XX      (GILE-) GILEAD SCIE INC.
XX
XX      Matteucci MD, Krawczyk S;
XX      WPI; 1992-007480/01.
XX
XX      New sequence-specific non-photo-activated crosslinking agents - bind to
XX      the major groove of duplex DNA and are esp. useful for treating latent
XX      infections e.g. HIV.
XX
XX      Example 4; Page 24; 42pp; English.
XX
XX      This sequence is designed to bind to the HIV target sequence 5'-
XX      AGAGAGAGAGAGAGAG-3'. See also AAQ20009-Q20025
XX
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4017 GAGAGAGAGAGAGAGAG 4031
Db      15 GAGAGAGAGAGAGAGAG 1
XX
RESULT 2678
AAQ33752
ID      AAQ33752 standard; DNA; 15 BP.
XX
XX      AAQ33752;
XX
XX      25-MAR-2003 (revised)
XX      02-FEB-1993 (first entry)
XX
XX      Microsatellite sequence from clone TGLA162.
XX
XX      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX      genetic mapping; traits; amplification; ss.
XX
XX      Bos taurus.
XX
XX      W09213102-A1.
XX
XX      06-AUG-1992.
XX
XX      15-JAN-1992; 92MO-US000340.
XX      15-JAN-1991; 91US-00642342.
XX      (GENM-) GENMARK.
XX      PA
XX      PI      George M, Massey JM;

```

```

XX DR WPI, 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 231; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 15 BP; 5 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCA 7429
Db 1 GCAGCAGCAGCAGCA 15
RESULT 2679
AAQ30250/c
ID AAQ30250 standard; DNA; 15 BP.
XX AC AAQ30250;
XX DT 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX DE Oligomer HIV132 for forming triplex with HIV target duplex.
XX KW Human immunodeficiency virus; AIDS; modified; HIV; hepatitis; herpes;
KW hepatitis; malignancy; inflammation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FH modified_base 2 /*tag= a
FT /*mod_base= m5c
FT modified_base 4 /*tag= b
FT /*mod_base= m5c
FT modified_base 6 /*tag= c
FT /*mod_base= m5c
FT modified_base 13 /*tag= d
FT /*mod_base= m5c
FT modified_base 15 /*tag= e
FT /*mod_base= OTHER
FT /*note= "OTHER= N4 N4 ethanocytosine"
XX PN W09209705-A1.
XX PD 11-JUN-1992.

```

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XX PF 25-NOV-1991; 91WO-US008811.
XX PR 23-NOV-1990; 90US-00617907.
PR 18-JUN-1991; 91US-00643382.
PR 08-APR-1991; 91US-00683420.
PR 17-APR-1991; 91US-00685444.
PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX PA (GILE-) GILEAD SCI INC.
XX PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX DR WPI, 1992-217083/26.
XX PT New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX PS Claim 12; Page 65; 77pp; English.
XX CC The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is an HIV
CC target duplex congy. a purine-rich region concentrated on one chain of
CC the duplex. The oligomer, and others like it are useful in diagnosis and
CC therapy of diseases characterised by specific DNA duplex targets, e.g.
CC HIV, hepatitis, herpes, malignant tumours and inflammation. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. Additional
CC modifications, such as altered inter- nucleotide linkages may also be
CC incorporated, rendering the oligomer e.g. stable to nuclease activity.
CC The oligomer is able to inhibit gene expression, as verified by in vitro
CC systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX SQ Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 0.24; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4017 GAGAAAAAAGAGAGA 4031
Db 15 GAGAAAAAAGAGAGA 1
RESULT 2680
AAQ30249/c
ID AAQ30249 standard; DNA; 15 BP.
XX AC AAQ30249;
XX DT 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX DE Oligomer HIV131 for forming triplex with HIV target duplex.
XX KW Human immunodeficiency virus; AIDS; modified; HIV; hepatitis; herpes;
KW hepatitis; malignancy; inflammation; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FH modified_base 2 /*tag= a
FT /*mod_base= m5c
FT modified_base 4 /*tag= b
FT /*mod_base= m5c
FT modified_base 6 /*tag= b
FT /*mod_base= m5c

```

```
FT      /*tag= c
FT      /mod_base= m5c
FT      modified_base
FT      /*tag= d
FT      /mod_base= m5c
FT      modified_base
FT      /*tag= e
FT      /mod_base= m5c
XX      W09209705-A1.
XX      11-JUN-1992.
XX      25-NOV-1991; 91WO-US008811.
XX      23-NOV-1990; 90US-00617907.
XX      18-JAN-1991; 91US-00643382.
XX      08-APR-1991; 91US-00683420.
XX      17-APR-1991; 91US-00686544.
XX      17-APR-1991; 91US-00686546.
XX      17-APR-1991; 91US-00686547.
XX      27-SEP-1991; 91US-007676733.
XX      (GILE-) GILEAD SCI INC.
XX      PI
XX      Firehler B, Krawczyk S, Matteucci MD, Milligan J;
XX      WPI; 1992-217083/26.
XX      New oligomers contg. modified bases - which form a triplex with G-C
XX      doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX      herpes malignancy and inflammation.
XX      PS
XX      Claim 12; Page 65; 77pp; English.
XX      CC
XX      The synthetic oligomer is capable of forming a triplex at physiological
XX      pH with a purine rich target sequence by coupling into the major groove
XX      of the duplex. The specific target sequence of this oligomer is an HIV
XX      target duplex contg. a purine-rich region concentrated on one chain of
XX      the duplex. The oligomer, and others like it are useful in diagnosis and
XX      therapy of diseases characterised by specific DNA duplex targets, e.g.
XX      HIV, hepatitis, herpes, malignant tumours and inflammation. The triple
XX      helices form under mild conditions thus assays may be carried out without
XX      subjecting the test specimen to harsh conditions. Additional
XX      modifications, such as altered inter-nucleotide linkages may also be
XX      incorporated, rendering the oligomer e.g. stable to nuclease activity.
XX      CC The oligomer is able to inhibit gene expression, as verified by in vitro
XX      CC systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-
XX      CC 2003 to correct PN field.)
XX      SQ
XX      Sequence 15 BP; 0 A; 5 C; 0 G; 10 T; 0 U; 0 Other;
XX      Query Match 0.2%; Score 15; DB 1; Length 15;
XX      Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Oy
XX      4017 GAGAAAAAGAGAGA 4031
XX      |||||
XX      15 GAGAAAAAGAGAGA 1
XX      Db
XX      RESULT 2681
XX      AAQ79185/c
XX      ID AAQ79185 standard; DNA; 15 BP.
XX      AC
XX      AAQ79185;
XX      XX
XX      25-MAR-2003 (revised)
XX      DT 21-JUN-1995 (first entry)
XX      XX
XX      Nuclease resistant oligonucleotide.
XX      DB
XX      Nuclease resistant oligonucleotide; inhibition of gene expression;
XX      XX
```

```
KW      9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX      f
XX      Synthetic.
XX      OS
XX      Key
XX      Location/Qualifiers
XX      modified_base
XX      13
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note="9-methyl-acyclo-adenosine"
XX      FT
XX      FT
XX      W09422864-A1.
XX      13-OCT-1994.
XX      PD
XX      21-MAR-1994; 94WO-US002995.
XX      PF
XX      30-MAR-1993; 93US-00040326.
XX      PR
XX      (STER ) STERLING WINTHROP INC.
XX      PA
XX      Cook PD, Delecki DJ, Guinasso C;
XX      FT
XX      WPI; 1994-333078/41.
XX      DR
XX      New acyclic nucleoside analogues - used to prepare nuclease resistant
XX      PT oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX      PS
XX      Example 11; Page 20; 37pp; English.
XX      XX
XX      AAQ79182-079186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX      CC nucleoside analogues which inhibit nuclease degradation. The nuclease
XX      CC resistant oligonucleotides can themselves be used to inhibit gene
XX      CC expression as antisense agents, in nucleic acid sequencing and diagnostic
XX      CC assays. (Updated on 25-MAR-2003 to correct PN field.)
XX      CC
XX      SQ
XX      Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX      Query Match 0.2%; Score 15; DB 1; Length 15;
XX      Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      Oy
XX      4464 TTTT TTTT TTTT TTTT 4478
XX      |||||
XX      15 TTTT TTTT TTTT TTTT 1
XX      Db
XX      RESULT 2682
XX      AAQ79184/c
XX      ID AAQ79184 standard; DNA; 15 BP.
XX      AC
XX      AAQ79184;
XX      XX
XX      25-MAR-2003 (revised)
XX      DT 21-JUN-1995 (first entry)
XX      XX
XX      Nuclease resistant oligonucleotide.
XX      DB
XX      Nuclease resistant oligonucleotide; inhibition of gene expression;
XX      KW 9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX      KW
XX      Synthetic.
XX      OS
XX      Key
XX      Location/Qualifiers
XX      modified_base
XX      14
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note="9-methyl-acyclo-adenosine"
XX      FT
XX      FT
XX      W09422864-A1.
XX      13-OCT-1994.
XX      PD
XX      21-MAR-1994; 94WO-US002995.
XX      PF
```

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XX 30-MAR-1993; 93US-00040326.
XX (STER ) STERLING WINTHROP INC.
XX Cook PD, Delecki DJ, Guinasso C;
XX WPI, 1994-333078/41.
XX New acyclic nucleoside analogues - used to prepare nuclease resistant
XX oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX Example 10; Page 20; 37pp; English.
XX AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
XX nucleoside analogues which inhibit nuclease degradation. The nuclease
XX resistant oligonucleotides can themselves be used to inhibit gene
XX expression as antisenese agents, in nucleic acid sequencing and diagnostic
XX assays. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 15 TTTT TTTT TTTT TTTT 1
RESULT 2683
AAT52136
ID AAT52136 standard; RNA; 15 BP.
XX
XX AAT52136;
AC
AC 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICM hammerhead ribozyme target sequence (nt. position 2910).
DE
DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KM gene expression; downregulation; interleukin-5; IL-5; ICM-1;
KM intercellular adhesion molecule; rel A; tumour necrosis factor;
KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KM Philadelphia chromosome; inflammatory leukæmia; CML; cancer;
KM atherosclerosis; myocardial infarction; autoimmune disease;
KM transplant rejection; rheumatoid arthritis; psoriasis;
KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KM human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KM ss.
XX
XX Homo sapiens.
OS
XX ID AAT52138 standard; RNA; 15 BP.
XX
XX W09523225-A2.
XX
XX 31-AUG-1995.
PD
PD 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.

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PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 94US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpelsky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Ueman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 175; 407pp; English.
XX
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICM-1 target sequences and thereby
XX inhibit ICM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 UUUUUUUUUUUUUU 15
RESULT 2684
AAT52138
ID AAT52138 standard; RNA; 15 BP.
XX
XX AAT52138;
AC
AC 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
XX Human ICM hammerhead ribozyme target sequence (nt. position 2911).
DE
DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KM gene expression; downregulation; interleukin-5; IL-5; ICM-1;
KM intercellular adhesion molecule; rel A; tumour necrosis factor;
KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KM Philadelphia chromosome; inflammatory leukæmia; CML; cancer;
KM atherosclerosis; myocardial infarction; autoimmune disease;
KM transplant rejection; rheumatoid arthritis; psoriasis;
KM

```

KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 ss.  
 XX Homo sapiens.  
 OS  
 XX MO9523225-A2.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX  
 XX 23-FEB-1995; 95WO-IB000156.  
 PF  
 XX 23-FEB-1994; 94US-00201109.  
 PR 23-FEB-1994; 94US-00218934.  
 PR 29-MAR-1994; 94US-00222795.  
 PR 04-APR-1994; 94US-00224483.  
 PR 07-APR-1994; 94US-00227958.  
 PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319492.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00324847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Stinchcomb DF, Chowrira B, Dierenzo A, Draper KG, Dudycz LM;  
 PI Grimm S, Kapelsky A, Kleich K, Matulic-Adamic J, McGwisgen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Siedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Wolf T;  
 XX  
 DR WPI; 1995-351090/45.  
 XX  
 PT Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 XX  
 PS Claim 2; Page 175; 407pp; English.  
 XX  
 CC The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesized with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 CC  
 XX  
 XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
 Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT 4478

DB 1 UUUUUUUUUUUUUU 15  
 RESULT 2685  
 AA06037  
 ID AA06037 standard; DNA; 15 BP.  
 XX  
 AC AA06037;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Oligonucleotide-anthracycline or anthracycline conjugate #3.  
 XX Anthracycline conjugate; anthracycline; triple-helix; tumour; virus;  
 KW intercalation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "conjugated via a linker molecule to anthracycline  
 FT or anthracycline"  
 XX  
 XX MO9733897-A1.  
 XX  
 PD 18-SEP-1997.  
 XX  
 XX 12-MAR-1997; 97WO-EP001246.  
 PF  
 XX 13-MAR-1996; 96IT-FI000044.  
 PR  
 XX (CMDR ) CONSIGLIO NAZ DELLE RICERCHE.  
 PA  
 PI Garbei AM, Bonazzi S, Zanello S, Capobianco ML, Gianini G;  
 PI Arcamone F;  
 PI  
 DR WPI; 1997-470805/43.  
 XX  
 XX  
 PT New oligo:nucleotide-anthracycline or anthracycline conjugates - which  
 PT form triple-helix complexes with DNA, used for targeting e.g. tumours or  
 PT viruses.  
 XX  
 PS Claim 7; Page 19; 25pp; English.  
 XX  
 CC This sequence represents a specifically claimed example of a conjugate  
 CC which consists of a natural or modified oligonucleotide capable of  
 CC forming a triple-helix complex with a double stranded DNA, linked, via an  
 CC appropriate linker, to the aglycone-moiety of an anthracycline or to an  
 CC anthracycline. The conjugates form triple-helix complexes with DNA of  
 CC higher stability compared with corresponding oligonucleotides, due to the  
 CC intercalation of the aglycone moiety in the DNA target. They can be used  
 CC against activated oncogenes in the treatment of tumours and against the  
 CC proviral genome of retroviruses. (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 XX  
 XX Sequence 15 BP; 10 A; 0 C; 5 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4017 GAGAAAAAGAGAGA 4031  
 DB 1 GAGAAAAAGAGAGA 15  
 RESULT 2686  
 AA06038/c  
 ID AA06038 standard; DNA; 15 BP.  
 XX





XX	AAV01603;
AC	
XX	25-MAR-2003 (revised)
DT	31-MAR-1998 (first entry)
XX	
DE	Oligonucleotide containing phosphoramidate linkages.
XX	
KM	phosphoramidate linkage; solid phase synthesis; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..15
FT	/tag= a
FT	/note= "these residues have N3' ->P5' phosphoramidate linkages"
PN	MO9731009-A1.
XX	
PD	28-AUG-1997.
XX	
PF	14-JUN-1996; 96WO-US010418.
XX	
PR	21-FEB-1996; 96US-00603566.
XX	
PA	(LYNX-) LYNX THERAPEUTICS INC.
XX	
PI	Hirschbein BL, Fearon KL, Graynov SM, McCurdy SN, Nelson JS,
PI	Schultz RG;
DR	WPI; 1997-435080/40.
XX	
PT	Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT	immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT	phosphoramidite then oxidation, useful as research, diagnostic and
PT	therapeutic agents.
XX	
PS	Disclosure; Page 28; 60pp; English.
XX	
CC	A new method is provided for the synthesis of oligonucleotides having N3'
CC	->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC	protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC	amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC	phosphoramidate monomer to form an internucleoside N3' -> P5'
CC	phosphoramidate link; (d) oxidising this link to phosphoramidate; and
CC	optionally repeating steps (b)-(d) until the required oligonucleotide is
CC	completed. This method provides better yields with lower reagent
CC	consumption than known processes, and can be operated on a large scale.
CC	The obtained oligos, containing phosphoramidate linkages, have favourable
CC	binding properties, nuclease resistance and solubility, and are useful as
CC	research, diagnostic and therapeutic agents. The present sequence is an
CC	example of an oligonucleotide in which N3' ->P5' phosphoramidate linkages
CC	have been introduced by the new method. (Updated on 25-MAR-2003 to
CC	correct PR field.)
XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX	
QY	Query Match 0.2%; Score 15; DB 1; Length 15;
XX	Best Local Similarity 100.0%; Pred. NO. 1.3e+03;
XX	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX	TTTT TTTT TTTT TTTT TTTT 15
XX	
RESULT 2689	
AAV07431	
ID	AAV07431 standard; DNA; 15 BP.
AC	AAV07431;
XX	

```

DE 27-OCT-1998 (first entry)
XX Synthetic peptide-labeled oligonucleotide primer.
XX
XX oligonucleotide; peptide; conjugate; release tag compound;
KM mass spectrometry; detection; identification; diagnosis; primer; ss.
XX
XX Synthetic.
OS
XX
XX WO9826095-A1.
XX
XX 18-JUN-1998.
XX
XX 10-DEC-1997; 97WO-US022639.
XX
XX 10-DEC-1996; 96US-0033037P.
XX
XX 16-MAY-1997; 97US-0046719P.
XX
XX (GENE-) GENETRACE SYSTEMS INC.
XX
XX Montforte JA, Becker CH, Pollart DJ, Shaler TA,
XX
XX WPI, 1998-348547/30.
XX
XX
XX New release tag compounds for detecting target molecule(s) - comprising a
XX reactive group, a release group and a releasable non-volatile mass label
XX detectable by mass spectrometry.
XX
XX
XX Example 3; Page 92; 170pp; English.
XX
XX
XX The sequence is that of an oligonucleotide primer which was produced as
XX part of an oligonucleotide peptide conjugate as an example of a release
XX tag compound (RTC). These comprise a reactive group, a release group and
XX a non-volatile mass label comprising a synthetic polymer or biopolymer
XX detectable by mass spectrometry. The RTCs can be used as probes for the
XX detection of TMs. They can be used for e.g. identification of gene
XX sequences, identification of non-coding nucleotide sequences,
XX identification of mutations within a gene or protein sequence, detection
XX of metals, detection of toxins, detection of receptors on an organism or
XX a cell, characterisation of antibody-antigen interactions, enzyme-
XX substrate interactions and characterisation of ligand interactions.
XX
XX Multiplex applications include multiple pathogen diagnostics, multi-gene
XX genotyping, clone and gene mapping, and gene expression analysis. The
XX RTCs permit the ready detection of releasable mass labels by mass
XX spectrometry. The releasable mass labels permit the multiplexing of tens,
XX hundreds and perhaps even thousands of different mass labels that can be
XX used to uniquely identify each desired target
XX
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. NO. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX |||||
XX 1 TTTTTTTTTTTTTT 15
XX
XX
XX RESULT 2690
XX AAT86675
XX AAT86675 standard; DNA; 15 BP.
XX
XX AAT86675;
XX
XX 04-JUN-1998 (first entry)
XX
XX Oligonucleotide linked to polyacrylamide.
XX
XX Capillary affinity gel electrophoresis; separation; polymer-gel;
XX polyacrylamide; ss.
XX
XX

```

```

OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1
FT /'cag= a
FT /note= "Thymine at 5' end attached to a polyacrylamide
FT gel via a linking group"
XX
XX MO9745721-A1.
XX
XX 04-DEC-1997.
XX
XX 23-MAY-1997; 97MO-EP002647.
XX
XX 24-MAY-1996; 96CH-00001320.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX Muscate A, Paulus A, Natt F;
XX
XX WPI; 1998-041763/04.
XX
XX Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors for
XX target molecules are bound.
XX
XX Example A1; Page 22; 41pp; English.
XX
XX This sequence represents an oligonucleotide receptor molecule covalently
XX bound to a polyacrylamide gel via a linking group. The invention relates
XX to selective separation of electrically charged target molecules in an
XX analytical mixture. It comprises capillary affinity gel electrophoresis
XX using a capillary tube which is at least partly filled with a polymer
XX gel. Receptors for target molecules are covalently bound to the polymer.
XX An electric field of at least 50 volts/cm is applied. The capillary tube
XX is charged with the analytical mixture. In a first separation stage, the
XX target molecules in the mixture are bound to the receptors and the
XX remaining components are eluted, optionally whilst splitting open. In a
XX second stage, the elution conditions are changed, optionally whilst
XX so that the affinity of the target molecules for the receptor is
XX eliminated and the target molecules are eluted and detected, optionally
XX whilst splitting open. The process is useful for selective separation
XX and/or determination of charged organic compounds, such as
XX oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
XX isolation of specific proteins and DNA molecules, purification of
XX antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity than
XX prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2691
XX AAT86605
XX ID AAT86605 standard; DNA; 15 BP.
XX
XX AAT86605;
XX
XX 04-JUN-1998 (first entry)
XX
XX Oligonucleotide separated by capillary affinity gel electrophoresis.
XX

```

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KM Capillary affinity gel electrophoresis; separation; polymer-gel;
KM polyacrylamide; ss.
XX
XX Synthetic.
XX
XX MO9745721-A1.
XX
XX 04-DEC-1997.
XX
XX 23-MAY-1997; 97MO-EP002647.
XX
XX 24-MAY-1996; 96CH-00001320.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX Muscate A, Paulus A, Natt F;
XX
XX WPI; 1998-041763/04.
XX
XX Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors for
XX target molecules are bound.
XX
XX Example D3; Page 25; 41pp; English.
XX
XX A mixture of oligonucleotides (AAT86604-7) were separated by a new
XX process using capillary affinity gel electrophoresis. The invention
XX relates to selective separation of electrically charged target molecules
XX in an analytical mixture. It comprises capillary affinity gel
XX electrophoresis using a capillary tube which is at least partly filled
XX with a polymer gel. Receptors for target molecules are covalently bound
XX to the polymer. An electric field of at least 50 volts/cm is applied. The
XX capillary tube is charged with the analytical mixture. In a first
XX separation stage, the target molecules in the mixture are bound to the
XX receptors and the remaining components are eluted, optionally whilst
XX splitting open. In a second stage, the elution conditions are changed,
XX optionally in stages, so that the affinity of the target molecules for
XX the receptor is eliminated and the target molecules are eluted and
XX detected, optionally whilst splitting open. The process is useful for
XX selective separation and/or determination of charged organic compounds,
XX such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
XX for isolation of specific proteins and DNA molecules, purification of
XX antibodies, analysis of antisense compounds or screening for enzyme
XX inhibitors. The process achieves higher resolution and selectivity than
XX prior art processes, especially in the case of complex biological
XX analytical mixtures. It has high sensitivity, even with small amounts of
XX samples. The derivatised polymers may be synthesised specifically using
XX standard methods
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2692
XX AAX00787
XX ID AAX00787 standard; DNA; 15 BP.
XX
XX AAX00787;
XX
XX 13-APR-1999 (first entry)
XX
XX N3-P5 phosphoramidate oligonucleotide #3.
XX
XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
XX Synthetic.
XX

```

```

XX Key Location/Qualifiers
FH misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
  internucleotide linkages"
XX US5859233-A.
XX 12-JAN-1999.
XX 20-DEC-1996; 96US-00771789.
XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX GYAZNOV SM, NELSON JS, MCCURDY SN, HIRSCHBEIN BL, SCHULTZ RG;
XX FEARON KL;
XX WPI; 1999-120007/10.
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX Example 10; Col 33; 34pp; English.
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2693
XX AAX00788/C
XX ID AAX00788 standard; DNA; 15 BP.
XX AAX00788;
XX 13-APR-1999 (first entry)
XX N3-P5 phosphoramidate oligonucleotide #4.
XX Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_difference 1..15
XX /tag= a
XX /note= "contains internucleotide N3-P5 phosphoramidate
  internucleotide linkages"
XX US5859233-A.
XX 12-JAN-1999.
XX 20-DEC-1996; 96US-00771789.

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```

XX 21-FEB-1996; 96US-00603566.
XX 14-JUN-1996; 96US-00663918.
XX (LYNX-) LYNX THERAPEUTICS INC.
XX GYAZNOV SM, NELSON JS, MCCURDY SN, HIRSCHBEIN BL, SCHULTZ RG;
XX FEARON KL;
XX WPI; 1999-120007/10.
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX the synthesis of oligo-nucleotide(s).
XX Example 10; Col 33; 34pp; English.
XX This sequence represents an example of an oligonucleotide containing
XX novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX sequence is generated synthetically by using an amine-exchange reaction
XX of phosphoramidites in which a deprotected 3'-amino group of an
XX oligonucleotide chain is exchanged for the amino portion of a 5'-
XX phosphoramidite with a protected 3' amino group. The resulting
XX phosphoramidite internucleotide linkage is oxidised to form a stable
XX protected phosphoramidate linkage
XX
XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX 15 TTTT TTTT TTTT TTTT 1
XX
XX RESULT 2694
XX AAX84262/C
XX ID AAX84262 standard; DNA; 15 BP.
XX AAX84262;
XX 08-SEP-1999 (first entry)
XX PCR primer for human Nck associated protein 1 coding sequence.
XX Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;
XX therapy; PCR primer; ss.
XX Synthetic.
XX Homo sapiens.
XX WO931239-A1.
XX 24-JUN-1999.
XX 14-DEC-1998; 98WO-JP005646.
XX 15-DEC-1997; 97JP-00363183.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX (SAKA/) SAKAKI Y.
XX SAKAKI Y;
XX WPI; 1999-395181/33.
XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of
XX Alzheimer's disease.
XX Example 1; Page 77; 90pp; Japanese.
XX This sequence represents a PCR primer used to isolate DNA encoding the

```

CC human Nck associated protein 1 (Napl) of the invention. Nap1 inhibits  
 CC apoptosis. The protein can be used in the investigation, diagnosis and  
 CC treatment (e.g. by gene therapy) of Alzheimer's disease  
 SX  
 SQ Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7413 CAGCAGCAGCAGCAG 7427  
 DB 15 CAGCAGCAGCAGCAG 1  
 RESULT 2695  
 AA261  
 ID AA261 standard; DNA; 15 BP.  
 XX  
 AC AAX84261;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE PCR primer for human Nck associated protein 1 coding sequence.  
 XX  
 KM Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
 KM therapy; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 PN WO9931239-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-JP005646.  
 XX  
 PR 15-DEC-1997; 97JP-00363183.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA (SAXA/) SAKAKI Y.  
 XX  
 PI Sakaki Y;  
 PI  
 DR WPI; 1999-395181/33.  
 XX  
 PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of  
 PT Alzheimer's disease.  
 XX  
 PS Example 1; Page 77; 90pp; Japanese.  
 XX  
 CC This sequence represents a PCR primer used to isolate DNA encoding the  
 CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits  
 CC apoptosis. The protein can be used in the investigation, diagnosis and  
 CC treatment (e.g. by gene therapy) of Alzheimer's disease  
 CC  
 SQ Sequence 15 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7413 CAGCAGCAGCAGCAG 7427  
 DB 1 CAGCAGCAGCAGCAG 15  
 RESULT 2696  
 AA26369/c  
 ID AA26369 standard; DNA; 15 BP.  
 XX  
 AC AA26369;  
 XX

DT 22-FEB-2000 (first entry)  
 XX  
 XX PCR primer used to amplify mouse testatin cDNA.  
 DE  
 XX  
 XX Mouse; cystatin-related protein; testatin; testis formation;  
 KM foetal gonad; testis tumour growth; tumour inhibiting cystatin;  
 KM genital tumour; testis malformation; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 OS  
 PN WO958565-A1.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 06-MAY-1999; 99WO-SF000764.  
 XX  
 XX  
 PR 08-MAY-1998; 98SE-00001617.  
 XX  
 PA (KARO-) KAROLINSKA INNOVATIONS AB;  
 PI Nordqvist K, Toehonen V;  
 PI  
 DR WPI; 2000-039071/03.  
 XX  
 PT Novel cystatin-related protein used for testis tumor diagnostics and  
 PT treatment.  
 XX  
 PS Example 1; Page 15; 37pp; English.  
 XX  
 CC The present sequence represents PCR primer used to amplify cDNA encoding  
 CC a mouse cystatin-related protein, designated testatin. The protein is  
 CC capable of inducing testis formation in foetal gonads. It is highly  
 CC probable that the protein inhibits testis tumour growth because of  
 CC structural and functional similarities with tumour inhibiting cystatins.  
 CC The cystatin-related protein testatin may be useful for inducing testis  
 CC formation in foetal gonads. Testatin polynucleotides are useful as a  
 CC source of primers and probes, which can be used to detect the presence of  
 CC testatin nucleic acid molecules in a sample. The testatin  
 CC polynucleotides, polypeptides, and compositions can be used for treating  
 CC genital tumours and may also be useful for creating a model for studying  
 CC testis malformations  
 CC  
 SQ Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7413 CAGCAGCAGCAGCAG 7427  
 DB 15 CAGCAGCAGCAGCAG 1  
 RESULT 2697  
 AA261854  
 ID AA261854 standard; RNA; 15 BP.  
 XX  
 AC AA261854;  
 XX  
 DT 28-MAR-2000 (first entry)  
 XX  
 DE HCV 3' non core region substrate for Hammerhead ribozyme HCV-3-118.  
 XX  
 KM Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;  
 KM cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;  
 KM autoimmune disease; ss.  
 XX  
 OS Hepatitis C virus.  
 OS  
 PN WO9955847-A2.  
 PN  
 PD 04-NOV-1999.

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XX 26-APR-1999; 99WO-US009027.
PE
XX 27-APR-1998; 98US-0083217P.
PR
XX 18-SEP-1998; 98US-0100842P.
PR
XX 25-FEB-1999; 99US-00257608.
PR
XX 23-MAR-1999; 99US-00274553.
PR
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
PI WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 49; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC HCV sequence was screened for optimal ribozyme target sites using a
CC computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases. The
CC ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred.No.1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
XXXXXXXXXXXXXXXXXXXX
RESULT 2698
AAZ64910
ID AAZ64910 standard; RNA; 15 BP.
XX
XX AAZ64910;
AC
XX 28-MAR-2000 (first entry)
DT
XX
XX Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
DE
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
XX Hepatitis C virus.
OS
XX
XX W09955847-A2.
FN
XX
XX 04-NOV-1999.
PD
XX
XX 26-APR-1999; 99WO-US009027.
PE
XX 27-APR-1998; 98US-0083217P.
PR
XX 18-SEP-1998; 98US-0100842P.
PR
XX 25-FEB-1999; 99US-00257608.
PR
XX 23-MAR-1999; 99US-00274553.
XX
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PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
PI WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
XX Claim 1; Page 102; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer.
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred.No.1.3e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 UUUUUUUUUUUUUU 15
XXXXXXXXXXXXXXXXXXXX
RESULT 2699
AAA46502
ID AAA46502 standard; cDNA; 15 BP.
XX
XX AAA46502;
AC
XX 04-SEP-2000 (first entry)
DT
XX
XX PCR primer used to amplify DNA encoding an endo-beta-mannanase.
DE
XX Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
XX
XX Coffea arabica.
OS
XX
XX W0200028046-A1.
FN
XX
XX 18-MAY-2000.
PD
XX 28-OCT-1999; 99WO-EP008314.
PE
XX 11-NOV-1998; 98EP-00203742.
PR
XX (NEST ) SOC PROD NESTLE SA.
PA
XX Marraccini P, Rogers J;
PI
XX
XX WPI; 2000-399535/34.
DR
XX
XX New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
PS Disclosure; Page 32; 41pp; French.
XX
XX PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
```

CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides  
 CC that consist of molecules of mannan, either simple or branched, linked  
 CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is  
 CC used for in vivo modification of the coffee endo-beta-mannanase gene. It  
 CC is also used to produce transgenic plant cells (especially coffee cells)  
 CC which have modified properties of mannan polysaccharide, and thus altered  
 CC flavour or structure. The enzyme is used for modification, degradation or  
 CC synthesis of mannan polysaccharides in vitro, particularly to treat  
 CC coffee beans to increase the percentage of dry matter extraction, and  
 CC thus reduce the quantity of sediment

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2700

AAA75048  
 ID AAA75048 standard; DNA; 15 BP.

XX AAA75048;

DT 15-JAN-2001 (first entry)

XX Primer used to reverse transcribe human RNA.

KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;  
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;  
 KW wound healing; infection; burn; angiogenesis; restenosis;  
 KW atherosclerosis; inflammation; neurodegenerative disease;  
 KW Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease; primer; ss.

XX Homo sapiens.

PN WO200052178-A1.

PD 08-SEP-2000.

PF 14-FEB-2000; 2000WO-US003542.

PR 01-MAR-1999; 99US-00258892.

XX (INST-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX (FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodavsky I, Feinstein E,

XX WPI; 2000-579289/54.

PT New polynucleotides encoding a polypeptide having heparanase activity,  
 PT useful in wound healing and in gene therapy, particularly in treating  
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.

XX Disclosure; Page 44; 152pp; English.

CC The present primer was used to reverse transcribe human RNA, from which a  
 CC cDNA sequence encoding a protein with heparanase catalytic activity was  
 CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,  
 CC particularly in treating tumour, inflammation or autoimmunity.  
 CC Particularly, the polynucleotide is useful in modulating the  
 CC bioavailability of heparin-binding growth factors, cellular responses to  
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.  
 CC interleukin (IL-8), cell interaction with plasma lipoproteins, cellular  
 CC susceptibility to certain viral and some bacterial and protozoa  
 CC infections, or disintegration of neurodegenerative plaques. The  
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or

CC radiation burns), and in the treatment of angiogenesis, restenosis,  
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-  
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,  
 CC bacterial or protozoa infections

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2701

AAA07792  
 ID AAA07792 standard; DNA; 15 BP.

XX AAA07792;

DT 23-JUN-2000 (first entry)

XX Nucleic acid sequence of ODN-e.

KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW peristalsis; duplex; ss.

XX Synthetic.

PN WO200011013-A1.

PD 02-MAR-2000.

PF 20-AUG-1999; 99WO-US019029.

PR 22-AUG-1998; 98US-0097712P.

XX (UYNE-) UNIV NEBRASKA.

PI Gold B;

DR WPI; 2000-246530/21.

PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.

XX Disclosure; Page 20; 42pp; English.

CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, cytokines, hormones, growth factors and  
 CC molecules, receptor molecules, cytochromes, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences

CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 CC  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 UTTTTTTTTTTTTTTU 15  
 RESULT 2702  
 AAA07794  
 ID AAA07794 standard; DNA; 15 BP.  
 XX  
 AC AAA07794;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-G.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 XX  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UNNE-) UNIV NEBRASKA.  
 XX  
 P1 Gold B;  
 P1  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences

XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 TTTTTTTT TTTT 15  
 RESULT 2703  
 AAA07828  
 ID AAA07828 standard; DNA; 15 BP.  
 XX  
 AC AAA07828;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of a strand of triplex oligomer 15.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; triplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 XX  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UNNE-) UNIV NEBRASKA.  
 XX  
 P1 Gold B;  
 P1  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 XX  
 PS Disclosure; Page 30; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07820-834 represent sequences forming triplex oligomers  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 1 TTTT TTTT TTTT TTTT TTTT 15  
 Db

RESULT 2704  
 AAA07790  
 ID AAA07790 standard; DNA; 15 BP.  
 AC AAA07790;  
 DT 23-JUN-2000 (first entry)  
 DE Nucleic acid sequence of ODN-c.  
 XX  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KM viral infection; inflammatory response; cellular proliferation;  
 KM psoriasis; duplex; ss.  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 PS  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutical acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.3e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 1 TTTT TTTT TTTT TTTT TTTT 15  
 Db

RESULT 2705  
 AAA07789  
 ID AAA07789 standard; DNA; 15 BP.  
 AC AAA07789;  
 DT 23-JUN-2000 (first entry)  
 DE Nucleic acid sequence of ODN-b.  
 XX  
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KM viral infection; inflammatory response; cellular proliferation;  
 KM psoriasis; duplex; ss.  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 PD 02-MAR-2000.  
 XX  
 PF 20-AUG-1999; 99WO-US019029.  
 PR 22-AUG-1998; 98US-0097712P.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Gold B;  
 DR WPI; 2000-246530/21.  
 XX  
 PT Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 PS  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutical acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
 CC infected cells. They are used in oligomers for gene regulation, antisense  
 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
 CC interleukins associated with pathological conditions such as inflammatory  
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
 CC infections and bacterial infections (see AAA07786 for details of other  
 CC uses for which the oligomers are suitable for). Oligomers comprising the  
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
 CC target nucleic acid sequences, are physiologically stable, non-toxic and  
 CC able to penetrate into cells while maintaining stringent base pair  
 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



OY 4464 TTTTUUUUUUUUUU 4478  
DB 1 TTTTUUUUUUUUUU 15

RESULT 2706  
ID AAA07795  
AC AAA07795 standard; DNA; 15 BP.  
XX  
XX AAA07795;  
XX  
XX 23-JUN-2000 (first entry)  
XX  
XX Nucleic acid sequence of ODN-h.  
XX  
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
XX  
XX viral infection; inflammatory response; cellular proliferation;  
XX  
XX psoriasis; duplex; ss.  
XX  
XX Synthetic.  
XX  
XX WO200011013-A1.  
XX  
XX 02-MAR-2000.  
XX  
XX 20-AUG-1999; 99WO-US019029.  
XX  
XX 22-AUG-1998; 98US-0097712P.  
XX  
XX (UYNE-) UNIV NEBRASKA.  
XX  
XX Gold B;  
XX  
XX WPI; 2000-246530/21.  
XX  
XX Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
XX  
XX Disclosure; Page 20; 42pp; English.

XX  
XX The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
CC uses for which the oligomers are suitable for). Oligomers comprising the  
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX

XX  
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
SQ

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTTUUUUUUUUUU 4478  
DB 1 TTTTUUUUUUUUUU 15

DB 1 TTTTUUUUUUUUUU 15

RESULT 2707  
ID AAA07797  
AC AAA07797 standard; DNA; 15 BP.  
XX  
XX AAA07797;  
XX  
XX 23-JUN-2000 (first entry)  
XX  
XX Nucleic acid sequence of ODN-j.  
XX  
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
XX  
XX viral infection; inflammatory response; cellular proliferation;  
XX  
XX psoriasis; duplex; ss.  
XX  
XX Synthetic.  
XX  
XX WO200011013-A1.  
XX  
XX 02-MAR-2000.  
XX  
XX 20-AUG-1999; 99WO-US019029.  
XX  
XX 22-AUG-1998; 98US-0097712P.  
XX  
XX (UYNE-) UNIV NEBRASKA.  
XX  
XX Gold B;  
XX  
XX WPI; 2000-246530/21.  
XX  
XX Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
XX  
XX Disclosure; Page 20; 42pp; English.

XX  
XX The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
CC uses for which the oligomers are suitable for). Oligomers comprising the  
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX

XX  
XX Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;  
SQ

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 1.3e+03;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTTUUUUUUUUUU 4478  
DB 1 TTTTUUUUUUUUUU 15

RESULT 2708

AAA07799 standard; DNA, 15 BP.

AAA07799;

23-JUN-2000 (first entry)

Nucleic acid sequence of ODN-1.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

proliferation; cellular proliferation; leukemias;

proliferation; cellular proliferation; leukemias;

Synthetic.

WO200011013-A1.

02-MAR-2000.

20-AUG-1999; 99WO-US019029.

22-AUG-1998; 98US-0097712P.

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic

oligomers used to inhibit expression of nucleic acids and in gene

regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.3e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2709

AAA07802 standard; DNA, 15 BP.

AAA07802;

23-JUN-2000 (first entry)

Nucleic acid sequence of ODN-0.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

proliferation; cellular proliferation; leukemias;

proliferation; cellular proliferation; leukemias;

Synthetic.

WO200011013-A1.

02-MAR-2000.

20-AUG-1999; 99WO-US019029.

22-AUG-1998; 98US-0097712P.

(UYNE-) UNIV NEBRASKA.

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic

oligomers used to inhibit expression of nucleic acids and in gene

regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.3e+03;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4478

1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2710

AAA07825 standard; DNA, 15 BP.



XX	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KM	psoriasis; duplex; ss.
XX	
OS	Synthetic.
PN	WO200011013-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UTNE-) UNIV NEBRASKA.
XX	
P1	Gold B;
DR	WPI; 2000-246530/21.
XX	
PT	Modified nucleomonomers, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
XX	regulation, antisense technology and diagnostics.
PS	
XX	Diaclosure; page 20; 42pp; English.
XX	
CC	The invention provides modified nucleomonomers of specified formula and
CC	their pharmacaceutically acceptable salts. The nucleomonomers are used as
CC	monomers in oligomers, which are used in pharmaceutical compositions to
CC	inhibit expression of nucleic acid molecules including DNA and RNA in
CC	cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC	infected cells. They are used in oligomers for gene regulation, antisense
CC	technology, diagnostic applications to detect target sequences in
CC	biological samples such as those containing pathogenic bacteria, fungi
CC	and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC	encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC	molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC	interleukins associated with pathological conditions such as inflammatory
CC	conditions, cardiovascular disorders, immune reactions, cancer, viral
CC	infections and bacterial infections (see AA07786 for details of other
CC	uses for which the oligomers are suitable for). Oligomers comprising the
CC	nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC	target nucleic acid sequences, are physiologically stable, non-toxic and
CC	able to penetrate into cells while maintaining stringent base pair
CC	fidelity for target DNA sequences. The oligomers demonstrate significant
CC	single- or double-stranded target nucleic acid binding activity to form
CC	duplexes, triplexes or other forms of stable association. Sequences
CC	AA07788-803 represent oligonucleotides forming a third strand along with
CC	the duplex sequences
CC	
XX	
XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
XX	
Query Match	0.2%; Score 15; DB 1; Length 15;
Best Local Similarity	0.0%; Pred. No. 1.3e+03;
Matches	0; Conservative 15; Mismatches 0; Indels 0; Gaps 0
Qy	4464 TTTT TTTT TTTT TTTT 4478
DB	1 UUUUUUUUUUUUUUUU 15
XX	
RESULT 2713	
AA07834	AAA07834 standard; DNA; 15 BP.
XX	
AC	AAA07834;
XX	
DT	23-UN-2000 (first entry)
XX	
DE	Nucleic acid sequence of a strand of triplex oligomer 17.
XX	
NK	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

KM	vital infection; inflammatory response; cellular proliferation;
XX	pooriastis; duplex; triplex; ss.
XX	Synthetic.
OS	
PN	WO200011013-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UTNE-) UNIV NEBRASKA.
XX	
PI	Gold B;
XX	
DR	WPI, 2000-246530/21.
XX	
PT	Modified nucleomonomers, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
PT	regulation, antisense technology and diagnostics.
XX	
PS	Disclosure; Page 30; 42pp; English.
XX	
CC	The invention provides modified nucleomonomers of specified formula and
CC	their pharmaceutically acceptable salts. The nucleomonomers are used as
CC	monomers in oligomers, which are used in pharmaceutical compositions to
CC	inhibit expression of nucleic acid molecules including DNA and RNA in
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CC	infected cells. They are used in oligomers for gene regulation, antisense
CC	technology, diagnostic applications to detect target sequences in
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CC	and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC	encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC	able to penetrate into cells while maintaining stringent base pair
CC	fidelity for target DNA sequences. The oligomers demonstrate significant
CC	single- or double-stranded target nucleic acid binding activity to form
CC	duplexes, triplexes or other forms of stable association. Sequences
CC	AAA07820-834 represent sequences forming triplex oligomers
CC	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
XX	
Query Match	0.2%; Score 15; DB 1; Length 15;
Best Local Similarity	86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	4464 TTTTTTTTTTTTTT 4478
	:
	1 TTTTTTTTUTTTTTT 15
DB	
RESULT 2714	
AAA07796	
ID	AAA07796 standard; DNA; 15 BP.
XX	
AC	AAA07796;
XX	
DT	23-UN-2000 (First entry)
XX	
DE	Nucleic acid sequence of ODN-1.
XX	
KM	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	psoriastis; duplex; ss.
XX	

PW	MO200011013-A1.
XX	.02-MAR-2000.
PD	
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UYNE-) UNIV NEBRASKA.
XX	
PI	Gold B;
XX	
WP	WPI; 2000-246530/21.
XX	
PT	Modified nucleomonomers, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
PT	regulation, antisense technology and diagnostics.
PS	
PS	Disclosure; Page 20; 42pp; English.
XX	
CC	The invention provides modified nucleomonomers of specified formula and
CC	their pharmaceutically acceptable salts. The nucleomonomers are used as
CC	monomers in oligomers, which are used in pharmaceutical compositions to
CC	inhibit expression of nucleic acid molecules including DNA and RNA in
CC	cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC	infected cells. They are used in oligomers for gene regulation, antisense
CC	technology, diagnostic applications to detect target sequences in
CC	biological samples such as those containing pathogenic bacteria, fungi
CC	and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC	encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC	molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC	interleukins associated with pathological conditions such as inflammatory
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CC	fidelity for target DNA sequences. The oligomers demonstrate significant
CC	single- or double-stranded target nucleic acid binding activity to form
CC	duplexes, triplexes or other forms of stable association. Sequences
CC	AAA07788-803 represent oligonucleotides forming a third strand along with
CC	the duplex sequences
CC	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
	Query Match 0.2%; Score 15; DB 1; Length 15;
	Best Local Similarity 86.7%; Pred. No. 1.3e+03;
	Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
OY	4464 TTTT TTTTTTTTTTTT 4478
	:     :
Dd	1 TTTTUTTTTUTTTT 15
	RESULT 2716
	AAA07793
ID	AAA07793 standard; DNA; 15 BP.
AC	AAA07793;
XX	
DT	23-JUN-2000 (first entry)
XX	
DE	Nucleic acid sequence of ODN-F.
XX	
KX	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	psoriasis; duplex; ss.
XX	
OS	Synthetic.
XX	
PN	WO200011013-A1.
XX	

PD 02-MAR-2000.  
 XX 20-AUG-1999; 99WO-US019029.  
 PF 22-AUG-1998; 98US-0097712P.  
 XX (UYNE-) UNIV NEBRASKA.  
 PA Gold B;  
 PI WPI; 2000-246530/21.  
 XX Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
 XX  
 CC The invention provides modified nucleomonomers of specified formula and  
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
 CC monomers in oligomers, which are used in pharmaceutical compositions to  
 CC inhibit expression of nucleic acid molecules including DNA and RNA in  
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
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 CC technology, diagnostic applications to detect target sequences in  
 CC biological samples such as those containing pathogenic bacteria, fungi  
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
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 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 CC  
 SO Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
 Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 Db 1 UUUUUUUUUUUUUU 15  
 RESULT 2717  
 AAA07798  
 ID AAA07798 standard; DNA; 15 BP.  
 XX  
 AC AAA07798;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-K.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.

PF 20-AUG-1999; 99WO-US019029.  
 XX 22-AUG-1998; 98US-0097712P.  
 ER (UYNE-) UNIV NEBRASKA.  
 PA Gold B;  
 XX PI WPI; 2000-246530/21.  
 DR Modified nucleomonomers, used in physiologically stable, non-toxic  
 PT oligomers used to inhibit expression of nucleic acids and in gene  
 PT regulation, antisense technology and diagnostics.  
 XX  
 PS Disclosure; Page 20; 42pp; English.  
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 CC The invention provides modified nucleomonomers of specified formula and  
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 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
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 CC fidelity for target DNA sequences. The oligomers demonstrate significant  
 CC single- or double-stranded target nucleic acid binding activity to form  
 CC duplexes, triplexes or other forms of stable association. Sequences  
 CC AAA07788-803 represent oligonucleotides forming a third strand along with  
 CC the duplex sequences  
 CC  
 SO Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
 Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 Db 1 UUUUUUUUUUUUUU 15  
 RESULT 2718  
 AAA07788  
 ID AAA07788 standard; DNA; 15 BP.  
 XX  
 AC AAA07788;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Nucleic acid sequence of ODN-a.  
 XX  
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
 KW viral infection; inflammatory response; cellular proliferation;  
 KW psoriasis; duplex; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200011013-A1.  
 XX  
 PD 02-MAR-2000.  
 PF 20-AUG-1999; 99WO-US019029.  
 XX

PR 22-AUG-1998; 98US-0097712P.  
XX  
XX (UNNE-) UNIV NEBRASKA.  
XX  
XX Gold B;  
XX  
XX WPI; 2000-246530/21.  
XX  
XX Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
XX  
XX Disclosure; Page 20; 42pp; English.  
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XX The invention provides modified nucleomonomers of specified formula and  
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CC technology, diagnostic applications to detect target sequences in  
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CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT TTTT 15  
RESULT 2719  
AAA07791 ID AAA07791 standard; DNA; 15 BP.  
XX  
XX AAA07791;  
AC  
XX 23-JUN-2000 (first entry)  
DT  
XX  
DE Nucleic acid sequence of ODN-d.  
XX  
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
XX Synthetic.  
OS  
XX WO200011013-A1.  
PN  
XX 02-MAR-2000.  
PD  
XX 20-AUG-1999; 99WO-US019029.  
PF  
XX 22-AUG-1998; 98US-0097712P.  
PR  
XX

PA (UNNE-) UNIV NEBRASKA.  
XX  
XX Gold B;  
XX  
XX WPI; 2000-246530/21.  
XX  
XX Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
XX  
XX Disclosure; Page 20; 42pp; English.  
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XX The invention provides modified nucleomonomers of specified formula and  
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CC technology, diagnostic applications to detect target sequences in  
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CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
OY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT TTTT 15  
RESULT 2720  
AAA07801 ID AAA07801 standard; DNA; 15 BP.  
XX  
XX AAA07801;  
AC  
XX 23-JUN-2000 (first entry)  
DT  
XX  
DE Nucleic acid sequence of ODN-n.  
XX  
XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
XX Synthetic.  
OS  
XX WO200011013-A1.  
PN  
XX 02-MAR-2000.  
PD  
XX 20-AUG-1999; 99WO-US019029.  
PF  
XX 22-AUG-1998; 98US-0097712P.  
PR  
XX (UNNE-) UNIV NEBRASKA.  
PA  
XX

PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS . Disclosure; Page 20; 42pp; English.  
XX  
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CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
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CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
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CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association. Sequences  
CC AAA07788-803 represent oligonucleotides forming a third strand along with  
CC the duplex sequences  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 73.3%; Pred. No. 1.3e+03;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTTTTTTTTTTTTTT 4478  
:|||||:|||||:  
Db 1 TTTTTTTTTTTTTT 15  
RESULT 2721  
AAA62350  
ID AAA62350 standard; DNA; 15 BP.  
XX  
AC AAA62350;  
XX  
DT 06-NOV-2000 (first entry)  
XX  
XX Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.  
XX  
XX Conformationally-locked oligonucleotide; antisense inhibitor;  
XX bicyclic sugar nucleoside analogue; gene probe; de.  
XX  
XX Synthetic.  
XX  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 7  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"  
FT modified\_base 9  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"  
XX  
XX US6083482-A.  
XX  
XX 04-JUL-2000.  
PD

XX  
PF 11-MAY-1999; 99US-00309742.  
XX  
PR 11-MAY-1999; 99US-00309742.  
XX  
PA (ICNC ) ICN PHARM INC.  
XX  
PI Wang G;  
XX  
DR WPI; 2000-451496/39.  
XX  
XX  
PT New conformationally restricted 3',5'-bridged nucleosides and  
PT oligonucleotides useful as antisense therapeutics or as gene-specific  
PT diagnostics.  
PS Example 20; Col 16; 10pp; English.  
XX  
XX The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-  
CC C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in  
CC the sequence were incorporated by phosphoramidite chemistry using a DNA  
CC synthesizer. Bicyclic sugar nucleosides are conformationally restricted  
CC 3',5'-bridged nucleosides which can be used as building blocks for  
CC oligonucleotides. Oligonucleotides can be produced that have certain,  
CC desired, geometrical shapes and entropy advantages. They may have  
CC superior hybridisation to DNA and RNA, and excellent biological  
CC stability. The conformationally-modified oligonucleotides may be useful  
CC as antisense inhibitors of gene expression or as gene probes, and may  
CC therefore be used in antisense therapeutics or gene-specific diagnostics  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTTTTTTTTTTTTTT 4478  
:|||||:|||||:  
Db 1 TTTTTTTTTTTTTT 15  
RESULT 2722  
AAA62347  
ID AAA62347 standard; DNA; 15 BP.  
XX  
AC AAA62347;  
XX  
DT 06-NOV-2000 (first entry)  
XX  
XX Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.  
XX  
XX Conformationally-locked oligonucleotide; antisense inhibitor;  
XX bicyclic sugar nucleoside analogue; gene probe; de.  
XX  
XX Synthetic.  
XX  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 3  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 5  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
FT modified\_base 9  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"  
XX  
XX modified\_base 11



FT	/*tag= e	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R) -C,3'-N-ethanothymidine"	
FT	13	
FT	/*tag= f	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R) -C,3'-N-ethanothymidine"	
FT	15	
FT	/*tag= g	
FT	/mod_base= OTHER	
FT	/note= "3',-C-amino-5' (R) -C,3'-N-ethanothymidine"	
PN	US6803482-A.	
PD	04-JUL-2000.	
XX		
PF	11-MAY-1999;	99US-00309742.
XX		
PR	11-MAY-1999;	99US-00309742.
XX		
PA	(ICNC ) ICN PHARM INC.	
XX		
PI	Wang G;	
XX		
DR	WPI; 2000-451496/39.	
XX		
PT	New conformationally restricted 3',5'-bridged nucleosides and	
PT	oligonucleotides useful as antisense therapeutics or as gene-specific	
PT	diagnostics.	
XX		
PS	Example 20; Col 15; 10pp; English.	
CC		
CC	The present sequence is an oligonucleotide containing 3',-C-amino-5' (R) -	
CC	C,3',-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in	
CC	the sequence were incorporated by phosphoramidite chemistry using a DNA	
CC	synthesizer. Bicyclic sugar nucleosides are conformationally restricted	
CC	3',5'-bridged nucleosides which can be used as building blocks for	
CC	oligonucleotides. Oligonucleotides can be produced that have certain,	
CC	desired, geometrical shapes and entropy advantages. They may have	
CC	superior hybridisation to DNA and RNA, and excellent biological	
CC	stability. The conformationally-modified oligonucleotides may be useful	
CC	as antisense inhibitors of gene expression or as gene probes, and may	
CC	therefore be used in antisense therapeutics or gene-specific diagnostics	
XX		
CC		
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;	
	Query Match	0.2%; Score 15; DB 1; Length 15;
	Best Local Similarity	100.0%; Pred. No. 1.3e+03;
	Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTTTTTTTTTTTT 4478	
Db	1 TTTTTTTTTTTTTT 15	
	RESULT 2723	
	AAA62348	
ID	AAA62348 standard; DNA; 15 BP.	
XX		
AC	AAA62348;	
XX		
DT	06-NOV-2000 (first entry)	
XX		
DE	Oligonucleotide #4 containing 3'-C-amino-5' (R) -C,3'-N-ethanothymidine.	
XX		
KM	Conformationally-locked oligonucleotide; antisense inhibitor;	
XX	bicyclic sugar nucleoside analogue; gene probe; ds.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	modified_base	7
FT	/*tag= a	

FT		/mod_base= OTHER
PT		/note= "3'-C-amino-5' (R) -C, 3'-3'-N-ethanothymidine"
FT	modified_base	9
FT		/*tag= b
FT		/mod base= OTHER
FT		/note= "3'-C-amino-5' (R) -C, 3'-3'-N-ethanothymidine"
XX		
FN	US6083482-A.	.
PD		
PD	04-JUL-2000.	
XX		
PE	11-MAY-1999;	99US-00309742.
XX		
PR	11-MAY-1999;	99US-00309742.
PA	(ICNC ) ICN PHARM INC.	
XX		
PI	Wang G;	
DR		
XX	WPI; 2000-451496/39.	
XX		
PT	New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific diagnostics.	
PT		
PS	Example 20; Col 15; 10pp; English.	
CC	The present sequence is an oligonucleotide containing 3'-C-amino-5' (R) - C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesizer. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA ,and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics	
CC		
CC		
XX		
SO	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other:	
	Query Match	0.2%; Score 15; DB 1; Length 15;
	Best Local Similarity	100.0%; Pred. No. 1.3e+03;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	4464 TTTTTTTTTTTT	4478
DB	1 TTTTTTTTTTTTTT	15
	RESULT 2724	
	AAH20308	
ID	AAH20308 standard; DNA; 15 BP.	
XX		
AC	AAH20308;	
DT	31-JUN-2001 (first entry)	
DE	Oligo dT15 EDTA labelled probe.	
XX		
KW	Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1
FT		/*tag= a
FT		/mod base= OTHER
FT		/note="Optionally thymidine has EDTA covalently attached at C-5"
FT	modified_base	5
FT		/*tag= b
FT		/mod base= OTHER

```
FT /note= "Optionally thymidine has EDTA covalently attached
FT at C-5"
FT modified_base
FT 8 /*tag= C
FT /mod_base= OTHER
FT /note= "Optionally thymidine has EDTA covalently attached
FT at C-5"
XX
XX US2001002314-A1.
XX
XX 31-MAY-2001.
XX
XX 04-AUG-1998; 98US-00128732.
XX
XX 30-OCT-1987; 87US-00115922.
XX 16-NOV-1990; 90US-00614205.
XX 12-NOV-1993; 93US-00152250.
XX
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
XX Dervan PB, Moser HE;
XX
XX WPI; 2001-342909/36.
XX
XX New hybridization probe for specific triplex formation with large double
XX helices, useful e.g. for site-specific diagnostic cleavage, contains
XX attached functional residue.
XX
XX Example 1; Fig 3B; 20pp; English.
XX
XX This invention relates to hybridisation probes which target a specific
XX sequence within a large double-helical nucleic acid. The probe is
XX complementary to the target sequence and contains at least one nucleotide
XX with an attached molecule that is able to cleave double-helical DNA e.g.
XX EDTA-Fe(II) (ethylenediaminetetracetic acid-iron complex). The probes
XX where the attached molecule is a label or compound that alters gene
XX expression, are used for specific detection and/or cleavage of double-
XX helical DNA, e.g. for diagnosis, for treatment of disease (particularly
XX caused by viruses, genetic defects or oncogenes), for chromosomal
XX analysis, and for the isolation and mapping of genes. The present
XX sequence represents probe of the invention used in an example
XX illustrating how the probe binds to and cleaves double stranded DNA
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2725
XX AAF30882
XX ID AAF30882 standard; DNA; 15 BP.
XX
XX AAF30882;
XX
XX 09-JUL-2001 (first entry)
XX
XX Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX Synthetic.
XX
XX WO200131063-A1.
XX
XX 03-MAY-2001.
XX
```

```
PF 26-OCT-2000; 2000WO-US029786.
XX
XX 26-OCT-1999; 99US-00428236.
XX
XX (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX Dempsy RO, Afonina IA, Vermeulen NMU;
XX
XX WPI; 2001-328656/34.
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component of an
XX ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX invention. MGBs bind in a non-intercalating manner to the minor groove of
XX non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX but in an intercalating manner, or lies in the minor groove, or is
XX oriented in some other way to the DNA molecule by MGB, such that it
XX becomes fluorescent (or its fluorescent properties change detectably).
XX The conjugates are used as hybridisation probes and amplification primers
XX for fluorescent detection of specifically hybridising sequences, for
XX analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX mismatch discrimination, target or signal amplification, array-based
XX assays and sequencing, including detection of double-stranded DNA by
XX triplex formation. Many different targets can be detected a single
XX reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX hybridisation-triggered fluorescence. Upon hybridisation to the
XX complementary target sequence there was an increase in fluorescence
XX yield, measured as the ratio of the fluorescence emitted by the hybrid
XX between the ODN-MGB-LF conjugate and its target sequence to the
XX fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX of 8.3
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2726
XX AAH20511
XX ID AAH20511 standard; DNA; 15 BP.
XX
XX AAH20511;
XX
XX 31-JUL-2001 (first entry)
XX
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..14
XX /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate deoxynucleotides"
XX
XX DE10051726-A1.
XX
XX 10-MAY-2001.
XX
```

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XX 18-OCT-2000; 2000DE-01051726.
XX
XX 30-OCT-1999; 99DE-01052376.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Seliger H, Sobkowski M, Hinz M;
XX
XX WPI; 2001-336414/36.
XX
XX Intermediate for oligonucleotide synthesis comprises partially hydrolysed
XX cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
XX
XX Example 2; Page 5; 8pp; German.
XX
XX This invention describes a novel chemical product comprising a partially
XX hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
XX with nucleotide derivative(s). The product is an intermediate for the
XX large (gram) scale solid phase synthesis of modified oligonucleotides
XX useful e.g. as clinical diagnostics and therapeutics, e.g. for the
XX treatment of AIDS and cancers. The presence of the partially hydrolysed
XX copolymer facilitates the synthesis of larger amounts of oligonucleotides
XX compared with the use of Merckxogel (RTM; macroporous polyvinyl acetate)
XX described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
XX Oligonucleotides are obtained in very good quality and high yields. Also,
XX the nucleosides do not display the reduced activity seen in some prior
XX art procedures, less carrier material, reagents and solvent are required.
XX Further, the carrier material is biodegradable and thus does not present
XX disposal problems. It also swells uniformly in a range of solvents, which
XX obviates expansion or contraction during use or solvent exchange.
XX AAH20510-AAH20513 represent oligonucleotides containing modified
XX deoxynucleotides which are used to illustrate the method of the invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2727
XX AAF49041
XX ID AAF49041 standard; DNA; 15 BP.
XX
XX AAF49041;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #1.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virocidic; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGBP-2; IGBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000MO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX

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XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 8; Page 60; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGBP]-2 or IGBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brian or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4470 TTTTTTTTTTTTTT 4484
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2728
XX AAF45344/C
XX ID AAF45344 standard; DNA; 15 BP.
XX
XX AAF45344;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGBP2 oligonucleotide #183.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytoskeletal; dermatological; cardiant; virocidic; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGBP-2; IGBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000MO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wright CJ, Werther GA, Edmondson SR;
XX

```

XX WPI; 2001-041421/05.  
DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.  
XX Example 6; Page 35; 201pp; English.  
XX  
XX The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, seborrhea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia  
XX  
XX Sequence 15 BP; 0 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7414 AGCAGCAGCAGCAGC 7428  
Db 15 AGCAGCAGCAGCAGC 1  
RESULT 2729  
AAH18783/C  
ID AAH18783 standard; DNA; 15 BP.  
XX  
XX AAH18783;  
XX  
XX 25-JUN-2001 (first entry)  
DE Human IL4 allele-specific primer SEQ ID NO: 42.  
XX  
XX Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;  
KW inflammatory disorder; immune disorder; population diversity;  
KW paternity test; forensic test; cytokine; chromosome 5q31.1; probe;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX MO200123404-A1.  
XX PN  
XX 05-APR-2001.  
XX PD  
XX 28-SEP-2000; 2000WO-US026608.  
XX PF  
XX 30-SEP-1999; 99US-0156825P.  
XX PR  
XX (GENA-) GENAISSANCE PHARM INC.  
XX PA  
XX Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;  
PI  
XX WPI; 2001-316132/33.  
DR  
XX  
XX Polynucleotide comprising novel single nucleotide polymorphisms in human  
PT interleukin-4 gene for use in studying expression, function of  
PT interleukin-4, in developing drugs, diagnosis and treatment of immune  
PT disorders.  
XX

PS Claim 12; Page 16; 71pp; English.  
XX  
XX The present invention provides the protein, cDNA and gene of human  
CC interleukin-4 (IL4). The coding sequences for this protein contain single  
CC nucleotide polymorphisms (SNPs) which may be associated with differences  
CC in susceptibility to atopy, inflammatory and immune diseases and  
CC different drug responses. They may also be used in applications such as  
CC forensic and paternity testing and studying population diversity and  
CC anthropological lineage. The IL4 gene is found on human chromosome 5q31.1  
XX  
XX Sequence 15 BP; 5 A; 3 C; 7 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5799 CCGCCTGCTGCTCT 5813  
Db 15 CCGCCTGCTGCTCT 1  
RESULT 2730  
AAH49243  
ID AAH49243 standard; DNA; 15 BP.  
XX  
XX AAH49243;  
XX  
XX 26-NOV-2001 (first entry)  
DE  
XX PNA-forming oligonucleotide #7.  
XX  
XX Polyamide-oligonucleotide derivative; anticancer; antiproliferative;  
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;  
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;  
KW peptide nucleic acid; ss.  
XX  
XX Synthetic.  
XX OS  
XX  
XX Key Location/Qualifiers  
FT modified\_base 9 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /note= "c-but"  
FT modified\_base 15 /\*tag= b  
FT /\*mod\_base= OTHER  
FT /note= "t-hex"  
XX  
XX EP1113021-A2.  
XX PN  
XX 04-JUL-2001.  
XX PD  
XX 08-MAR-1995; 2001EP-00104012.  
XX PF  
XX 14-MAR-1994; 94DE-04408528.  
XX PR  
XX 08-MAR-1995; 95EP-00103332.  
XX XX  
XX (AVENT ) AVENTIS PHARMA DEUT GMBH.  
XX PA  
XX Uhlmann E, Breipohl G;  
PI  
XX WPI; 2001-591267/67.  
DR  
XX  
XX New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents  
PT for treating e.g. cancer, also as diagnostic probes and primers.  
PT  
XX  
XX Example 26; Page 40; 54pp; German.  
PS  
XX  
XX This invention describes novel polyamide-oligonucleotide derivatives (I)  
CC and their physiologically acceptable salts of formula P(DNA)-Li<sub>1</sub>q(PNA-  
CC Li<sub>1</sub>-r(DNA-Li<sub>1</sub>s(PNA)-t"x" where q, r, s, t = 0 or 1, with the sum of  
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid  
CC (such as DNA or RNA or their known derivatives); Li<sub>1</sub> = covalent linkage

CC between DNA and PNA, i.e. a bond or a residue containing at least one  
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure  
CC containing at least one nucleobase different from thymine, and F, F' =  
CC end groups and/or are connected through a covalent bond. The products of  
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic  
CC and vasotropic activity and can be used for the inhibition of gene  
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by  
CC binding to proteins (aptamers). (1) are used for treating diseases caused  
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular  
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-  
CC cell adhesion reactions, for treating cancer, or for inhibiting  
CC resection, particularly as antisense reagents. They are also useful in  
CC heterogeneous or homogeneous assays, as primers or probes, particularly  
CC where the target is amplified before being detected by hybridization, for  
CC diagnosis of genetic, malignant or pathogen-related diseases. (1) retain  
CC the increased affinity for complementary strands and better stability in  
CC serum, associated with conventional peptide nucleic acids (PNA), but lack  
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate  
CC in aqueous solution, and have reduced affinity for purification  
CC materials, reduced cytotoxicity, better sequence specificity. They are  
CC more active than either DNA or PNA oligomers. When used as probes, (1)  
CC show different responses to base-pair mismatches in the DNA and PNA  
CC segments, allowing better discrimination between pathogenic and non-  
CC pathogenic conditions such as the transition from proto-oncogene to  
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,  
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme  
CC to be used to eliminate RNA or DNA primers. The DNA component allows  
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (1)  
CC may be incorporated into a gene. AAH49208-AAH49264 represent  
CC oligonucleotides used to illustrate the method of the invention  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4478  
|||||  
DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2731  
ABLA0743  
ID ABLA0743 standard; DNA; 15 BP.  
XX  
AC ABLA0743;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE Chicken heparanase (hpa) cDNA cloning oligo dt(15) primer.  
XX  
KW Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;  
XX anti-protoczoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.  
XX  
OS Gallus gallus.  
XX  
PN US2002034810-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 16-AUG-2001; 2001US-00930218.  
XX  
PR 20-SEP-2000; 2000US-00666390.  
XX  
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.  
XX  
PI Goldsmith O, Becker I, Vlodevsky I, Michal I, Zeharia E;  
XX  
DR WPI; 2002-338926/37.  
XX  
PT Nucleic acid encoding avian and reptile heparanase polypeptide is useful  
PT to treat various heparin-related disorders and the signal peptide is

PT useful in production of membrane-targeted or secreted recombinant  
PT proteins.  
XX  
XX Disclosure; Page 13; 39pp; English.  
XX

CC The invention relates to an isolated avian and reptile nucleic acid,  
CC encoding a polypeptide with heparanase catalytic activity. The signal  
CC peptide of the nucleic acid can be used to express membrane-associated or  
CC secreted proteins in heterologous expression systems. The encoded  
CC polypeptides can be used to prevent tumor angiogenesis, metastasis and  
CC invasion, and to intervene with pathologies associated with impaired  
CC heparin-binding growth factors, cellular responses to heparin-binding  
CC growth factors and cytokines, cell interaction with plasma lipoproteins,  
CC cellular susceptibility to viral, protozoa and bacterial infections or  
CC disintegration of neurodegenerative plaques. The present sequence  
CC represents a chicken heparanase (hpa) cDNA cloning oligo dt(15) primer  
XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4478  
|||||  
DB 1 TTTT TTTT TTTT TTTT 15

RESULT 2732  
ABA97403  
ID ABA97403 standard; DNA; 15 BP.  
XX  
AC ABA97403;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Nucleotide sequence of oligomer # 10 used to compare mismatches.

XX  
KW Protein nucleic acid molecule; PNA; ds.  
XX  
OS Synthetic.  
XX  
PN WO200168673-A1.  
XX  
PD 20-SEP-2001.  
XX  
PF 13-MAR-2001; 2001WO-US008111.  
XX  
PR 14-MAR-2000; 2000US-0189190P.  
XX  
PR 30-NOV-2000; 2000US-0250334P.  
XX  
PA (ACTI-) ACTIVE MOTIF.

XX  
PI Eftimov V, Fernandez J, Archdeacon D, Archdeacon J;  
PI Chikhakhchean O, Buryakova A, Choob M, Hondorp K;  
XX  
DR WPI; 2002-041177/05.  
XX  
PT Oligonucleotides analogs useful in detection, separation and purification  
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.  
XX  
XX Example 20; Page 123; 197pp; English.

CC This invention relates to oligonucleotide analogues comprising a protein  
CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
CC separation of nucleic acid molecules and as probes, primers, linkers,  
CC adaptors and antisense agents on solid supports. Modifications enhance  
CC their use as capture and detection probes e.g. by the incorporation of  
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
CC fluorescein and reporter molecules such as alkaline phosphatase. They are  
CC also used for enhancing or inhibiting the activity of an enzyme or  
CC cellular activity. The compounds are stable to nucleases and proteases,  
CC have high affinity, binding specificity and solubility. The polyamide

CC backbone of pNAs is resistant to both nucleases and proteases. pNAs bind  
CC nucleic acid molecules with greater affinity than DNA or RNA  
CC concentration. The compounds are relatively simple to synthesize and are  
CC used in a wide variety of applications. This sequence represents a DNA  
CC oligomer which is used to represent the effect of single base mismatches  
CC on oligonucleotides

XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
15 TTTT TTTT TTTT TTTT TTTT 15

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2733  
AAL49453/c  
ID AAL49453 standard; DNA; 15 BP.  
XX  
AC AAL49453;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 1.  
XX  
KM Mutation detection; primer; mutant; tag; tumour suppressor gene;  
KM protein production; cancer; ds.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..15  
FT /\*tag= a  
FT /product= "tag peptide"  
FT /partial  
FT /note= "no start or stop"

XX  
PN WO200266675-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 15-FEB-2002; 2002WO-EP001651.  
XX  
PR 16-FEB-2001; 2001DE-01007317.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Kahmann S, Mueller O;  
XX  
XX WPI: 2002-674959/72.  
DR P-PSDB; AAO19054.  
XX  
XX  
PT Detecting mutations in nucleic acid, useful for diagnosis and  
PT characterization of tumors, by amplification, in vitro transcription and  
PT translation, then protein detection.

XX  
PS Claim 11; Fig 5; 62pp; German.

CC The present invention relates to a method of detecting mutations in a  
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded  
CC amplicon, in vitro transcription and translation of this amplicon, and  
CC detection of the translated protein. The primers used for amplification  
CC are designed to produce an amplicon that is translatable and allows  
CC differentiation between translation products of wild-type and mutated  
CC nucleic acids. The method is used to detect mutations in tumour  
CC suppressor genes, for (early) diagnosis, monitoring and characterisation  
CC of tumours (especially of bladder and intestines) and in the germ line  
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector  
CC is used to detect or verify the reading frame of a nucleic acid cloned in  
CC it, and to determine the suitability of detectable peptides for analysis

CC and/or purification of a recombinant protein, expressed from a sequence  
CC cloned in the vector. The present sequence encodes a tag peptide and was  
CC used in the invention

XX  
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
15 TTTT TTTT TTTT TTTT TTTT 1

Db 15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2734  
AAL49455/c  
ID AAL49455 standard; DNA; 15 BP.  
XX  
AC AAL49455;  
XX  
DT 14-NOV-2002 (first entry)  
XX  
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 3.  
XX  
KM Mutation detection; primer; mutant; tag; tumour suppressor gene;  
KM protein production; cancer; ds.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..15  
FT /\*tag= a  
FT /product= "tag peptide"  
FT /partial  
FT /note= "no start or stop"

XX  
PN WO200266675-A2.  
XX  
PD 29-AUG-2002.  
XX  
PF 15-FEB-2002; 2002WO-EP001651.  
XX  
PR 16-FEB-2001; 2001DE-01007317.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Kahmann S, Mueller O;  
XX  
XX WPI: 2002-674959/72.  
DR P-PSDB; AAO19056.  
XX  
XX  
PT Detecting mutations in nucleic acid, useful for diagnosis and  
PT characterization of tumors, by amplification, in vitro transcription and  
PT translation, then protein detection.

XX  
PS Claim 11; Fig 5; 62pp; German.

CC The present invention relates to a method of detecting mutations in a  
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded  
CC amplicon, in vitro transcription and translation of this amplicon, and  
CC detection of the translated protein. The primers used for amplification  
CC are designed to produce an amplicon that is translatable and allows  
CC differentiation between translation products of wild-type and mutated  
CC nucleic acids. The method is used to detect mutations in tumour  
CC suppressor genes, for (early) diagnosis, monitoring and characterisation  
CC of tumours (especially of bladder and intestines) and in the germ line  
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector  
CC is used to detect or verify the reading frame of a nucleic acid cloned in  
CC it, and to determine the suitability of detectable peptides for analysis  
CC and/or purification of a recombinant protein, expressed from a sequence  
CC cloned in the vector. The present sequence encodes a tag peptide and was  
CC used in the invention

XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2735  
 AAD29506  
 ID AAD29506 standard; DNA; 15 BP.  
 AC AAD29506;  
 XX 17-MAY-2002 (first entry)  
 DE Primer used for the expression of adipocytes in human preadipose cells.  
 XX Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;  
 KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;  
 KM ss.  
 OS Unidentified.  
 XX MO200206450-A1.  
 PN 24-JAN-2002.  
 PD 13-JUL-2001; 2001WO-EP008165.  
 PP 18-JUL-2000; 2000EP-00115489.  
 PR (NEST ) SOC PROD NESTLE SA.  
 PA Darimont C, Mace K, Pfeiffer A;  
 XX WPI; 2002-188539/24.  
 DR New human pre-adipose cell line capable of differentiating to adipose  
 PT cells; useful in developing drug, food ingredients, and supplements  
 PT against obesity, diabetes and cardiovascular diseases.  
 XX Example 5; Page 10; 30pp; English.

CC The present invention relates to new human pre-adipose cell lines capable  
 CC to differentiate to white adipose cells, exhibiting essentially the same  
 CC cellular properties of normal white adipose cells. The human pre-adipose  
 CC cell lines are useful for the identification of substances controlling  
 CC the regulation of lipid uptake and release by human white adipocytes, and  
 CC substances controlling the differentiation of preadipocytes into mature  
 CC adipocytes. They are useful for screening compounds capable to regulate  
 CC the secretion of any metabolites or hormones from human white adipocytes.  
 CC Sequences of the invention are useful for developing drugs, food  
 CC ingredients and supplements against obesity, diabetes and cardio-  
 CC vascular diseases. The present DNA sequence is a reverse transcription  
 CC (RT)-PCR primer which is used for the expression of adipocytes in  
 CC differentiated immortalised human preadipose cells. This primer is used  
 CC in the amplification of the invention  
 CC  
 CC Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
 SQ Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2736  
 AAD22531/C  
 ID AAD22531 standard; RNA; 15 BP.  
 XX AAD22531;  
 AC AAD22531;  
 XX 29-AUG-2003 (revised)  
 DT 07-AUG-2003 (revised)  
 DT 12-FEB-2002 (first entry)  
 DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.  
 XX RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;  
 KW virucide; oncogene; cancer; transcription; translation; leukaemia virus;  
 KW hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];  
 KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.  
 XX  
 OS unidentified retrovirus.  
 OS Unidentified.  
 PN US6291438-B1.  
 PD 18-SEP-2001.  
 PP 06-OCT-1998; 98US-00167375.  
 PR 24-FEB-1993; 93US-00022055.  
 PR 23-FEB-1994; 94US-00200650.  
 PR 22-FEB-1996; 96US-00604871.  
 XX (WANG/) WANG J H.  
 PA Wang JH;  
 PI WPI; 2002-009339/01.  
 DR Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral  
 PT reverse transcriptase comprises at the 2'-O position of the  
 PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly  
 PT substituted phenyl compound.  
 XX Example 3; Col 24; 56pp; English.

CC The invention relates to derivatised antisense oligoribonucleotides with  
 CC enhanced membrane permeability and stability. The derivatised antisense  
 CC oligoribonucleotide complementary to a sequence of nucleotides found in a  
 CC virus or a cell is useful for inhibiting e.g., viral reverse  
 CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at  
 CC the 2'-O position with a hydrophobic carrier reagent containing a poly  
 CC substituted phenyl compound. The derivatised oligoribonucleotides are  
 CC used to decrease the expression of oncogenes and thereby decrease the  
 CC expression of cancer cells which rely upon oncogene expression for their  
 CC phenotypic and pathological properties. The oligoribonucleotides are also  
 CC used for increasing the effectiveness of antisense oligonucleotide  
 CC targeted to a gene associated with a disease or a condition in an  
 CC animal. To alter gene transcription and/or translation for any gene or  
 CC gene segment responsible for expression, to inhibit viral reverse  
 CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis  
 CC virus, oncogenes and human immunodeficiency virus. The present sequence  
 CC is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment  
 CC which is used in the treatment of moloney murine leukaemia virus (MuLV)  
 CC in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-  
 CC AUG-2003 to standardise OS field)  
 CC  
 CC Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 1 TTTT TTTT TTTT TTTT TTTT 15

Db 15 TTTTTTTTTTTTTT 1

RESULT 2737  
ABQ82140/c  
ID ABQ82140 standard; DNA; 15 BP.  
XX  
XX ABQ82140;  
XX  
XX 11-DEC-2002 (first entry)  
XX  
XX  
DE Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO.23.  
XX  
XX Chimeric nucleic acid construct; recombinational cloning; silencing;  
XX  
XX recombination site; double stranded RNA; plant; ds.  
XX  
XX Synthetic.  
XX  
XX WO200259294-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-AU000073.  
XX  
XX 26-JAN-2001; 2001US-0264067P.  
XX  
XX 29-NOV-2001; 2001US-0333743P.  
XX  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX Weeley S, Waterhouse P, Helliwell C;  
XX  
XX WPI; 2002-682669/73.  
XX  
XX  
XX New vectors comprising operably linked DNA fragments having an origin of  
PT replication, a selectable marker and a chimeric DNA construct, useful for  
PT silencing target nucleic acids and for producing large amounts of double-  
PT stranded RNA.

Claim 14; Page 74; 104pp; English.

The present invention describes a vector (i) comprising operably linked  
CC DNA fragments having: (a) origin of replication allowing replication in a  
CC recipient cell, preferably in bacteria such as *Escherichia coli*; (b)  
CC selectable marker region capable of being expressed in the recipient cell  
CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter  
CC region capable of being recognized by RNA polymerases of a eukaryotic  
CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and  
CC fourth recombination sites; (iii) 3' transcription terminating and  
CC polyadenylation region functional in the eukaryotic cell. The first and  
CC fourth recombination sites, or the second and third recombination sites  
CC are capable of reacting with a same recombination site, and preferably  
CC are identical. The first and second recombination sites, or the third and  
CC fourth recombination sites, do not recombine with each other or with a  
CC same recombination site. The vector is useful for producing large amounts  
CC of double-stranded RNA which can be used for silencing target nucleic  
CC acid sequences. The vectors can also be used to convert a DNA fragment  
CC into an inverted repeat structure. Plants transformed with a vector from  
CC the present invention can be used in a conventional breeding scheme to  
CC produce more plants with the same characteristics or to introduce a  
CC chimeric gene for reduction of the phenotypic expression of nucleic  
CC acids. The present sequence represents an acceptor vector nucleotide  
CC sequence from the present invention

XX  
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478  
15 TTTTTTTTTTTTTT 1  
Db

RESULT 2738  
ABX00240  
ID ABX00240 standard; RNA; 15 BP.  
XX  
XX ABX00240;  
XX  
XX 23-DEC-2002 (first entry)  
XX  
XX  
DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.  
XX  
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; viraemia;  
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
XX type I interferon; interferon alpha; interferon beta; cytostatic;  
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
XX substrate; hammerhead ribozyme; HH ribozyme; ss.  
XX  
XX  
XX Hepatitis C virus.  
XX  
XX US2002082225-A1.  
XX  
XX 27-JUN-2002.  
XX  
XX 23-MAR-1999; 99US-00274553.  
XX  
XX 23-MAR-1999; 99US-00274553.  
XX  
XX (BLATT/) BLATT L.  
XX (MCSW/) MCSWIGEN J A.  
XX (ROBE/) ROBERTS B.  
XX (PAVCO/) PAVCO P A.  
XX (MACE/) MACEJACK D.  
XX  
XX Blatt L, Mewiggen JA, Roberts B, Pavco PA, Macejack D;  
PI  
XX WPI; 2002-617759/66.  
XX  
XX  
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
PT replication and are useful to treat hepatitis C virus infections and  
PT cirrhosis, liver failure or hepatocellular carcinoma.

Claim 1; Page 21; 80pp; English.

The present invention relates to enzymatic nucleic acids which  
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
CC (HP) motif where the binding arms comprise sequences complementary to one  
CC of the substrate sequences defined in the specification. The HCV  
CC ribozymes are useful for modulating the expression and/or replication of  
CC HCV. They can be used to treat cirrhosis, liver failure and/or  
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
CC a condition associated with HCV infection in conjunction with one or more  
CC other drug therapies, particularly type I interferon, especially  
CC interferon alpha, beta or gamma or consensus interferon. The present  
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:  
CC Some of the sequence data for this patent did not form part of the  
CC printed specification. The complete sequence data for this patent was  
CC obtained in electronic format directly from the USPTO web site at  
CC [seqdata.uspto.gov/patididentry.html](http://seqdata.uspto.gov/patididentry.html)

XX  
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 15;  
Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478  
1 UUUUUUUUUUUUUU 15  
Db

RESULT 2739



ABX03406  
 ID ABX03406 standard; RNA; 15 BP.  
 AC  
 XX ABX03406;  
 XX  
 DT 24-DEC-2002 (first entry)  
 DE  
 XX Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; viraemia;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytosolic;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;  
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (BLATT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswigen JA, Roberts B, Pavco PA, Macejack D;  
 DR  
 XX WPI; 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 64; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:  
 CC Some of the sequence data for this patent did not form part of the  
 CC printed specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/patseqidbentry.html  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
 Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 1 UUUUUUUUUUUUUUUU 15

RESULT 2740  
 ABL57064  
 ID ABL57064 standard; DNA; 15 BP.

XX  
 AC ABL57064;  
 XX  
 DT 22-JUL-2002 (first entry)  
 DE  
 XX Hydrazide precursor phosphoramidite oligonucleotide O35.  
 XX  
 KW Macromolecule; hydrazide; immobilisation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key  
 FT modified\_base  
 FT 1. .15  
 FT /cag= b  
 FT /note= "phosphoramidite linkage"  
 FT modified\_base  
 FT 1  
 FT /cag= a  
 FT /mod\_base= OTHER  
 FT /note= "diethyl 5-((2-cyanoethoxy)(diisopropylamino)  
 FT phosphanyloxy)methyl) isophthalate, synthetic branching  
 FT amidite"  
 FT 15  
 FT modified\_base  
 FT 15  
 FT /cag= c  
 FT /mod\_base= OTHER  
 FT /note= "3' Cy3 dye"  
 XX  
 PN W0200214558-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US041663.  
 XX  
 PR 11-AUG-2000; 2000WO-US022205.  
 XX  
 PA (NANO-) NANOGEN INC.  
 XX  
 PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TV, Greef CH, Wang D;  
 DR  
 XX WPI; 2002-404476/43.  
 XX  
 PT Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula.  
 XX  
 PS Example 4; Page 44; 120pp; English.  
 XX  
 CC The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 15-mer, designated oligo O35, which was produced in an  
 CC example from the invention and which includes a synthetic branching  
 CC amide compound. The invention describes an improved process for  
 CC immobilisation of macromolecules including DNA, RNA, peptide nucleic  
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing  
 CC multiple reactive sites, to a substrate surface or other conjugation  
 CC target. It also describes the preparation of oligos containing one or  
 CC more hydrazides, which can be used for conjugation to surface binding  
 CC moieties, or for other conjugation reactions. The process is useful e.g.  
 CC in nucleic acid hybridisation based assays, DNA chip technology and  
 CC biosensor applications  
 XX  
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2741  
 ABL57054

```
ID ABL57054 standard; DNA; 15 BP.
XX
AC ABL57054;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide phosphoramidite oligonucleotide O9.
XX
KM Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key
FT modified_base 1.15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "6-(2-cyanoethoxy) (diisopropylamino)
FT phosphanyloxy)-N'-cetylhexanohydrazide"
FT
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 2; Page 40; 120pp; English.
XX
CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 15-mer, designated oligo O9, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT TTTT 15
```

```
RESULT 2742
ABL57063
ID ABL57063 standard; DNA; 15 BP.
XX
AC ABL57063;
XX
DT 22-JUL-2002 (first entry)
```

```
XX
DE Hydrazide precursor phosphoramidite oligonucleotide O39.
XX
KM Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Key
FT modified_base 1.15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzyloxy)-5
FT -(2'-cyanoethyl) (diisopropylamino) phosphanyloxy)methyl)-
FT benzene"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
FT
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX
DR WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 3; Page 43; 120pp; English.
XX
CC The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O39, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 1 TTTT TTTT TTTT TTTT TTTT 15
```

```
RESULT 2743
ABL57066
ID ABL57066 standard; DNA; 15 BP.
XX
AC ABL57066;
XX
DT 22-JUL-2002 (first entry)
```

```

XX DE Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX KM Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base
XX FT 1 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Amino-C6 modification"
XX FT modified_base
XX FT 15
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N,
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 12; Page 57; 120pp; English.
XX CC The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
XX CC oligonucleotide that was used in a comparison of hydrazine and amine
XX CC attachment moieties on active ester surfaces in an example from the
XX CC invention. The invention describes an improved process for immobilisation
XX CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX CC RNA and peptides, especially macromolecules containing multiple reactive
XX CC sites, to a substrate surface or other conjugation target. It also
XX CC describes the preparation of oligos containing one or more hydrazides,
XX CC which can be used for conjugation to surface binding moieties, or for
XX CC other conjugation reactions. The process is useful e.g. in nucleic acid
XX CC hybridisation based assays, DNA chip technology and biosensor
XX CC applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

```

```

XX OS Synthetic.
XX KM Key
XX FH modified_base
XX FT 1.15
XX FT /*tag= b
XX FT /note= "phosphoramidite linkage"
XX FT modified_base
XX FT 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "4-(2-cyanoethyl)(diisopropylamino)
XX FT phosphanyloxyethyl)-benzoic acid methyl ester"
XX FT modified_base
XX FT 15
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "3' Cy3 dye"
XX PN WO200214558-A2.
XX PD 21-FEB-2002.
XX PF 10-AUG-2001; 2001WO-US041663.
XX PR 11-AUG-2000; 2000WO-US022205.
XX PA (NANO-) NANOGEN INC.
XX PI Raddatz S, Mueller-Ibel J, Schweitzer M, Bruecher C, Windhab N,
XX PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX DR WPI; 2002-404476/43.
XX PT Compound for binding macromolecule to substrate surface or conjugation
XX PT targets, contains phosphorous containing reactive group, hydrazide
XX PT protecting group and benzene ring, and has predefined formula.
XX PS Example 3; Page 43; 120pp; English.
XX CC The present sequence is of a hydrazine treated hydrazide precursor
XX CC phosphoramidite 15-mer, designated oligo 033, which was produced in an
XX CC example from the invention. The invention describes an improved process
XX CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX CC multiple reactive sites, to a substrate surface or other conjugation
XX CC target. It also describes the preparation of oligos containing one or
XX CC more hydrazides, which can be used for conjugation to surface binding
XX CC moieties, or for other conjugation reactions. The process is useful e.g.
XX CC in nucleic acid hybridisation based assays, DNA chip technology and
XX CC biosensor applications
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
XX DB 1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 2744
ABLS7059
ID ABL57059 standard; DNA; 15 BP.
XX AC ABL57059;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide 033.
XX KW Macromolecule; hydrazide; immobilisation; ss.

```

```

RESULT 2745
ABLS7061
ID ABL57061 standard; DNA; 15 BP.
XX AC ABL57061;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide 037.
XX KW Macromolecule; hydrazide; immobilisation; ss.

```

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-(2',-cyanoethylloxy)
FT (diisopropyl amino)-phosphanyloxy)-propane"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N,
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O37, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15
```

RESULT 2746  
ABLS7056  
ID ABL57056 standard; DNA; 15 BP.  
XX  
XX ABL57056;  
XX  
XX 22-JUL-2002 (first entry)  
XX  
XX Hydrazide phosphoramidite oligonucleotide O31.  
XX  
XX Macromolecule; hydrazide; immobilisation; ss.  
XX  
XX Synthetic.

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanoethoxy) (diisopropylamino)
FT phosphanyloxy)-N'-crtilyhexanohydrazide"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 2; Page 40; 120pp; English.
XX
XX The present sequence is of a trityl deprotected hydrazide phosphoramidite
XX 15-mer, designated oligo O31, which was produced in an example from the
XX invention. The invention describes an improved process for immobilisation
XX of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
XX RNA and peptides, especially macromolecules containing multiple reactive
XX sites, to a substrate surface or other conjugation target. It also
XX describes the preparation of oligos containing one or more hydrazides,
XX which can be used for conjugation to surface binding moieties, or for
XX other conjugation reactions. The process is useful e.g. in nucleic acid
XX hybridisation based assays, DNA chip technology and biosensor
XX applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15
```

RESULT 2747  
ABLS7060  
ID ABL57060 standard; DNA; 15 BP.  
XX  
XX ABL57060;  
XX  
XX 22-JUL-2002 (first entry)  
XX  
XX Hydrazide precursor phosphoramidite oligonucleotide O34.  
XX  
XX Macromolecule; hydrazide; immobilisation; ss.  
XX  
XX Synthetic.

```

XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
FT phosphonyloxy)methyl)isophthalate"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"
XX
XX WO200214558-A2.
XX
XX 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-US041663.
XX
XX 11-AUG-2000; 2000WO-US022205.
XX
XX (NANO-) NANOGEN INC.
XX
XX Raddatz S, Mueller-Ibeier J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Omlety TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX
XX Example 3; Page 43; 120pp; English.
XX
XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O34, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilization of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2748
XX ABR98141
XX ID ABR98141 standard; DNA; 15 BP.
XX
XX ABR98141;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #26.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

```

```

XX Key Location/Qualifiers
XX Synthetic.
XX US6403302-B1.
XX 11-JUN-2002.
XX
XX 16-DEC-1993; 93US-00168920.
XX
XX 17-SEP-1992; 92US-00946976.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX
XX Example 1; Fig 3B; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or repressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTTTTTTTTTTTT 4478
XX 1 TTTTTTTTTTTTTT 15
XX
XX RESULT 2749
XX ABR98184
XX ID ABR98184 standard; DNA; 15 BP.
XX
XX ABR98184;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #48.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;

```

KM oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
 OS Synthetic.  
 XX US6403302-B1.  
 PN 11-JUN-2002.  
 PD 16-DEC-1993; 93US-00168920.  
 PF 17-SEP-1992; 92US-00946976.  
 PR (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 PA Dervan PB, Beal PA;  
 PI WPI; 2002-536030/57.  
 DR A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.  
 PS Example 7; Fig 24A; 108pp; English.  
 XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation,  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC method of the present invention  
 CC  
 SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 TTTT TTTT TTTT TTTT TTTT 15  
 RESULT 2750  
 AB237501  
 ID AB237501 standard; DNA; 15 BP.  
 AC AB237501;  
 XX 18-FEB-2003 (first entry)  
 DT Oligonucleotide SEQ ID NO:622.  
 DE Library; cleavage; display; diverse family; ss.  
 XX  
 KM

OS Synthetic.  
 XX WO200283872-A2.  
 PN 24-OCT-2002.  
 PD 17-APR-2002; 2002WO-US012405.  
 PF 17-APR-2001; 2001US-00837306.  
 PR 24-OCT-2001; 2001US-0000516.  
 PR 25-OCT-2001; 2001US-00045674.  
 XX (LADN/) LADNER R. C.  
 PA (COHE/) COHEN E. H.  
 PA (NAST/) NASTRI H. G.  
 PA (ROOK/) ROOKEY K. L.  
 PA (HOET/) HOET R.  
 PA (HOOG/) HOOGENDOORN H R J M.  
 XX Ladtner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;  
 PI Hoogenboom HRJM;  
 PI WPI; 2003-093015/08.  
 DR Cleaving single-stranded nucleic acid sequences at a desired location by  
 PT contacting the nucleic acid with an single strand oligonucleotide  
 PT complementary to a nucleic acid region where cleavage is desired.  
 XX Disclosure; Page 481; 485pp; English.  
 PS The present invention describes a method for cleaving single-stranded  
 CC nucleic acid sequences at a desired location. Also described: (1) methods  
 CC for displaying or expressing a member of a diverse family of peptides,  
 CC polypeptides or proteins on the surface of a genetic package and  
 CC collectively displaying at least a part of the diversity of the family,  
 CC where the displayed or expressed peptide, polypeptide or protein is  
 CC encoded at least in part by a nucleic acid that has been cleaved at a  
 CC desired location; (2) a method for preparing single-stranded nucleic  
 CC acids; (3) a method for preparing a library comprising a collection of  
 CC genetic packages that display a member of a diverse family of peptides,  
 CC polypeptides or proteins and that collectively display at least a portion  
 CC of the family; (4) a vector comprising a DNA sequence encoding an  
 CC antibody variable region linked to a version of pIII anchor which does  
 CC not mediate infection of phage particles, and wild-type gene III; (5) a  
 CC method for producing a population or a library of immunoglobulin genes;  
 CC and (6) a library of immunoglobulins that comprise members having at  
 CC least one variable domain in which at least one of CDR1 and CDR2 contain  
 CC synthetic diversity and CDR3 diversity is captured from B cells. The  
 CC method is useful for cleaving single-stranded nucleic acid sequences at a  
 CC desired location, which can be subsequently used to produce libraries or  
 CC genetic packages that display and/or express a diverse family of  
 CC peptides, polypeptides or proteins. AB236912 to AB237510 and AB25464 to  
 CC AB255499 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 TTTT TTTT TTTT TTTT TTTT 15  
 RESULT 2751  
 ABV74142/C  
 ID ABV74142 standard; DNA; 15 BP.  
 AC ABV74142;  
 XX 23-JAN-2003 (first entry)  
 DT

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XX DB 5' End of cDNA library clone.
XX KM G-protein coupled receptor; odourant; receptor; olfaction; array;
XX KW microarray; anosmia; attractant; aromatic; pesticide; ss.
XX OS Synthetic.
XX PN WO200277200-A2.
XX PD 03-OCT-2002.
XX PE 26-MAR-2002; 2002WO-US009559.
XX PR 27-MAR-2001; 2001US-0279168P.
XX PR 31-JAN-2002; 2002US-0353392P.
XX PA (INSC-) INSCENT INC.
XX PI Woods D, Dimitratos S;
XX DR WPI; 2003-029930/02.
XX PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX PT receptors, useful for isolating odorant binding proteins or pesticide
XX PT alternatives, by analyzing sequences from a male- and female-specific
XX PT nucleic acid library.
XX PS Disclosure; Fig 5; 83pp; English.
XX CC The present sequence is that of the 5' end of a cDNA clone isolated from
XX CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
XX CC using a method designed to rapidly array and normalize a complex cDNA
XX CC library obtained from a target species. Clones are arrayed into multi-
XX CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
XX CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
XX CC and a unique 3' sequence, which allows an anchored oligonucleotide in
XX CC each well to selectively hybridise only to those cDNA clones with a
XX CC complementary 5' end. The unique 3' key sequences are designed to give a
XX CC comprehensive level of degeneracy since they are diverse and numerous
XX CC enough to ensure that every possible cDNA sequence can be bound by an
XX CC individual, specific oligonucleotide in a single well. The cDNA library
XX CC is heated to denature the clones into single stranded DNA, and an aliquot
XX CC is added to every well. The anchored oligonucleotide serves as the 3'
XX CC primer in PCR, and the common 5' region present in every cDNA clone
XX CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
XX CC in each well. The library is now arrayed and normalised. The method was
XX CC used to identify and isolate clones encoding G-protein coupled receptors,
XX CC especially odourant receptors, and active effectors involved in the
XX CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
XX CC proteins, or other olfactory or neuronal proteins. The identified
XX CC receptors and proteins are useful for identifying compounds that reduce a
XX CC target animal's sensitivity to odours, for manufacturing compounds or
XX CC devices that mask odours, or trapping invertebrates with odourants.
XX CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
XX CC with desirable effects on specific species, for the development of pest
XX CC monitoring systems or non-toxic, species-specific pesticide alternatives,
XX CC for controlling insect feeding and breeding behaviour, detecting the
XX CC presence of small air-borne molecules, etc
XX SO Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT 4478
XX 15 TTTT TTTT TTTT TTTT 1

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ID ABV74141 standard; DNA; 15 BP.
XX AC ABV74141;
XX AC 23-JAN-2003 (first entry)
XX DT 23-JAN-2003 (first entry)
XX DE Oligonucleotide used in cDNA library array.
XX KM G-protein coupled receptor; odourant; receptor; olfaction; array;
XX KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "5' polylinker"
XX PN WO200277200-A2.
XX PD 03-OCT-2002.
XX PE 26-MAR-2002; 2002WO-US009559.
XX PR 27-MAR-2001; 2001US-0279168P.
XX PR 31-JAN-2002; 2002US-0353392P.
XX PA (INSC-) INSCENT INC.
XX PI Woods D, Dimitratos S;
XX DR WPI; 2003-029930/02.
XX PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX PT receptors, useful for isolating odorant binding proteins or pesticide
XX PT alternatives, by analyzing sequences from a male- and female-specific
XX PT nucleic acid library.
XX PS Disclosure; Fig 5; 83pp; English.
XX CC The present sequence is that of a poly-T oligonucleotide used in a method
XX CC designed to rapidly array and normalize a complex cDNA library obtained
XX CC from a target species. Clones are arrayed into multi-well plates. Each
XX CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
XX CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
XX CC which allows an anchored oligonucleotide in each well to selectively
XX CC hybridise only to those cDNA clones with a complementary 5' end. The
XX CC unique 3' key sequences are designed to give a comprehensive level of
XX CC degeneracy since they are diverse and numerous enough to ensure that
XX CC every possible cDNA sequence can be bound by an individual, specific
XX CC oligonucleotide in a single well. The cDNA library is heated to denature
XX CC the clones into single stranded DNA, and an aliquot is added to every
XX CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
XX CC the common 5' region present in every cDNA clone serves as the 5' priming
XX CC site. Denaturing and washing leave anchored cDNA in each well. The
XX CC library is now arrayed and normalised. The method was used to identify
XX CC and isolate clones encoding G-protein coupled receptors, especially
XX CC odourant receptors, and active effectors involved in the olfactory
XX CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
XX CC or other olfactory or neuronal proteins. The identified receptors and
XX CC proteins are useful for identifying compounds that reduce a target
XX CC animal's sensitivity to odours, for manufacturing compounds or devices
XX CC that mask odours, or trapping invertebrates with odourants.
XX CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
XX CC with desirable effects on specific species, for the development of pest
XX CC monitoring systems or non-toxic, species-specific pesticide alternatives,
XX CC for controlling insect feeding and breeding behaviour, detecting the
XX CC presence of small air-borne molecules, etc
XX SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 15;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2753

ABV75865  
ID ABV75865 standard; DNA; 15 BP.

AC ABV75865;

DT 05-FEB-2003 (first entry)

DE Oligonucleotide T15-Q-CDPI3.

KM Deprotection; phosphoramidite; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..15

FT /\*tag= a

FT /note= "phosphoramidite linkage"

FT modified\_base 15

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "3' Q-CDPI3"

XX W0200272864-A2.

PD 19-SEP-2002.

PF 04-MAR-2002; 2002WO-US006739.

PR 08-MAR-2001; 2001US-0274309P.

PA (PEKE ) PE CORP NY.

PI Nelson J;

DR WPI; 2003-046740/04.

PT New oligonucleotide deprotection reagent useful for deprotecting

PT oligonucleotide comprises an active methylene compound and an amine

PS reagent.

XX Example 2; Page 25; 46pp; English.

CC The present invention provides a method for deprotection of an

CC oligonucleotide. This involves reacting a protected oligonucleotide,

CC which is preferably covalently attached to a solid support through a

CC linkage, with a deprotection reagent comprising an active methylene

CC compound and an amine reagent. The process and reagent minimize side-

CC reactions leading to certain impurities that contaminate synthetic

CC oligonucleotides. The present sequence is a T15 phosphoramidite

CC oligonucleotide having a quencher moiety (Q) and minor groove binder

CC (CPBI) at the 3' end, which was synthesised in an example of the

CC invention. This protected oligonucleotide was treated either with 15%

CC ethanollic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%

CC deprotection without DEM yielded a complex mixture of products containing

CC only 26.5% of the desired product. When DEM was used, 76.8% of the

CC desired product was obtained

SO Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2754

ADA14836/c  
ID ADA14836 standard; DNA; 15 BP.

AC ADA14836;

DT 06-NOV-2003 (first entry)

DE Hairpin target sequence, #1, used in an example of the invention.

KM Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;

KM quencherable fluorescing agent; microarray; semiconductor; nanocrystal;

XX rhodamine B-labelled dye; detection; gold support; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc\_binding 1..15

FT /\*tag= a

FT /bound\_moiety= "Hairpin oligonucleotide #1"

FT /note= "Forms a double-stranded region with the hairpin

FT oligonucleotide shown in example 2"

XX US2003013109-A1.

PD 16-JAN-2003.

PF 21-JUN-2002; 2002US-00176055.

PR 21-JUN-2001; 2001US-0299460P.

PA (BAL/) BALINGER C T.

PA (LOCA/) LOCASCIO M.

PA (LAND/) LANDRY D P.

PI Ballinger CT, Locascio M, Landry DP;

DR WPI; 2003-596312/56.

PT Hairpin sensor useful for detecting a target nucleotide sequence in a

PT sample, comprises a hairpin loop assembly including a complementary probe

PT and a quencherable fluorescing agent.

PS Example 2; Page 11; 16pp; English.

CC The invention discloses a hairpin sensor comprising a hairpin loop

CC assembly including a complementary probe positioned between a first

CC inverse repeat arm and a second inverse repeat arm, and a quencherable

CC fluorescing agent joined, directly or indirectly, to the end of the

CC second inverse repeat arm of the hairpin loop assembly opposite the

CC complementary probe. Also claimed is a microarray comprising the hairpin

CC sensor, where the end of the first inverse repeat arm opposite the

CC complementary probe is bound, directly or indirectly, to a support, a kit

CC for detecting a target nucleotide sequence in a sample comprising the

CC hairpin sensor, and a support, and a hairpin sensor system, in which the

CC particle is conductive or semi-conductive, including at least one of the

CC above hairpin sensor assemblies. The hairpin sensor further comprises a

CC functional group joined to the end of the first inverse repeat arm

CC opposite the complementary probe, or first spacer opposite the first

CC inverse repeat arm, the functional group selected from amino, carboxyl,

CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned

CC between the second inverse repeat arm and the quencherable fluorescing

CC agent, where the ligand is selected from mercapto, hydroxyl, amino,

CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The

CC second spacer is positioned between the second inverse repeat arm and the

CC quencherable fluorescing agent which comprises a semiconductor nanocrystal

CC or rhodamine B-labelled dye. Within the microarray the support is capable



CC of accepting a charge. At least one hairpin sensor comprises two or more  
CC hairpin sensors. The two or more hairpin sensors include complementary  
CC probes that are the same or different and respective quenchable  
CC fluorescing agents that are the same or different. The two or more  
CC hairpin sensors are arranged in a spatially-defined pattern. The sensor  
CC and system are useful for detecting a target nucleotide sequence in a  
CC sample. Further, the method involves identifying the target nucleotide  
CC sequence by the location of the complementary probe to which the target  
CC nucleotide sequence binds. The two or more hairpin sensors include  
CC complementary probes or quenchable fluorescing agents, that are  
CC different. The sequence presented is the hairpin oligonucleotide target  
CC sequence, #1, used in an example of the invention.

Qy                    4464 TTTT TTTT TTTT TTTT 4478  
                      |||||  
Db                    15 TTTT TTTT TTTT TTTT 1

RESULT 2755  
ADB68520            0.2%; Score 15; DB 1; Length 15;  
ID    ADB68520 standard; DNA; 15 BP.  
AC    ADB68520;  
XX  
XX    ADB68520;  
XX  
DT    04-DEC-2003 (first entry)  
XX  
DE    Single-base mismatch oligonucleotide SEQ ID 10 DNA.  
XX  
XX    hydroxyproline nucleic acid; HYPNA; PNA; peptide nucleic acid;  
KW    gene expression; respiration; secretion; signalling;  
KW    ion-channel activity; cell motility; developmental phenotype;  
KW    tumour regression; single-base mismatch; ss;  
XX    phosphono-peptide nucleic acid; pPNA.  
XX  
OS    Synthetic.  
XX  
XX    WO2003068798-A2.  
PN  
XX    21-AUG-2003.  
PD  
XX    07-FEB-2003; 2003WO-US003904.  
PF  
XX    09-FEB-2002; 2002US-00072975.  
PR  
XX    (ACTI-) ACTIVE MOTIF.  
PA  
XX  
XX    Efilnov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;  
PI    WPI; 2003-689653/65.  
DR  
XX    WPI; 2003-689653/65.  
XX  
PT    Method of inhibiting expression of genes or RNA transcripts, useful for  
PT    therapy and determining effects of genes, by administering oligomers  
PT    containing hydroxyproline nucleic acid.  
XX  
XX    Example 20; Page 234; 240pp; English.  
PS  
XX    The invention relates to a novel method of inhibiting the expression of  
CC    one or more genes or RNA transcripts by administering at least one  
CC    oligonucleotide analogue that includes at least one hydroxyproline  
CC    nucleic acid (HYPNA) monomer to a cell or organism or their extracts. The  
CC    oligonucleotides of the invention may be used to monitor properties  
CC    including gene expression, respiration, secretion, signalling, ion-  
CC    channel activity, cell motility, developmental phenotype and tumour  
CC    regression. Furthermore, they may be utilised to determine the effects of  
CC    particular genes, as antisense or homologous recombination constructs  
CC    e.g. for creating animal models of disease and finally, for increasing  
CC    the activity of some enzymes, such as polymerases. The current sequence

CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the  
CC invention. This sequence may also comprise a peptide nucleic acid (PNA),  
CC a phosphono-PNA (pPNA) or a HYPNA.  
XX  
XX    Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
SQ    Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
Qy                    4464 TTTT TTTT TTTT TTTT 4478  
                      |||||  
Db                    1 TTTT TTTT TTTT TTTT 15

RESULT 2756  
ADC18592  
ID    ADC18592 standard; DNA; 15 BP.  
AC    ADC18592;  
XX  
XX    ADC18592;  
XX  
DT    18-DEC-2003 (first entry)  
XX  
DE    Annealing control primer Oligo-dT15 SEQ ID NO:54.  
XX  
XX    annealing control primer; ACP; annealing specificity;  
KW    nucleic acid amplification; hybridisation; DNA fingerprinting;  
KW    genomic DNA; RNA fingerprint; primer; ss.  
XX  
OS    Synthetic.  
XX  
XX    WO2003050305-A1.  
FN  
XX    19-JUN-2003.  
PD  
XX    19-SEP-2002; 2002WO-KR001781.  
PE  
XX    08-DEC-2001; 2001WO-KR002133.  
PR    01-MAY-2002; 2002WO-KR000816.  
XX  
XX    (SEEG-) SEEGENE INC.  
PA  
XX  
XX    Chun J;  
PI  
XX    WPI; 2003-627256/59.  
DR  
XX    WPI; 2003-627256/59.  
XX  
PT    Annealing control primer to improve annealing specificity in nucleic acid  
PT    amplification, has region complementary to target, arbitrary nucleotide  
PT    sequence, regulator with universal base/non-discriminatory base analog.  
XX  
XX    Example 2; SEQ ID NO 54; 190pp; English.  
PS  
XX  
XX    The present invention describes an annealing control primer (ACP) (I) for  
CC    improving the annealing specificity in nucleic acid amplification. (I)  
CC    has a 3'-end portion with a nucleotide sequence complementary to a site  
CC    on a template nucleic acid for hybridisation, a 5'-end portion having a  
CC    pre-selected arbitrary nucleotide sequence, and a regulator portion  
CC    between the 3' and 5'-end portions, comprising a universal or non-  
CC    discriminatory base analogue, where the regulator portion is capable of  
CC    regulating an annealing portion of the primer in association with  
CC    annealing temperature. (I) is useful for improving annealing specificity  
CC    in nucleic acid amplification. (I) is useful for amplifying a nucleic  
CC    acid sequence from a DNA or a mixture of nucleic acids, for selectively  
CC    amplifying a target nucleic acid sequence from a DNA, and for selectively  
CC    amplifying a target nucleic acid sequence from a mRNA, by reverse  
CC    transcribing the mRNA and performing an amplification reaction using (I).  
CC    (I) is also useful for detecting DNA complementary to differentially  
CC    expressed mRNA in two or more nucleic acid samples, by reverse  
CC    transcribing the mRNA and performing an amplification reaction using (I).  
CC    (I) is also useful for rapidly amplifying a target cDNA fragment  
CC    comprising a cDNA region corresponding to the 3'-end or 5'-end region of  
CC    an mRNA, for amplifying a population of full-length double-stranded cDNAs  
CC    complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs



[illegible]

XX allergic diseases; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
OS Homo sapiens.  
XX  
XX WO200009525-A2.  
XX  
XX PD 24-FEB-2000.  
XX  
XX PE 03-AUG-1999; 99WO-US017712.  
XX  
XX PR 03-AUG-1998; 98US-0095212P.  
XX  
XX PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX NYce JW;  
PI WPI; 2000-205971/18.  
DR  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
PS Disclosure; Page 539; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinoma, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing

XX SQ Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 68 GCCGGCGGCGCGCGCG 82  
|||  
Db 2 CGCGGCGCGCGCGCG 16

RESULT 2761  
AAF20624  
ID AAF20624 standard; DNA; 16 BP.

AC AAF20624;

XX

14-MAR-2001 (first entry)  
 XX Human C/EBP polynucleotide fragment #2191.  
 XX Low adenosine antisease oligonucleotide; phosphorothioate; allergy;  
 XX human; airway disorder; bronchoconstriction; lung inflammation;  
 XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 XX immunosuppressive; antihistaminic; analgesic; hypotensive; cytostatic;  
 XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
 XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 XX cancer; ss.  
 XX Homo sapiens.  
 XX WO200062736-A2.  
 XX 26-OCT-2000.  
 XX 24-MAR-2000; 2000WO-US008020.  
 XX 06-APR-1999; 99US-0127958P.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX (NYCE/) NYCE J W.  
 XX NYCE JW;  
 XX WPI; 2000-679539/66.  
 XX Low adenosine (A) content antisease oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX Claim 14; Page 264; 1592pp; English.  
 XX The present invention describes low adenosine (A) content antisease  
 CC oligonucleotides and compositions (I) comprising them. In the antisease  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antihistaminic, hypotensive and cytostatic activities.  
 CC The antisease oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisease oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF19434 to AAF21543 represent human polynucleotide  
 CC fragments and antisease oligonucleotides used in the exemplification of  
 CC the present invention  
 XX Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 GCGGGGCGGCGGCG 82  
 DB 2 GCGGGGCGGCGGCG 16  
 RESULT 2762  
 ID ABL57075/c  
 ABL57075 standard; DNA; 16 BP.  
 XX ABL57075;  
 XX 22-JUL-2002 (first entry)  
 XX Molecular beacon target sequence.  
 DE Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.  
 XX Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT key 1.16  
 FT msc\_binding /tag= a  
 FT /bound\_molecy= "Molecular beacon"  
 FT /note= "forms double-stranded region with bases 5-21 of  
 sequence in ABL57069"  
 XX NO200218951-A2.  
 XX 07-MAR-2002.  
 XX 29-AUG-2001; 2001WO-US041941.  
 XX 28-AUG-2000; 2000US-0228728P.  
 XX 30-MAR-2001; 2001US-0280350P.  
 XX (UYRQ ) UNIV ROCKEFELLER.  
 XX Dubertret B, Calame M, Libhaber A;  
 XX WPI; 2002-404569/43.  
 XX Sensitive detecting proximity changes in a system that utilizes an  
 PT intersecting fluorophore and quencher, for high sensitivity applications,  
 PT involves utilizing a metal surface as quencher.  
 XX Example 3; Page 30; 62pp; English.  
 XX The present sequence is that of a perfectly matched target sequence for a  
 CC molecular beacon comprising an oligonucleotide probe (see ABL57069)  
 CC covalently attached at the 3' end to fluorescent dye and at the 5' end to  
 CC a nanoparticle. In the native state, the probe forms a hairpin  
 CC conformation with hybridised termin. The proximity of the fluorophore  
 CC and quencher (gold nanoparticle) in the molecular beacon results in  
 CC little or no detectable fluorescence. Upon hybridisation of the central  
 CC complementary stretch of the probe to a target sequence, such as the  
 CC present sequence, the hairpin undergoes a conformational change resulting  
 CC in an increase in fluorescence, the extent of which is proportional to  
 CC the amount of target sequence present. Single mismatches can be detected.  
 CC The invention relates generally to the use of metal surface quenchers  
 CC such as particles or films for high sensitivity applications in, for  
 CC example, detection and diagnostic systems  
 XX Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 DB 16 TTTT TTTT TTTT TTTT TTTT 2



```

XX Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /mod base= OTHER
FT /note= "OTHER = P (Phosphono PNA monomer with phenyl
PT group attached to terminal phosphate"
XX
XX WO2003068798-A2.
XX
XX 21-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003904.
XX
XX 09-FEB-2002; 2002US-00072975.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX WPI; 2003-689653/65.
XX
XX Method of inhibiting expression of genes or RNA transcripts, useful for
XX therapy and determining effects of genes, by administering oligomers
XX containing hydroxyproline nucleic acid.
XX
XX Example 17; Page 148; 240pp; English.
XX
XX The invention relates to a novel method of inhibiting the expression of
XX one or more genes or RNA transcripts by administering at least one
XX oligonucleotide analogue that includes at least one hydroxyproline
XX nucleic acid (HYPNA) monomer to a cell or organism or their extracts. The
XX oligonucleotides of the invention may be used to monitor properties
XX including gene expression, respiration, secretion, signalling, ion-
XX channel activity, cell motility, developmental phenotype and tumour
XX regression. Furthermore, they may be utilised to determine the effects of
XX particular genes, as antisense or homologous recombination constructs
XX e.g. for creating animal models of disease and finally, for increasing
XX the activity of some enzymes, such as polymerases. The current sequence
XX is that of the PNA-HYPNA hybridisation oligomer of the invention. This
XX sequence may also comprise phosphono-PNA (PPNA) and serine nucleic acid
XX (SerNA) components.
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT 4478
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX RESULT 2766
XX AAX69797
XX ID AAX69797 standard; RNA; 17 BP.
XX
XX AAX69797;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme subterrate #1092.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX

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```

XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX
XX Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(e) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular disease, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 13.3%; Pred. No. 1.5e+03;
XX Matches 2; Conservative 13; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4462 ACCTTT TTTT TTTT TTTT 4476
XX 3 ACUUUUUUUUUUUUUU 17
XX
XX RESULT 2767
XX AAX69802
XX ID AAX69802 standard; RNA; 17 BP.
XX
XX AAX69802;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme subterrate #1097.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX foetal liver kinase 1; ss.
XX
XX Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR ) CHIRON CORP.
XX

```

PI Pavco F, Mcswiggen J, Stinchcomb D, Bacobedo J;  
 XX  
 DR WPI: 1997-259017/23.  
 XX  
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 79; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 0.0%; Pred. No. 1.5e+03;  
 Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 1 UUUUUUUUUUUUUUUU 15  
 RESULT 2768  
 AAV37934  
 ID AAV37934 standard; cDNA; 17 BP.  
 XX  
 AC AAV37934;  
 XX  
 DT 05-OCT-1998 (first entry)  
 XX  
 DE Primer of the specification.  
 XX  
 KM Leukocyte; IGA nephropathy; diagnosis; treatment; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9824815-A1.  
 PD 11-JUN-1998.  
 XX  
 PF 05-DEC-1997; 97WO-JP004469.  
 XX  
 PR 05-DEC-1996; 96JP-00325752.  
 XX  
 PA (KYOW ) KYOMA HAKKO KOGYO KK.  
 PA (KAZU-) KAZUSA DNA RES INST FOUND.  
 XX  
 PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;  
 PI Nomura N, Nagase T, Sawada S, Takei M;  
 XX  
 DR WPI: 1998-333259/29.  
 XX  
 PT Protein from leukocytes and DNA encoding it - useful as reagents for  
 PT diagnosing and treating IGA nephropathy.  
 XX  
 PS Example 2; Page 33; 41pp; Japanese.  
 XX  
 CC PCR primers AAV37933-39 are used in the course of the invention. The  
 CC specification describes a novel protein isolated from leukocytes of  
 CC patients with IGA nephropathy. Oligonucleotides based on the DNA sequence  
 CC encoding this protein are useful as reagents for diagnosing and treating  
 CC IGA nephropathy  
 XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2769  
 AAV49503  
 ID AAV49503 standard; cDNA to mRNA; 17 BP.  
 XX  
 AC AAV49503;  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Human eosinophil cell activator HVC002 primer #1.  
 XX  
 KM Eosinophil cell activator; treatment; diagnosis; malignant tumour;  
 KM parasitic infection; allergic inflammation; eosinophilic pneumonia;  
 KM rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9824817-A1.  
 PD 11-JUN-1998.  
 XX  
 PF 05-DEC-1997; 97WO-JP004470.  
 XX  
 PR 05-DEC-1996; 96JP-00325762.  
 XX  
 PA (KYOW ) KYOMA HAKKO KOGYO KK.  
 XX  
 PI Yoshizue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;  
 PI Nishi T;  
 XX  
 DR WPI: 1998-333261/29.  
 XX  
 PT DNA and encoded protein which activates eosinophil cells - for treatment  
 PT of cancer, parasite infection, autoimmune disease and allergic  
 PT inflammation.  
 XX  
 PS Example 1; Page 64; 92pp; Japanese.  
 XX  
 CC AAV49503-V49507 are primers used in the isolation of a human eosinophil  
 CC cell activator. This protein and antibodies generated from the protein  
 CC can be used for treatment and diagnosis of malignant tumours, parasitic  
 CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset  
 CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and  
 CC the antisense DNA in gene therapy of these disorders. The protein can be  
 CC used for screening of potential agonists or antagonists of its activity  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 Db 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2770  
 AAX18370  
 ID AAX18370 standard; DNA; 17 BP.  
 XX  
 AC AAX18370;

```

XX
DT 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 11.
DE
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JP1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
XX PS Disclosure; Page 11; 19pp; Japanese.
XX
XX CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma; in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
XX SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX |||||
XX 1 TTTT TTTT TTTT TTTT 15
XX
XX Db
XX
XX RESULT 2771
XX AAA30179
XX ID AAA30179 standard; DNA; 17 BP.
XX
XX AC AAA30179;
XX
XX DT 16-AUG-2000 (first entry)
XX
XX DE PCR primer GT15A used in pollenosis associated gene identification.
XX
XX KM Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200020575-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 06-OCT-1999; 99WO-JP005506.
XX
XX PR 06-OCT-1998; 98JP-00284610.
XX
XX

```

```

PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kaehiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
XX DR WPI; 2000-317712/27.
XX
XX PT Gene highly expressed in patients with high cedar pollen-specific IGE
XX PT levels, useful for diagnosing pollenosis, and screening candidate
XX PT compounds for pollenosis treatment.
XX
XX PS Example 6; Page 38; 44pp; Japanese.
XX
XX CC This sequence represents a PCR primer used in the identification of a
XX CC human pollenosis associated gene. The gene is highly expressed in
XX CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
XX CC invention relates to the nucleotide sequence encoding the pollenosis
XX CC associated protein, diagnosing pollenosis and screening candidate
XX CC compounds for treating pollenosis. The gene can be used in diagnosing
XX CC pollenosis, particularly cedar pollenosis, and screening candidate
XX CC compounds for pollenosis treatment
XX
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT 4478
XX |||||
XX 2 TTTT TTTT TTTT TTTT 16
XX
XX Db
XX
XX RESULT 2772
XX AAA30180
XX ID AAA30180 standard; DNA; 17 BP.
XX
XX AC AAA30180;
XX
XX DT 16-AUG-2000 (first entry)
XX
XX DE PCR primer GT15C used in pollenosis associated gene identification.
XX
XX KM Pollenosis-associated protein; high pollen-specific immunoglobulin E;
XX KM IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200020575-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 06-OCT-1999; 99WO-JP005506.
XX
XX PR 06-OCT-1998; 98JP-00284610.
XX
XX PA (GENO-) GENOX RES INC.
XX
XX PI Nagasu T, Sugita Y, Kaehiwabara T, Oshida T, Obayashi M, Gunji S;
XX PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
XX DR WPI; 2000-317712/27.
XX
XX PT Gene highly expressed in patients with high cedar pollen-specific IGE
XX PT levels, useful for diagnosing pollenosis, and screening candidate
XX PT compounds for pollenosis treatment.
XX
XX PS Example 6; Page 38; 44pp; Japanese.
XX
XX CC This sequence represents a PCR primer used in the identification of a
XX CC human pollenosis associated gene. The gene is highly expressed in
XX CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
XX CC invention relates to the nucleotide sequence encoding the pollenosis

```



CC associated protein, diagnosing pollenosis and screening candidate  
 CC compounds for treating pollenosis. The gene can be used in diagnosing  
 CC pollenosis, particularly cedar pollenosis, and screening candidate  
 CC compounds for pollenosis treatment

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16

RESULT 2773  
 AAX82722  
 ID AAX82722 standard; DNA; 17 BP.

AC AAX82722;

DT 10-NOV-2000 (first entry)

DE Human IGA nephropathy-associated cDNA primer #63.

KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;  
 human; primer; ss.

OS Homo sapiens.

PN WO9963085-A1.

PD 09-DEC-1999.

PF 28-MAY-1999; 99WO-JP002855.

PR 02-JUN-1998; 98JP-00152603.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 Sawada S, Takei M, Shibata K, Furiya A;

DR WPI; 2000-097328/08.

PT DNA sequences preferentially expressed in IGA nephropathy patients,  
 proteins encoded by them, and antibodies to those proteins.

PS Claim 3; Page 170; 180pp; Japanese.

XX This invention describes novel DNA sequences preferentially expressed in  
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to  
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy  
 CC incorporating the antisense sequences; the treatment of IGA nephropathy  
 CC using the antisense sequences; for mRNA inhibition; proteins associated  
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;  
 CC antibodies recognizing these proteins; the production of the proteins by  
 CC culture of host cells transformed with DNA encoding them; diagnostic  
 CC reagents for IGA nephropathy containing the antibodies; and compositions  
 CC for the treatment of IGA nephropathy which contain the antibodies. The  
 CC products of the invention can be used for the diagnosis and treatment of  
 CC IGA nephropathy. This sequence represents a primer used in the isolation  
 CC and identification of the human IGA nephropathy-associated proteins  
 CC described in the method of the invention

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478

DB 4464 TTTT TTTT TTTT TTTT 16

RESULT 2774  
 AAX82720  
 ID AAX82720 standard; DNA; 17 BP.

AC AAX82720;

DT 10-NOV-2000 (first entry)

DE Human IGA nephropathy-associated cDNA primer #61.

KW IGA nephropathy-associated protein; diagnosis; treatment; antisense;  
 human; primer; ss.

OS Homo sapiens.

PN WO9963085-A1.

PD 09-DEC-1999.

PF 28-MAY-1999; 99WO-JP002855.

PR 02-JUN-1998; 98JP-00152603.

PA (KYOW ) KYOWA HAKKO KOGYO KK.

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
 Sawada S, Takei M, Shibata K, Furiya A;

DR WPI; 2000-097328/08.

PT DNA sequences preferentially expressed in IGA nephropathy patients,  
 proteins encoded by them, and antibodies to those proteins.

PS Claim 3; Page 169; 180pp; Japanese.

XX This invention describes novel DNA sequences preferentially expressed in  
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to  
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy  
 CC incorporating the antisense sequences; the treatment of IGA nephropathy  
 CC using the antisense sequences; for mRNA inhibition; proteins associated  
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;  
 CC antibodies recognizing these proteins; the production of the proteins by  
 CC culture of host cells transformed with DNA encoding them; diagnostic  
 CC reagents for IGA nephropathy containing the antibodies; and compositions  
 CC for the treatment of IGA nephropathy which contain the antibodies. The  
 CC products of the invention can be used for the diagnosis and treatment of  
 CC IGA nephropathy. This sequence represents a primer used in the isolation  
 CC and identification of the human IGA nephropathy-associated proteins  
 CC described in the method of the invention

XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16

RESULT 2775

AAZ89372  
 ID AAZ89372 standard; DNA; 17 BP.

AC AAZ89372;

DT 15-JUN-2000 (first entry)

DE RNA detecting primer #2.  
 XX Amplification; detection; gene expression; primer; ss.  
 KW Unidentified.  
 OS  
 XX DE19840731-A1.  
 PN  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 07-SEP-1998; 98DE-01040731.  
 XX  
 PR 07-SEP-1998; 98DE-01040731.  
 XX  
 PA (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.  
 XX  
 DR WPI; 2000-257789/23.  
 XX  
 PT Analysis of RNA samples, useful for detection of differential gene  
 expression uses two differently labeled primers.  
 PS  
 XX Disclosure; Page 10; 10pp; German.  
 CC  
 CC This invention describes a novel method for analysis of an RNA sample  
 CC which comprises amplifying cDNA with first and second differentially labeled  
 CC primers and analysis of the amplified labeled cDNA. The method is useful  
 CC for analyzing differential gene expression, for identifying and/or  
 CC characterizing pharmacological activities or for identifying target  
 CC genes. The use of different primer combinations allow more cDNAs to be  
 CC amplified. The method also provides a more detailed analysis than prior  
 CC art methods. This sequence represents a primer used to illustrate the  
 CC method of the invention  
 XX  
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTTTTTTTTTTTTTT 4478  
 Db 1 TTTTTTTTTTTTTTTT 15  
 RESULT 2776  
 AA236739  
 ID AA236739 standard; DNA; 17 BP.  
 XX  
 AC AA236739;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Anchored oligo(dT) primer AT15A used for modified differential display.  
 XX  
 KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;  
 KW differentially expressed nucleic acid; disease state; cancer; disease;  
 KW autoimmune disease; infectious disease; aging; developmental disorder;  
 KW proliferative disorder; neurological disorder; toxicity; primer;  
 KW treatment resistance; differential expression; drug discovery;  
 KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9955913-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 27-APR-1999; 99WO-US0009119.  
 XX  
 PR 27-APR-1998; 98US-0083331P.  
 PR 27-AUG-1998; 98US-0098070P.  
 PR 04-FEB-1999; 99US-0118624P.  
 XX

PA (KIMM-) KIMMEL CANCER CENT SIDNEY.  
 XX  
 PI McCelland M, Welsh J, Trenkle T;  
 XX  
 DR WPI; 2000-086388/07.  
 XX  
 XX Measuring expression of low abundance reduced complexity target nucleic  
 PT acid molecules.  
 PS  
 XX Example 3; Page 91, 187pp; English.  
 CC  
 CC AA236739-41 represent oligo(dT) primers used for modified differential  
 CC display, in the method of the invention. The specification describes a  
 CC method for measuring the level of two or more nucleic acid molecules in a  
 CC target. The method comprises contacting a probe with an arbitrarily or  
 CC statistically sampled target and detecting the amount of specific binding  
 CC of the target to the probe. The method can be used to identify disease  
 CC states, such as cancer, autoimmune disease, infectious disease, aging,  
 CC developmental disorder, proliferative disorder or neurological disorder.  
 CC Alternatively the method can be used to assess the efficacy or toxicity  
 CC of or a resistance to a treatment. Also the methods can be used to  
 CC determine differential expression of nucleic acid molecules in response  
 CC to a stimulus, e.g. a chemical, drug or growth factor (especially  
 CC epidermal growth factor), radiation, stress or a pathogen. The methods  
 CC can also be used to determine co-regulated genes that can be potential  
 CC targets for drug discovery  
 XX  
 SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTTTTTTTTTTTTTT 4478  
 Db 2 TTTTTTTTTTTTTTTT 16  
 RESULT 2777  
 AAC64202  
 ID AAC64202 standard; DNA; 17 BP.  
 XX  
 AC AAC64202;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.  
 XX  
 KW Human; polliosis-associated gene 373; IGF; immunoglobulin E;  
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KW drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200065046-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 26-APR-2000; 2000WO-JP002730.  
 XX  
 PR 27-APR-1999; 99JP-00120489.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2000-687339/67.  
 XX  
 PT Polliosis-associated gene 373 undergoing significantly low expression in  
 subjects with high cedar pollen-specific immunoglobulin-E levels, useful  
 in diagnosis of allergic diseases and screening drug candidates.

XX Example 6; Page 69; 80pp; Japanese.  
PS  
XX  
CC The invention relates to the human pollinosis-associated gene 373 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis gene 373; expression constructs and  
CC host cells comprising pollinosis-associated gene 373 nucleic acids;  
CC pollinosis-associated gene 373 primers and probes; antibodies against the  
CC protein encoded by the gene; methods of detection of pollinosis-  
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic  
CC diseases via the detection of pollinosis-associated gene 373 nucleic  
CC acids. The invention additionally encompasses methods of screening drug  
CC candidates for the treatment of allergic disease by measuring the  
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated  
CC T-cells in the presence of a test compound relative to a control.  
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic  
CC diseases and in the screening of drug candidates for the treatment of  
CC such diseases. The present sequence represents a PCR primer used in the  
CC isolation of human pollinosis-associated gene 373 cDNA  
CC  
SQ  
Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 4464 TTTT TTTT TTTT TTTT 4478  
Db 2 TTTT TTTT TTTT TTTT 16  
RESULT 2778  
AAC64203  
ID AAC64203 standard; DNA; 17 BP.  
XX  
AC AAC64203;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.  
XX  
KW Human; pollinosis-associated gene 373; IGE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO200065046-A1.  
XX  
PD 02-NOV-2000.  
XX  
PE 26-APR-2000; 2000WO-JP002730.  
XX  
PR 27-APR-1999; 99JP-00120489.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687339/67.  
XX  
PT Pollinosis-associated gene 373 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific immunoglobulin E levels, useful  
PT in diagnosis of allergic diseases and screening drug candidates.  
XX  
XX Example 6; Page 70; 80pp; Japanese.  
PS  
CC The invention relates to the human pollinosis-associated gene 373 which  
CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis gene 373; expression constructs and  
CC host cells comprising pollinosis-associated gene 373 nucleic acids;  
CC pollinosis-associated gene 373 primers and probes; antibodies against the  
CC protein encoded by the gene; methods of detection of pollinosis-  
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic  
CC diseases via the detection of pollinosis-associated gene 373 nucleic  
CC acids. The invention additionally encompasses methods of screening drug  
CC candidates for the treatment of allergic disease by measuring the  
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated  
CC T-cells in the presence of a test compound relative to a control.  
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic  
CC diseases and in the screening of drug candidates for the treatment of  
CC such diseases. The present sequence represents a PCR primer used in the  
CC isolation of human pollinosis-associated gene 373 cDNA  
CC  
SQ  
Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 4464 TTTT TTTT TTTT TTTT 4478  
Db 2 TTTT TTTT TTTT TTTT 16  
RESULT 2779  
AAC64181  
ID AAC64181 standard; DNA; 17 BP.  
XX  
AC AAC64181;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.  
XX  
KW Human; pollinosis-associated gene 419; FAF-1 homologue;  
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;  
KW T-cell; reduced expression; detection; diagnosis; drug screening;  
KW allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO200065045-A1.  
XX  
PD 02-NOV-2000.  
XX  
PE 26-APR-2000; 2000WO-JP002729.  
XX  
PR 27-APR-1999; 99JP-00120490.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687338/67.  
XX  
PT Pollinosis-associated gene 419 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
XX Example 6; Page 49; 77pp; Japanese.  
PS  
CC The invention relates to the human pollinosis-associated gene 419 which  
CC exhibits reduced expression in the T-cells of individuals with high cedar  
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from  
CC T-cells from individuals allergic to cedar pollen using the differential  
CC display method. Pollinosis-associated gene 419 has homology with the gene  
CC encoding human Fas-associated factor-1 (FAF-1). The invention also

CC relates to the protein encoded by pollinosis gene 419; expression  
 CC constructs and host cells comprising pollinosis- associated gene 419  
 CC nucleic acids; pollinosis-associated gene 419 primers and probes;  
 CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 419 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-  
 CC associated gene 419 nucleic acids. The invention additionally encompasses  
 CC methods of screening drug candidates for the treatment of allergic  
 CC disease by measuring the expression of pollinosis-associated gene 419 in  
 CC pollen antigen-stimulated T-cells in the presence of a test compound  
 CC relative to a control. Pollinosis-associated gene 419 is useful in the  
 CC diagnosis of allergic diseases and in the screening of drug candidates  
 CC for the treatment of such diseases. The present sequence represents a PCR  
 CC primer used in the isolation of human pollinosis-associated gene 419 cDNA  
 CC  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2780  
 AAC64182  
 ID AAC64182 standard; DNA; 17 BP.  
 XX  
 AC AAC64182;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.  
 XX  
 KM Human; pollinosis-associated gene 419; PAF-1 homologue;  
 KM Fae-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;  
 KM T-cell; reduced expression; detection; diagnosis; drug screening;  
 KM allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX WO200065045-A1.  
 PN  
 PD 02-NOV-2000.  
 PD  
 XX 26-APR-2000; 2000WO-JP002729.  
 PF  
 XX 27-APR-1999; 99JP-00120490.  
 PR  
 XX (GENO-) GENOX RES INC.  
 PA  
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 PI WPI; 2000-687338/67.  
 DR  
 XX Pollinosis-associated gene 419 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 PT  
 XX Example 6; Page 49; 77pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 419 which  
 CC exhibits reduced expression in the T-cells of individuals with high cedar  
 CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from  
 CC T-cells from individuals allergic to cedar pollen using the differential  
 CC display method. Pollinosis-associated gene 419 has homology with the gene  
 CC encoding human Fae-associated factor-1 (FAF-1). The invention also  
 CC relates to the protein encoded by pollinosis gene 419; expression  
 CC constructs and host cells comprising pollinosis- associated gene 419  
 CC nucleic acids; pollinosis-associated gene 419 primers and probes;

CC antibodies against the protein encoded by the gene; methods of detection  
 CC of pollinosis-associated gene 419 nucleic acids; and a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-  
 CC associated gene 419 nucleic acids. The invention additionally encompasses  
 CC methods of screening drug candidates for the treatment of allergic  
 CC disease by measuring the expression of pollinosis-associated gene 419 in  
 CC pollen antigen-stimulated T-cells in the presence of a test compound  
 CC relative to a control. Pollinosis-associated gene 419 is useful in the  
 CC diagnosis of allergic diseases and in the screening of drug candidates  
 CC for the treatment of such diseases. The present sequence represents a PCR  
 CC primer used in the isolation of human pollinosis-associated gene 419 cDNA  
 CC  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2781  
 AAC64171  
 ID AAC64171 standard; DNA; 17 BP.  
 XX  
 AC AAC64171;  
 XX  
 DT 21-FEB-2001 (first entry)  
 XX  
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.  
 XX  
 KM Human; pollinosis-associated gene 513; IGE; immunoglobulin E;  
 KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
 KM drug screening; allergic disease; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX WO200065049-A1.  
 PN  
 PD 02-NOV-2000.  
 PD  
 XX 26-APR-2000; 2000WO-JP002733.  
 PF  
 XX 27-APR-1999; 99JP-00120491.  
 PR  
 XX (GENO-) GENOX RES INC.  
 PA  
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 PI WPI; 2000-687342/67.  
 DR  
 XX Pollinosis-associated gene 513 undergoing significantly low expression in  
 PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis  
 PT of allergic diseases and screening drug candidates.  
 PT  
 XX Example 6; Page 38; 46pp; Japanese.  
 XX  
 CC The invention relates to the human pollinosis-associated gene 513 which  
 CC exhibits significantly reduced expression in the T-cells of individuals  
 CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene  
 CC was isolated from T-cells from individuals allergic to cedar pollen using  
 CC the differential display method. The invention also relates to methods of  
 CC detection of pollinosis-associated gene 513 nucleic acids; a method of  
 CC diagnosis of allergic diseases via the detection of pollinosis-associated  
 CC gene 513 nucleic acids; and methods of screening drug candidates for the  
 CC treatment of allergic disease by measuring the expression of pollinosis-  
 CC associated gene 513 in pollen antigen-stimulated T-cells in the presence  
 CC of a test compound relative to a control. Pollinosis-associated gene 513  
 CC is useful in the diagnosis of allergic diseases and in the screening of  
 CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 513 cDNA  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4464 TTTTTTTTTTTTTT 4478  
DB 2 TTTTTTTTTTTTTT 16  
RESULT 2782  
AAC64172  
ID AAC64172 standard; DNA; 17 BP.  
XX  
AC AAC64172;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.  
XX  
KW Human; pollinosis-associated gene 513; IGE; immunoglobulin E;  
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
OS Synthetic.  
XX  
PN WO20065049-A1.  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002733.  
XX  
PR 27-APR-1999; 99JP-00120491.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687342/67.  
XX  
PT Pollinosis-associated gene 513 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
PS Example 6; Page 38; 46pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 513 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates to methods of  
CC detection of pollinosis-associated gene 513 nucleic acids; a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 513 nucleic acids; and methods of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 513  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 513 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTTTTTTTTTTTT 4478  
DB 2 TTTTTTTTTTTTTT 16  
RESULT 2783  
AAC64161  
ID AAC64161 standard; DNA; 17 BP.  
XX  
AC AAC64161;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.  
XX  
KW Human; pollinosis-associated gene 581; IGE; immunoglobulin E;  
KM cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
OS Synthetic.  
XX  
PN WO20065048-A1.  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002732.  
XX  
PR 27-APR-1999; 99JP-00120492.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687341/67.  
XX  
PT Pollenosis-associated gene 581 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
PS Example 6; Page 39; 69pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 581 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates to methods  
CC to the protein encoded by pollinosis-associated gene 581; to expression  
CC constructs and host cells comprising pollinosis-associated gene 581  
CC nucleic acids; pollinosis-associated gene 581 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 581 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 581 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by  
CC measuring the expression of pollinosis-associated gene 581 in pollen  
CC antigen-stimulated T-cells in the presence of a test compound relative to  
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of  
CC allergic diseases and in the screening of drug candidates for the  
CC treatment of such diseases. The present sequence represents a PCR primer  
CC used in the isolation of human pollinosis-associated gene 581 cDNA  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 4464 TTTTTTTTTTTTTT 4478  
DB 2 TTTTTTTTTTTTTT 16

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RESULT 2784
AAC64162
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KM Human; pollinosis-associated gene 581; IGE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KM drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000MO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagaau T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels; useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16

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XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX
KM Human; pollinosis-associated gene 627; IGE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KM drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000MO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagaau T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels; useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 41; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
DB 2 TTTT TTTT TTTT TTTT 16

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RESULT 2785
AAC64213
ID AAC64213 standard; DNA; 17 BP.
XX
AC AAC64213;
XX

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RESULT 2786
AAC64214
ID AAC64214 standard; DNA; 17 BP.
XX
AC AAC64214;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KM Human; pollinosis-associated gene 627; IGE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KM drug screening; allergic disease; PCR primer; ss.
XX

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OS Synthetic.  
XX  
XX WO200065051-A1.  
XX  
XX 02-NOV-2000.  
XX  
XX 26-APR-2000; 2000WO-JP002735.  
XX  
XX 27-APR-1999; 99JP-00120493.  
XX  
XX (GENO-) GENOX RES INC.  
XX  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX WPI; 2000-687344/67.  
XX  
XX Pollinosis-associated gene 627 undergoing significantly low expression in  
XX subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
XX of allergic diseases and screening drug candidates.  
XX  
XX Example 6; Page 42; 51pp; Japanese.  
XX  
XX The invention relates to the human pollinosis-associated gene 627 which  
XX exhibits significantly reduced expression in the T-cells of individuals  
XX with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
XX was isolated from T-cells from individuals allergic to cedar pollen using  
XX the differential display method. The invention also relates to methods of  
XX detection of pollinosis-associated gene 627 nucleic acids; a method of  
XX diagnosis of allergic diseases via the detection of pollinosis-associated  
XX gene 627 nucleic acids; and a method of screening drug candidates for the  
XX treatment of allergic disease by measuring the expression of pollinosis-  
XX associated gene 627 in pollen antigen-stimulated T-cells in the presence  
XX of a test compound relative to a control. Pollinosis-associated gene 627  
XX is useful in the diagnosis of allergic diseases and in the screening of  
XX drug candidates for the treatment of such diseases. The present sequence  
XX represents a PCR primer used in the isolation of human pollinosis-  
XX associated gene 627 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT 4478  
DB 2 TTTT TTTT TTTT TTTT 16  
RESULT 2787  
AAC64231  
ID AAC64231 standard; DNA; 17 BP.  
XX  
XX AAC64231;  
XX  
XX 21-FEB-2001 (first entry)  
XX  
XX PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.  
XX  
XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
XX immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
XX detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO200065050-A1.  
XX  
XX 02-NOV-2000.  
XX  
XX 26-APR-2000; 2000WO-JP002734.  
XX  
XX 27-APR-1999; 99JP-00120494.  
XX  
XX (GENO-) GENOX RES INC.

XX  
XX (GENO-) GENOX RES INC.  
XX  
XX (EISA) EISAI CO LTD.  
XX  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
XX Yokoi A;  
XX WPI; 2000-687343/67.  
XX  
XX Pollinosis-associated gene 795 undergoing significantly low expression in  
XX subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
XX of allergic diseases and screening drug candidates.  
XX  
XX Page 45; Example 6; 73pp; Japanese.  
XX  
XX The invention relates to the human pollinosis-associated gene 795 which  
XX exhibits significantly reduced expression in the T-cells of individuals  
XX with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
XX was isolated from T-cells from individuals allergic to cedar pollen using  
XX the differential display method. Pollinosis-associated gene 795 has  
XX homology with the human vimentin gene. The invention also relates also  
XX relates to the protein encoded by pollinosis gene 795; to expression  
XX constructs and host cells comprising pollinosis-associated gene 795  
XX nucleic acids; pollinosis-associated gene 795 primers and probes;  
XX antibodies against the protein encoded by the gene; methods of detection  
XX of pollinosis-associated gene 795 nucleic acids; and a method of  
XX diagnosis of allergic diseases via the detection of pollinosis-associated  
XX gene 795 nucleic acids. The invention additionally encompasses methods of  
XX screening drug candidates for the treatment of allergic disease by  
XX measuring the expression of pollinosis-associated gene 795 in pollen  
XX antigen-stimulated T-cells in the presence of a test compound relative to  
XX a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
XX allergic diseases and in the screening of drug candidates for the  
XX treatment of such diseases. The present sequence represents a PCR primer  
XX used in the isolation of human pollinosis-associated gene 795 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT 4478  
DB 2 TTTT TTTT TTTT TTTT 16  
RESULT 2788  
AAC64230  
ID AAC64230 standard; DNA; 17 BP.  
XX  
XX AAC64230;  
XX  
XX 21-FEB-2001 (first entry)  
XX  
XX PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.  
XX  
XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
XX immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
XX detection; diagnosis; drug screening; allergic disease; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO200065050-A1.  
XX  
XX 02-NOV-2000.  
XX  
XX 26-APR-2000; 2000WO-JP002734.  
XX  
XX 27-APR-1999; 99JP-00120494.  
XX  
XX (GENO-) GENOX RES INC.

PA (EISA ) EISAI CO LTD.  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;  
XX WPI; 2000-667343/67.  
DR  
PT Pollinosis-associated gene 795 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
PS Page 45; Example 6; 73pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 795 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. Pollinosis-associated gene 795 has  
CC homology with the human vimentin gene. The invention also relates also  
CC relates to the protein encoded by pollinosis gene 795; to expression  
CC constructs and host cells comprising pollinosis-associated gene 795  
CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 795 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 795 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by  
CC measuring the expression of pollinosis-associated gene 795 in pollen  
CC antigen-stimulated T-cells in the presence of a test compound relative to  
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
CC allergic diseases and in the screening of drug candidates for the  
CC treatment of such diseases. The present sequence represents a PCR primer  
CC used in the isolation of human pollinosis-associated gene 795 cDNA  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 2 TTTT TTTT TTTT TTTT 16  
RESULT 2789  
AAC92292  
ID AAC92292 standard; DNA; 17 BP.  
XX  
AC AAC92292;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.  
XX  
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;  
KW allergic disease; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200073439-A1.  
XX PD 07-DEC-2000.  
XX  
PF 18-MAY-2000; 2000WO-JP003191;  
XX  
PR 27-MAY-1999; 99JP-00148784.  
XX (GENO-) GENOX RES INC.  
PA (EISA ) EISAI CO LTD.  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;  
XX WPI; 2001-061528/07.  
XX  
PT Pollinosis-associated gene 465 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
PS Example 6; Page 43; 61pp; Japanese.  
XX  
CC The present invention describes the human pollinosis-associated gene 465  
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in  
CC (AAC92291), that undergoes significantly low expression in subjects after  
CC pollen scattering, and is useful in the diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen. The gene is useful in  
CC the diagnosis of allergic diseases and screening candidate compounds for  
CC remedies capable of regulating the response of T cells to the stimulus by  
CC an antigen. The present sequence represents a PCR primer which is used in  
CC an example from the present invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db 2 TTTT TTTT TTTT TTTT 16  
RESULT 2790  
AAC92293  
ID AAC92293 standard; DNA; 17 BP.  
XX  
AC AAC92293;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.  
XX  
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;  
KW allergic disease; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200073439-A1.  
XX PD 07-DEC-2000.  
XX  
PF 18-MAY-2000; 2000WO-JP003191.  
XX  
PR 27-MAY-1999; 99JP-00148784.  
XX (GENO-) GENOX RES INC.  
PA (EISA ) EISAI CO LTD.  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;  
XX WPI; 2001-061528/07.  
XX  
PT Pollinosis-associated gene 465 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
PS Example 6; Page 44; 61pp; Japanese.  
XX



CC The present invention describes the human pollinosis-associated gene 465  
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in  
CC (AAC92291), that undergoes significantly low expression in subjects after  
CC pollen scattering, and is useful in the diagnosis of allergic diseases  
CC and screening candidate compounds for remedies capable of regulating the  
CC response of T cells to the stimulus by an antigen. The gene is useful in  
CC the diagnosis of allergic diseases and screening candidate compounds for  
CC remedies capable of regulating the response of T cells to the stimulus by  
CC an antigen. The present sequence represents a PCR primer which is used in  
CC an example from the present invention  
CC  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
QY Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 4464 TTTT TTTT TTTT TTTT 4478  
2 TTTT TTTT TTTT TTTT 16  
RESULT 2791  
AAC91720  
ID AAC91720 standard; DNA; 17 BP.  
AC AAC91720;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.  
XX  
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;  
KW reduced expression; detection; diagnosis; drug screening;  
KW allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200073440-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 18-MAY-2000; 2000WO-JP003192.  
XX  
PR 27-MAY-1999; 99JP-00148785.  
XX  
PA (GENO-) GENOX RES INC.  
PA (EISA) EISAI CO LTD.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;  
XX  
DR WPI; 2001-032159/04.  
XX  
PT Pollinosis-associated gene 787 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
PS Example 6; Page 40; 54pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 787 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC after the pollen-scattering season, relative to expression levels in T-  
CC cells before the pollen-scattering season. The gene was isolated from T-  
CC cells from individuals allergic to pollen using the differential display  
CC method. The invention also relates to pollinosis-associated gene 787  
CC primers and probes; methods of detection of pollinosis-associated gene  
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the  
CC detection of pollinosis-associated gene 787 nucleic acids. The invention  
CC additionally encompasses a method of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 787 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 787  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 787 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
QY Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 4464 TTTT TTTT TTTT TTTT 4478  
2 TTTT TTTT TTTT TTTT 16  
RESULT 2792  
AAC91719  
ID AAC91719 standard; DNA; 17 BP.  
AC AAC91719;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.  
XX  
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;  
KW reduced expression; detection; diagnosis; drug screening;  
KW allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200073440-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 18-MAY-2000; 2000WO-JP003192.  
XX  
PR 27-MAY-1999; 99JP-00148785.  
XX  
PA (GENO-) GENOX RES INC.  
PA (EISA) EISAI CO LTD.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;  
XX  
DR WPI; 2001-032159/04.  
XX  
PT Pollinosis-associated gene 787 undergoing significantly low expression in  
PT subjects after pollen scattering, useful in diagnosis of allergic  
PT diseases and screening candidate compounds to regulate response of T  
PT cells to antigen stimulus.  
XX  
PS Example 6; Page 40; 54pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 787 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC after the pollen-scattering season, relative to expression levels in T-  
CC cells before the pollen-scattering season. The gene was isolated from T-  
CC cells from individuals allergic to pollen using the differential display  
CC method. The invention also relates to pollinosis-associated gene 787  
CC primers and probes; methods of detection of pollinosis-associated gene  
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the  
CC detection of pollinosis-associated gene 787 nucleic acids. The invention  
CC additionally encompasses a method of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 787  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-associated gene 787 cDNA  
 CC associated gene 787 cDNA  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2793  
 AAC82875  
 ID AAC82875 standard; DNA; 17 BP.  
 XX  
 AC AAC82875;  
 XX  
 DT 20-MAR-2001 (first entry)  
 XX  
 DE Human pollinosis-associated gene 441 primer #2.  
 XX  
 KM Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
 KW pollen scattering; antigen; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073435-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 18-MAY-2000; 2000WO-JP003190.  
 XX  
 PR 27-MAY-1999; 99JP-00148783.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kaishibara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2001-061526/07.  
 XX  
 PT Pollinosis-associated gene 441 which undergoes lower expression in  
 PT subjects after pollen scattering, useful in diagnosis of allergic  
 PT diseases and screening candidate compounds to regulate response of T  
 PT cells to antigen stimulus.  
 XX  
 PS Example 6; Page 35; 42pp; Japanese.  
 XX  
 CC This invention describes a novel nucleic acid molecule comprising a  
 CC sequence (I) which undergoes significantly low expression in subjects  
 CC after pollen scattering, and is useful in diagnosis of allergic diseases  
 CC and screening candidate compounds for remedies capable of regulating the  
 CC response of T cells to the stimulus by an antigen  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2794  
 AAC82874  
 ID AAC82874 standard; DNA; 17 BP.  
 XX  
 AC AAC82874;

XX  
 DT 20-MAR-2001 (first entry)  
 XX  
 DE Human pollinosis-associated gene 441 primer #1.  
 XX  
 KM Pollinosis; pollinosis-associated gene 441; allergy; T cell;  
 KW pollen scattering; antigen; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073435-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PF 18-MAY-2000; 2000WO-JP003190.  
 XX  
 PR 27-MAY-1999; 99JP-00148783.  
 XX  
 PA (GENO-) GENOX RES INC.  
 XX  
 PI Nagasu T, Sugita Y, Kaishibara T, Oshida T, Obayashi M, Gunji S;  
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
 XX  
 DR WPI; 2001-061526/07.  
 XX  
 PT Pollinosis-associated gene 441 which undergoes lower expression in  
 PT subjects after pollen scattering, useful in diagnosis of allergic  
 PT diseases and screening candidate compounds to regulate response of T  
 PT cells to antigen stimulus.  
 XX  
 PS Example 6; Page 35; 42pp; Japanese.  
 XX  
 CC This invention describes a novel nucleic acid molecule comprising a  
 CC sequence (I) which undergoes significantly low expression in subjects  
 CC after pollen scattering, and is useful in diagnosis of allergic diseases  
 CC and screening candidate compounds for remedies capable of regulating the  
 CC response of T cells to the stimulus by an antigen  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2795  
 AAH47127  
 ID AAH47127 standard; DNA; 17 BP.  
 XX  
 AC AAH47127;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of primer GT15C.  
 XX  
 KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;  
 KW PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200165259-A1.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-JP001372.  
 XX  
 PR 02-MAR-2000; 2000JP-00061832.  
 XX  
 PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saico H;  
 PI WPI; 2001-557789/62.  
 XX  
 XX  
 PT Diagnosis of allergies including atopic dermatitis.  
 PS Example 6; Page 66; 83pp; Japanese.  
 XX  
 CC The invention provides a method of diagnosis of allergies that involves:  
 CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151  
 CC in T-cells; and comparing them with the level of expression in healthy T-  
 CC cells. The method is useful for diagnosing allergies, particularly atopic  
 CC dermatitis. The present sequence represents a PCR primer used for  
 CC analysis of the expression of the above genes  
 CC  
 XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2796  
 AAH47126  
 ID AAH47126 standard; DNA; 17 BP.  
 XX  
 AC AAH47126;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of primer GT15A.  
 XX  
 KM B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;  
 KM PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200165259-A1.  
 PN  
 XX  
 PD 07-SEP-2001.  
 PD  
 PF 23-FEB-2001; 2001WO-JP001372.  
 PF  
 XX  
 PR 02-MAR-2000; 2000JP-00061832.  
 PR  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saico H;  
 PI WPI; 2001-557789/62.  
 DR  
 XX  
 PT Diagnosis of allergies including atopic dermatitis.  
 PS Example 6; Page 65; 83pp; Japanese.  
 XX  
 CC The invention provides a method of diagnosis of allergies that involves:  
 CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151  
 CC in T-cells; and comparing them with the level of expression in healthy T-  
 CC cells. The method is useful for diagnosing allergies, particularly atopic  
 CC dermatitis. The present sequence represents a PCR primer used for  
 CC analysis of the expression of the above genes  
 CC  
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT 4478  
 DB 2 TTTT TTTT TTTT TTTT 16  
 RESULT 2797  
 ABN01547/C  
 ID ABN01547 standard; DNA; 17 BP.  
 XX  
 AC ABN01547;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1539.  
 XX  
 KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KM skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200192524-A2.  
 PN  
 XX  
 PD 06-DEC-2001.  
 PD  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR  
 XX  
 PA (AEOM-) AEOMICA INC.  
 PA  
 XX  
 PI Gu Y, Yi Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 DR  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 1539; 214pp; English.  
 PS  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterize and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognize hGDMLP-  
 CC 1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart

CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2474 TCCAGGGCACACGCC 2488  
Db 15 TCCAGGGCACACGCC 1  
RESULT 2798  
ABN01546/c  
ID ABN01546 standard; DNA; 17 BP.  
XX  
AC ABN01546;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1538.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
XX  
PS Disclosure; SEQ ID NO 1538; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
CC -1 protein, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2474 TCCAGGGCACACGCC 2488  
Db 16 TCCAGGGCACACGCC 2  
RESULT 2799  
ABN01545/c  
ID ABN01545 standard; DNA; 17 BP.  
XX  
AC ABN01545;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1537.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX

PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT description ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 1537; 214pp; English.  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from Wipo  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 XX Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2474 TCCAGGCGACCGCC 2488  
 DB 17 TCCAGGCGACCGCC 3  
 RESULT 2800  
 ABK49634  
 ID ABK49634 standard; DNA; 17 BP.  
 XX  
 AC ABK49634;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.  
 XX  
 KM Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
 KM differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200224903-A1.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-JP008246.  
 XX  
 PR 25-SEP-2000; 2000JP-00291318.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G,  
 PI Takahashi E;  
 DR WPI; 2002-315738/35.  
 XX  
 PT Examining allergic diseases by differential display of gene showing

PT different expression particularly increased expression in remission stage  
 PT in eosinophils of patients, also applicable in screening candidate  
 PT compounds for remedies.  
 XX  
 XX Example 1; Page 56; 72pp; Japanese.  
 CC The invention relates to a method for examining allergic diseases  
 CC comprising determining the expression level of a gene containing the  
 CC human cDNA appearing as ABK49633 which has homology with  
 CC acetyltransferases in the eosinophils of a patient and comparing the  
 CC expression level with that in the eosinophils of a healthy individual  
 CC (i.e. differential display). Also included are methods of screening for  
 CC candidate compounds which affect the expression level of the gene or the  
 CC activity of the protein encoded by the gene (including related proteins  
 CC and mutants), the use of probes based on the gene sequence in the  
 CC examination of allergic diseases, the use of reporter constructs in the  
 CC screening of candidate compounds, a vector containing a the transcription  
 CC -controlling region of the gene, cells transformed with the vector, an  
 CC antibody against the protein and a model animal for allergic diseases  
 CC which is a transgenic non-human vertebrate with lowering of expression  
 CC intensity of the gene in eosinophils. The method is examining allergic  
 CC diseases particularly atopic dermatitis which is also applicable in  
 CC screening candidate compounds for remedies. Such method can be performed  
 CC in high throughput, at low cost. The present sequence is a differential  
 CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
 CC protein 20-90-05  
 XX  
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTTTTTTTTTTTTT 4478  
 DB 2 TTTTTTTTTTTTTTT 16  
 RESULT 2801  
 ABK49635  
 ID ABK49635 standard; DNA; 17 BP.  
 XX  
 AC ABK49635;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.  
 XX  
 KM Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
 KM differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200224903-A1.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 21-SEP-2001; 2001WO-JP008246.  
 XX  
 PR 25-SEP-2000; 2000JP-00291318.  
 XX  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 PA (EISA) EISAI CO LTD.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G,  
 PI Takahashi E;  
 DR WPI; 2002-315738/35.  
 XX  
 PT Examining allergic diseases by differential display of gene showing  
 PT different expression particularly increased expression in remission stage  
 PT in eosinophils of patients, also applicable in screening candidate

PT compounds for remedies.  
XX  
PS Example 1; Page 56; 72pp; Japanese.  
XX  
CC The invention relates to a method for examining allergic diseases  
CC comprises determining the expression level of a gene containing, the  
CC human cDNA appearing as ABK49633 which has homology with  
CC acetyltransferases in the eosinophils of a patient and comparing the  
CC expression level with that in the eosinophils of a healthy individual  
CC (i.e. differential display). Also included are methods of screening for  
CC candidate compounds which affect the expression level of the gene or the  
CC activity of the protein encoded by the gene (including related proteins  
CC and mutants), the use of probes based on the gene sequence in the  
CC examination of allergic diseases, the use of reporter constructs in the  
CC screening of candidate compounds, a vector containing a the transcription  
CC -controlling region of the gene, cells transformed with the vector, an  
CC antibody against the protein and a model animal for allergic diseases  
CC which is a transgenic non-human vertebrate with lowering of expression  
CC intensity of the gene in eosinophils. The method is examining allergic  
CC diseases particularly atopic dermatitis which is also applicable in  
CC screening candidate compounds for remedies. Such method can be performed  
CC in high throughput, at low cost. The present sequence is a differential  
CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
CC protein 20-90-05  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
DB 2 TTTT TTTT TTTT TTTT 16  
RESULT 2802  
ABLS9038  
ID ABL59038 standard; DNA; 17 BP.  
XX  
AC ABL59038;  
XX  
DT 20-AUG-2002 (first entry)  
XX  
DE Nucleotide sequence of PCR primer GT15A.  
XX  
KM Human; allergosis; eosinophil; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002095500-A.  
XX  
PD 02-APR-2002.  
XX  
PE 25-SEP-2000; 2000JP-00291316.  
XX  
PR 25-SEP-2000; 2000JP-00291316.  
XX  
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.  
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.  
XX  
DR WPI; 2002-439993/47.  
XX  
PT Examining allergosis, involves measuring the expression levels of a  
PT specific gene, and comparing it to the levels in the eosinophils of a  
PT healthy control.  
XX  
PS Example 1; Page 17; 20pp; Japanese.  
XX  
CC The specification describes a method for examining allergosis. The method  
CC comprises measuring the expression level of the gene given in ABL59037,  
CC and comparing it with the expression level of the gene in the eosinophils  
CC of a healthy person. The method is used for the examination of

CC allergosis. The present sequence represents a PCR primer, which is used  
CC in the course of the invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
DB 2 TTTT TTTT TTTT TTTT 16  
RESULT 2803  
ABLS9039  
ID ABL59039 standard; DNA; 17 BP.  
XX  
AC ABL59039;  
XX  
DT 20-AUG-2002 (first entry)  
XX  
DE Nucleotide sequence of PCR primer GT15C.  
XX  
KM Human; allergosis; eosinophil; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002095500-A.  
XX  
PD 02-APR-2002.  
XX  
PE 25-SEP-2000; 2000JP-00291316.  
XX  
PR 25-SEP-2000; 2000JP-00291316.  
XX  
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.  
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.  
XX  
DR WPI; 2002-439993/47.  
XX  
PT Examining allergosis, involves measuring the expression levels of a  
PT specific gene, and comparing it to the levels in the eosinophils of a  
PT healthy control.  
XX  
PS Example 1; Page 17; 20pp; Japanese.  
XX  
CC The specification describes a method for examining allergosis. The method  
CC comprises measuring the expression level of the gene given in ABL59037,  
CC and comparing it with the expression level of the gene in the eosinophils  
CC of a healthy person. The method is used for the examination of  
CC allergosis. The present sequence represents a PCR primer, which is used  
CC in the course of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
DB 2 TTTT TTTT TTTT TTTT 16  
RESULT 2804  
ABN99829  
ID ABN99829 standard; DNA; 17 BP.  
XX  
AC ABN99829;  
XX  
DT 15-AUG-2002 (first entry)  
XX

DE Human allergic disease related PCR primer SEQ ID NO: 18.  
XX (NIGGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
XX primer; ss.  
XX Homo sapiens.  
XX WO200233069-A1.  
XX 25-APR-2002.  
XX 28-SEP-2001; 2001WO-JP008574.  
XX 13-OCT-2000; 2000JP-00314093.  
XX (GENO-) GENOX RES INC.  
XX (NIGGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
XX WPI; 2002-372311/40.  
XX  
XX  
XX Method for examining allergic diseases by differential display of  
PT seventeen genes showing different expression particularly significant  
PT increase in eosinophils in patients with mild atopic dermatitis, also  
PT applicable in screening compounds.  
XX Example 1; Page 109; 165pp; Japanese.  
XX  
XX The present invention relates to a method for examining allergic diseases  
CC which involves determining the expression level of a gene, having one of  
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
CC eosinophils in a patient and comparing the expression level with that in  
CC the eosinophils of a healthy individual. The method can be used to  
CC examine allergic diseases, particularly atopic dermatitis, and its early  
CC diagnosis, which is also applicable in screening candidate compounds for  
CC remedies. The present sequence is a PCR primer described in the  
CC exemplification of the invention  
XX  
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db |||||  
2 TTTT TTTT TTTT TTTT TTTT 16  
RESULT 2805  
ABN99830  
ID ABN99830 standard; DNA; 17 BP.  
XX  
XX ABN99830;  
AC  
XX 15-AUG-2002 (first entry)  
DT  
XX Human allergic disease related PCR primer SEQ ID NO: 19.  
DE  
XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;  
KW primer; ss.  
XX Homo sapiens.  
XX WO200233069-A1.  
XX 25-APR-2002.  
XX 28-SEP-2001; 2001WO-JP008574.  
XX 13-OCT-2000; 2000JP-00314093.  
XX

PA (GENO-) GENOX RES INC.  
XX (NIGGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;  
XX WPI; 2002-372311/40.  
XX  
XX  
XX Method for examining allergic diseases by differential display of  
PT seventeen genes showing different expression particularly significant  
PT increase in eosinophils in patients with mild atopic dermatitis, also  
PT applicable in screening compounds.  
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XX The present invention relates to a method for examining allergic diseases  
CC which involves determining the expression level of a gene, having one of  
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the  
CC eosinophils in a patient and comparing the expression level with that in  
CC the eosinophils of a healthy individual. The method can be used to  
CC examine allergic diseases, particularly atopic dermatitis, and its early  
CC diagnosis, which is also applicable in screening candidate compounds for  
CC remedies. The present sequence is a PCR primer described in the  
CC exemplification of the invention  
XX  
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
Db |||||  
2 TTTT TTTT TTTT TTTT TTTT 16  
RESULT 2806  
AAL49948  
ID AAL49948 standard; DNA; 17 BP.  
XX  
XX AAL49948;  
AC  
XX 10-DEC-2002 (first entry)  
DT  
XX Human B1153 expression in allergic disease related PCR primer GT15A.  
DE  
XX Human; allergy; B1153; differential expression; anti-allergic; asthma;  
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;  
KW ss.  
XX Unidentified.  
XX  
XX WO200250269-A1.  
XX 27-JUN-2002.  
XX 21-DEC-2001; 2001WO-JP011286.  
XX 21-DEC-2000; 2000JP-00389476.  
XX  
XX (GENO-) GENOX RES INC.  
XX (NIGGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;  
XX WPI; 2002-713252/77.  
XX  
XX Examination of allergic diseases comprises detecting gene B1153 over-  
PT expressed in T cells of allergy patients for diagnosis treatment and  
PT investigation of atopic skin inflammation and asthma.  
XX Example 6; Page 81; 102pp; Japanese.  
XX  
XX The present invention relates to a method of examining allergic diseases

CC which comprises comparing the expression level of gene B153 in allergy  
 CC patients with the expression level in healthy subjects. The method is  
 CC useful for the treatment, prevention, diagnosis and study of allergic  
 CC diseases including atopic skin inflammation and asthma. The present  
 CC sequence is a PCR primer described in the exemplification of the  
 CC invention

XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2807  
 AAL49949  
 ID AAL49949 standard; DNA; 17 BP.  
 AC AAL49949;  
 XX  
 DT 10-DEC-2002 (first entry)  
 DE Human B153 expression in allergic disease related PCR primer GT15C.  
 XX  
 KM Human; allergy; B153; differential expression; antiallergic; asthma;  
 KM antiaesthetic; antiinflammatory; atopic skin inflammation; PCR; primer;  
 KM ss.  
 OS Unidentified.  
 XX  
 PN WO200250269-A1;  
 PD 27-JUN-2002.  
 PF 21-DEC-2001; 2001WO-JP011286.  
 PR 21-DEC-2000; 2000JP-00389476.  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 XX  
 PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagaau T, Tsujimoto G;  
 XX WPI; 2002-713252/77.  
 DR  
 XX  
 PT Examination of allergic diseases comprises detecting gene B153 over-  
 PT expressed in T cells of allergy patients for diagnosis treatment and  
 PT investigation of atopic skin inflammation and asthma.  
 XX  
 PS Example 6; Page 82; 102pp; Japanese.  
 XX  
 CC The present invention relates to a method of examining allergic diseases  
 CC which comprises comparing the expression level of gene B153 in allergy  
 CC patients with the expression level in healthy subjects. The method is  
 CC useful for the treatment, prevention, diagnosis and study of allergic  
 CC diseases including atopic skin inflammation and asthma. The present  
 CC sequence is a PCR primer described in the exemplification of the  
 CC invention

XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2808  
 AAL47234  
 ID AAL47234 standard; DNA; 17 BP.  
 AC AAL47234;  
 XX  
 DT 22-AUG-2002 (first entry)  
 DE Allergic disease examination method related anchor primer SEQ ID NO: 2.  
 XX  
 KM Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;  
 KM atopic dermatitis; human; PCR; primer; ss.  
 OS Unidentified.  
 XX  
 PN WO200233122-A1.  
 PD 25-APR-2002.  
 PF 11-OCT-2001; 2001WO-JP008937.  
 PR 13-OCT-2000; 2000JP-00314093.  
 PA (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
 PA (RISA ) RISA CO LTD.  
 XX  
 PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagaau T, Saito H;  
 PI Takahashi E;  
 DR WPI; 2002-372313/40.  
 PT Method for examining allergic diseases by differential display of  
 PT intersectin 2 gene showing different expression particularly significant  
 PT increase in eosinophils in patients.  
 XX  
 PS Example 1; Page 52; 90pp; Japanese.  
 XX  
 CC The present invention relates to a method for examining allergic diseases  
 CC with intersectin 2 gene or a gene with equivalent function of intersectin  
 CC 2 as an indicator gene, which comprises determining the expression level  
 CC of the gene in the eosinophils in a patient, and comparing the expression  
 CC level with that in the eosinophils of a healthy individual. The method is  
 CC for examining allergic diseases, particularly atopic dermatitis, which is  
 CC also applicable in screening candidate compounds for remedies. The  
 CC present sequence is an anchor primer described in the exemplification of  
 CC the invention

XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2809  
 AAL47235  
 ID AAL47235 standard; DNA; 17 BP.  
 AC AAL47235;  
 XX  
 DT 22-AUG-2002 (first entry)  
 DE Allergic disease examination method related anchor primer SEQ ID NO: 3.  
 XX  
 KM Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;  
 KM atopic dermatitis; human; PCR; primer; ss.  
 XX



OS Unidentified.

PN WO200233122-A1.

PD 25-APR-2002.

PF 11-OCT-2001; 2001WO-JP008937.

PR 13-OCT-2000; 2000JP-00314093.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagaue T, Saito H, Takahashi E;

DR WPI; 2002-372313/40.

PT Method for examining allergic diseases by differential display of

PT intersectin 2 gene showing different expression particularly significant

PS increase in eosinophils in patients.

PS Example 1; Page 53; 90pp; Japanese.

CC The present invention relates to a method for examining allergic diseases

CC with intersectin 2 gene or a gene with equivalent function of intersectin

CC 2 as an indicator gene, which comprises determining the expression level

CC of the gene in the eosinophils in a patient, and comparing the expression

CC level with that in the eosinophils of a healthy individual. The method is

CC for examining allergic diseases, particularly atopic dermatitis, which is

CC also applicable in screening candidate compounds for remedies. The

CC present sequence is an anchor primer described in the exemplification of

CC the invention

CC Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 15; DB 1; Length 17;

QY Best Local Similarity 100.0%; Pred. No. 1.5e+03;

DB Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTTTTTTTTTTTT 4478

DB 2 TTTTTTTTTTTTTT 16

RESULT 2810

ABK57743

ID ABK57743 standard; RNA; 17 BP.

XX

AC ABK57743;

XX

DT 02-JUL-2002 (first entry)

XX

DB Human CLCA1 gene enzymatic nucleic acid #2114.

XX

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

XX

XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

XX

XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

XX

XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

XX

XX acetylcysteine.

XX

XX Homo sapiens.

OS

XX

PN WO200211674-A2.

XX

PD 14-FEB-2002.

XX

PF 09-AUG-2001; 2001WO-US024970.

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

```

PA      (SYNTE ) SYNTEX USA LLC.
PA      (THOM/) THOMPSON J.
PA      Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI      Gruppe A;
PI      WPI, 2002-217145/27.
XX
XX      Enzymatic polynucleotide that down regulates expression of chloride
PT      channel calcium activated gene, useful for treating Chronic obstructive
PT      pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX      Claim 4; Page 134; 152pp; English.
XX
XX      The invention relates to enzymatic nucleic acid molecules that down
CC      regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC      by cleaving RNA derived from the genes. The nucleic acid sequences are
CC      useful as pharmaceutical agents for treating conditions such as chronic
CC      obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC      fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC      that are related to or will respond to the levels of CLCA1 in a cell or
CC      tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC      hence, are useful for treatment of a patient having a condition
CC      associated with the level of CLCA1, where the invention further comprises
CC      the use of one or more therapies under conditions suitable for the
CC      treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC      antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC      nucleic acids of the invention are also used as diagnostic tools to
CC      examine genetic drift and mutations within diseased cells or to detect
CC      the presence of CLCA1 RNA in a cell. This sequence represents an
CC      enzymatic nucleic acid molecule of the invention
XX
XX      Sequence 17 BP; 2 A; 3 C; 9 G; 0 T; 3 U; 0 Other;
SQ
SQ      Query March          0.2%; Score 15; DB 1; Length 17;
SQ      Match Local Similarity 86.7%; Pred. No. 1.5e+03;
SQ      Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
OY      5017 GGGCTCTGGAGGAG 5031
OY      |||::|||||
DB      2 GGGCTCTGGAGGAG 16
DB
DB      RESULT 2811
DB      ABRK57744
DB      ID ABRK57744 standard; RNA; 17 BP.
AC      ABRK57744;
AC
AC      02-JUL-2002 (first entry)
DT
DT      XX
DE      Human CLCA1 gene enzymatic nucleic acid #2115.
XX
XX      Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KM      antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KM      chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KM      oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KM      acetylcysteine.
XX
XX      Homo sapiens.
OS
OS      MO200211674-A2.
XX
XX      14-FEB-2002.
PD
PD      09-AUG-2001, 2001WO-US024970.
XX
XX      09-AUG-2000; 2000US-0224383P.
PR
PR      (RIBO-) RIBOZYME PHARM INC.
XX
XX      (SYNTE ) SYNTEX USA LLC.
PA
PA      (THOM/) THOMPSON J.
XX

```

```

PI Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PI Grube A;
XX
XX MPI; 2002-217145/27.
DR
XX Enzymatic polymnucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX Claim 4; Page 135; 152pp; English.
XX
XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
Query Match 0.2%; Score 15; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 1.5e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5017 GGGCTCTGGGAGAG 5031
DB 1 GGGCTCTGGGAGAG 15
|||||
RESULT 2812
ABK49757
ID ABK49757 standard; DNA; 17 BP.
XX
XX ABK49757;
XX AC
XX DT 15-JUL-2002 (first entry)
XX
XX Human atopic dermatitis cDNA related PCR primer G715c.
DE
XX Atopic dermatitis; se; differential display; primer; PCR; eosinophil;
XX allergic disease; antiallergic; dermatological; G715c.
KW
XX Synthetic.
OS
XX WO200226962-A1.
PN
XX 04-APR-2002.
PD
XX 21-SEP-2001; 2001WO-JP008247.
XX
XX 26-SEP-2000; 2000JP-00293021.
PR
XX
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PI Sugita Y, Haehida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI
XX MPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.

```

XX Example 1; Page 55; 74pp; Japanese.

PS

CC This invention relates to gene sequences that are differentially  
CC expressed in eosinophils from patients with atopic dermatitis in the  
CC increment stage as compared with those in the remission stage. These  
CC sequences are used in a novel method for examining allergic diseases  
CC comprising determining the expression levels of these genes and comparing  
CC the expression level with that in the eosinophils of a healthy  
CC individual. The method of the invention may have antiallergic or  
CC dermatological activities. The method can be used to diagnose allergic  
CC diseases particularly atopic dermatitis, and may also be used to screen  
CC candidate compounds for remedies. The method of the invention can be  
CC performed in high throughput, at low cost. The present sequence  
CC represents the G15C PCR primer used to amplify the differentially  
CC amplified atopic dermatitis related cDNA sequences of the invention

CC

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 4464 TTTTCTTTTTTTTT 4478  
|||||  
2 TTTTCTTTTTTTTT 16

Db

RESULT 2013

ID ABK49756  
AC ABK49756 standard; DNA; 17 BP.  
XX ABK49756;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human atopic dermatitis cDNA related PCR primer G15a.  
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;  
KM allergic disease; antiallergic; dermatological; G15a.  
XX  
OS Synthetic.  
XX WO200226962-A1.  
PN 04-APR-2002.  
PD  
XX 21-SEP-2001; 2001WO-JP008247.  
PF  
XX 26-SEP-2000; 2000JP-00293021.  
PR  
XX (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;  
DR WPI; 2002-330097/36.  
XX  
PT Examining allergic diseases by differential display of genes showing  
PT different expression particularly increase in remission stage in  
PT eosinophils in patients.  
XX  
XX Example 1; Page 54; 74pp; Japanese.  
XX  
XX This invention relates to gene sequences that are differentially  
CC expressed in eosinophils from patients with atopic dermatitis in the  
CC increment stage as compared with those in the remission stage. These  
CC sequences are used in a novel method for examining allergic diseases  
CC comprising determining the expression levels of these genes and comparing  
CC the expression level with that in the eosinophils of a healthy  
CC individual. The method of the invention may have antiallergic or  
CC dermatological activities. The method can be used to diagnose allergic  
CC diseases particularly atopic dermatitis, and may also be used to screen

CC candidate compounds for remedies. The method of the invention can be  
CC performed in high throughput, at low cost. The present sequence  
CC represents the G15a PCR primer used to amplify the differentially  
CC amplified atopic dermatitis related cDNA sequences of the invention  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478  
Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2814  
ACC52645  
ID ACC52645 standard; DNA; 17 BP.

XX  
AC ACC52645;  
XX  
DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #1412.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
KM tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.

XX Homo sapiens.

PN FR2826373-A1.

XX 27-DEC-2002.

PF 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

PA (MOLE-) MOLECULAR ENGINES LAB SA.

PI Tuijnder M, Teleman A, Amson R;

XX WPI; 2003-250498/25.

PT New nucleic acid sequences associated with tumor suppression, regression,  
PT apoptosis or virus resistance are useful to diagnose and treat viral  
PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 366; 798bp; French.

CC This sequence represents an isolated nucleic acid sequence associated  
CC with tumour suppression or regression, apoptosis or virus resistance. The  
CC invention relates to these sequences or sequences having at least 80%  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences. The  
CC invention is used to diagnose or treat viral disease or disease  
CC characterized by development of tumour cells or cellular degeneration  
XX

SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2395 ATCCAGCTGGAGC 2409  
Db 2 ATCCAGCTGGAGC 16

RESULT 2815  
ABX79793

ID ABX79793 standard; cDNA; 17 BP.

XX ABX79793;

XX 17-APR-2003 (first entry)

DE EST polymorphic DNA repeat polynucleotide #118.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

PN US6472154-B1.

XX 29-OCT-2002.

PF 31-DEC-1999; 99US-00475947.

PR 31-DEC-1999; 99US-00475947.

XX (TEXA ) UNIV TEXAS SYSTEM.

PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX WPI; 2003-208818/20.

PT Identifying a candidate polymorphic repeat within a coding sequence, for  
PT understanding or treating genetic disease, comprises detecting tandem  
PT repeats in a target coding sequence and scoring the repeats for  
PT polymorphic probability.

XX Example; Col 483; 588bp; English.

CC The invention discloses a method for identifying a candidate polymorphic  
CC repeat within a coding sequence (expressed sequence tag, EST), which  
CC comprises detecting tandem repeats in a target coding sequence, scoring  
CC the repeats for polymorphic probability and generating a dataset  
CC correlating the repeats with polymorphic probability to identify a  
CC candidate polymorphic repeat. The computational methods (polymorphic  
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
CC useful for identifying and detecting candidate polymorphic repeats in  
CC human genes, which can be used to understand, treat or eliminate genetic  
CC diseases, predispositions or adverse drug-treatment reactions. Examples  
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,  
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
CC the polymorphic repeats identified for a search of human ESTs

SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478  
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2816

ID ABT36431/c

XX ABT36431 standard; DNA; 17 BP.

XX ABT36431;

XX 12-JUN-2003 (first entry)

DE Tumour suppression related human fukutin oligo SEQ ID NO 2068.  
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW anticense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrentia; protein chip; gene therapy; tumour suppression;  
 XX human fukutin; ds.  
 OS Homo sapiens.  
 XX WO2003025175-A2.  
 PN 27-MAR-2003.  
 PD 17-SEP-2002; 2002MO-IB004208.  
 PF 17-SEP-2001; 2001FR-00011978.  
 PR 17-SEP-2001; 2001FR-00011978.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 PA Telerman A, Amson R, Tuijnder M;  
 PI WPI; 2003-313353/30.  
 DR New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PS Disclosure; Page 274; 720pp; French.  
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optional  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrentia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6294 CTGGCCTCCAGGAT 6308  
 DB 16 CTGGCCTCCAGGAT 2  
 XX  
 RESULT 2817  
 ADB04274  
 ID ADB04274 standard; DNA; 17 BP.  
 XX  
 AC ADB04274;  
 XX 20-NOV-2003 (first entry)  
 DT Human MD27 scanning oligonucleotide SEQ ID 5260.  
 DE  
 XX

KM Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
 KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 XX developmental disorder; ss.  
 OS Homo sapiens.  
 XX EP1281758-A2.  
 PN 05-FEB-2003.  
 PD 30-JUL-2002; 2002EP-00016874.  
 PF 02-AUG-2001; 2001US-00922181.  
 PR (AEOM-) AEOMICA INC.  
 PA Shannon M, Gu Y, Nguyen C;  
 PI WPI; 2003-423107/40.  
 DR New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 PS Example 8; SEQ ID NO 5260; 103pp; English.  
 XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4470 TTTT TTTT TTTT TTTT G 4484  
 DB 1 TTTT TTTT TTTT TTTT G 15  
 XX  
 RESULT 2818  
 ADC84469  
 ID ADC84469 standard; DNA; 17 BP.  
 XX  
 AC ADC84469;  
 XX 01-JAN-2004 (first entry)  
 DT PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.  
 XX Plant blastogenesis; transformation; gene expression; tissue specific;  
 KW PCR; primer; ss.  
 XX Synthetic.  
 OS Jp2003159071-A.  
 XX Jp2003159071-A.  
 PN 03-JUN-2003.  
 PD

XX 22-NOV-2001; 2001JP-00358366.  
 PF 22-NOV-2001; 2001JP-00358366.  
 PR 22-NOV-2001; 2001JP-00358366.  
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 PA WPI; 2003-818676/77.  
 DR  
 XX New naturally derived DNA specifically expressed during blastogenesis of  
 PT a plant, useful for producing a transformed plant and for compulsive  
 PT expression of a protein.  
 XX  
 PS Example 3; SEQ ID NO 2; 43pp; Japanese.  
 CC The invention relates to naturally derived DNA specifically expressed  
 CC during plant blastogenesis. The DNA of the invention is useful for  
 CC producing a transformed plant. Methods of the invention are also useful  
 CC for compulsive expression of this DNA. Methods of the invention are  
 CC useful for plant tissue specific expression of genes. Also, the growth  
 CC stage of a plant can be controlled specifically. The current sequence  
 CC represents a PCR primer for amplifying a plant blastogenesis specific  
 CC gene of the invention.  
 XX  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 SO  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT 4478  
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2819  
 ADC84468  
 ID ADC84468 standard; DNA; 17 BP.  
 AC  
 XX ADC84468;  
 AC  
 XX 01-JAN-2004 (first entry)  
 DT  
 XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.  
 DE  
 XX Plant blastogenesis; transformation; gene expression; tissue specific;  
 KM PCR; primer; ss.  
 KM  
 XX Synthetic.  
 OS  
 XX JP2003159071-A.  
 PN  
 XX 03-JUN-2003.  
 PD  
 XX 22-NOV-2001; 2001JP-00358366.  
 PF  
 XX 22-NOV-2001; 2001JP-00358366.  
 PR  
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 PA WPI; 2003-818676/77.  
 DR  
 XX New naturally derived DNA specifically expressed during blastogenesis of  
 PT a plant, useful for producing a transformed plant and for compulsive  
 PT expression of a protein.  
 XX  
 PS Example 3; SEQ ID NO 1; 43pp; Japanese.  
 CC The invention relates to naturally derived DNA specifically expressed  
 CC during plant blastogenesis. The DNA of the invention is useful for  
 CC producing a transformed plant. Methods of the invention are also useful  
 CC for compulsive expression of this DNA. Methods of the invention are  
 CC useful for plant tissue specific expression of genes. Also, the growth

CC stage of a plant can be controlled specifically. The current sequence  
 CC represents a PCR primer for amplifying a plant blastogenesis specific  
 CC gene of the invention.  
 XX  
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
 SO  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT 4478  
 Db 2 TTTT TTTT TTTT TTTT 16

RESULT 2820  
 ADE77745  
 ID ADE77745 standard; DNA; 17 BP.  
 AC  
 XX ADE77745;  
 AC  
 XX 29-JAN-2004 (first entry)  
 DT  
 XX DNA oligo (SeqID 5) related to the human B1799 gene.  
 DE  
 XX ss; allergic disease; B1799; anti-allergic; anti-inflammatory;  
 KM dermatological; gene therapy; atopic dermatitis.  
 KM  
 XX Unidentified.  
 OS  
 XX WO2003083139-A1.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 25-FEB-2003; 2003WO-JP002047.  
 PF  
 XX 03-APR-2002; 2002JP-00100908.  
 PR  
 XX (GENO-) GENOX RES INC.  
 PA (NIGE-) JAPAN GEN AGENCY NATION.  
 PA  
 XX Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;  
 PI WPI; 2003-804076/75.  
 DR  
 XX Examining allergic diseases, such as atopic dermatitis, comprises  
 DT comparing the expression levels of gene B1799 in T cells in a patient and  
 XX a healthy individual.  
 XX  
 PS Example 1; SEQ ID NO 5; 87pp; Japanese.  
 PS  
 XX This invention relates to a novel method for screening and examining  
 XX allergic diseases by the use of B1799 as the indicator gene.  
 CC Specifically, it comprises determining the expression level of this  
 CC indicator gene in a biological sample obtained from the patient, and  
 CC identifying differential expression (increased expression of B1799) in  
 CC invention describes the B1799 protein as anti-allergic, anti-inflammatory  
 CC and dermatological. As such, through the use of gene therapy, this method  
 CC can be used to treat allergic diseases particularly atopic dermatitis.  
 CC Furthermore, it is useful for determining a diagnosis that is convenient  
 CC and non-invasive, and is also applicable in high throughput screening to  
 CC identify candidate compounds for additional remedies. This  
 CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human  
 CC B1799 gene of the invention.  
 CC  
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
 SO  
 Query Match 0.2%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT 4478

Db 2 TTTTTTTTTTTTTT 16

RESULT 2821  
ID AAV54175 standard; cDNA; 18 BP.  
XX AAV54175;  
AC AAV54175;  
XX 21-DEC-1998 (first entry)  
XX Nucleotide sequence PCR primer 12.  
DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
XX Immunohistological staining.  
KM Synthetic.  
XX WO9839437-A1.  
XX 11-SEP-1998.  
XX 05-MAR-1998; 98WO-JP000905.  
XX 05-MAR-1997; 97JP-00050302.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Sakaki Y;  
XX WPI; 1998-495844/42.  
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or  
PT treating diseases associated with apoptosis.  
XX Example 1; Page 51; 70pp; Japanese.  
XX This is the nucleotide sequence of a PCR primer used in the method of the  
CC invention, involving the use of novel apoptosis-related DNAs and  
CC proteins. The inventions can be used as diagnostic reagents for apoptosis  
e.g. (monoclonal) antibodies for the protein, as a reagent in  
CC immunohistological staining, as apoptosis inhibitors. It can also be used  
CC for treatment of apoptosis-related diseases  
XX Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;  
SQ

Query Match 0.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478  
Db 2 TTTTTTTTTTTTTT 16

RESULT 2822  
ID AAV54173 standard; cDNA; 18 BP.  
XX AAV54173;  
AC AAV54173;  
XX 21-DEC-1998 (first entry)  
XX Nucleotide sequence PCR primer 10.  
DE PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
XX Immunohistological staining.  
KM Synthetic.  
XX WO9839437-A1.

PD 11-SEP-1998.  
XX 05-MAR-1998; 98WO-JP000905.  
XX 05-MAR-1997; 97JP-00050302.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Sakaki Y;  
XX WPI; 1998-495844/42.  
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or  
PT treating diseases associated with apoptosis.  
XX Example 1; Page 50; 70pp; Japanese.  
XX This is the nucleotide sequence of a PCR primer used in the method of the  
CC invention, involving the use of novel apoptosis-related DNAs and  
CC proteins. The inventions can be used as diagnostic reagents for apoptosis  
e.g. (monoclonal) antibodies for the protein, as a reagent in  
CC immunohistological staining, as apoptosis inhibitors. It can also be used  
CC for treatment of apoptosis-related diseases  
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
SQ

Query Match 0.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTT 4478  
Db 2 TTTTTTTTTTTTTT 16

RESULT 2823  
ID AAV54164 standard; cDNA; 18 BP.  
XX AAV54164;  
AC 21-DEC-1998 (first entry)  
XX Nucleotide sequence PCR primer 1.  
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;  
XX Immunohistological staining.  
KM Synthetic.  
XX WO9839437-A1.  
XX 11-SEP-1998.  
XX 05-MAR-1998; 98WO-JP000905.  
XX 05-MAR-1997; 97JP-00050302.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX Sakaki Y;  
XX WPI; 1998-495844/42.  
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or  
PT treating diseases associated with apoptosis.  
XX Example 1; Page 47; 70pp; Japanese.  
XX This is the nucleotide sequence of a PCR primer used in the method of the  
CC invention, involving the use of novel apoptosis-related DNAs and  
CC proteins. The inventions can be used as diagnostic reagents for apoptosis  
e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used  
 CC for treatment of apoptosis-related diseases

XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2824

AAV54166

AAV54166 standard; cDNA; 18 BP.

XX AAV54166;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 3.

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;

XX immunohistological staining.

XX Synthetic.

XX WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP000905.

XX 05-MAR-1997; 97JP-00050302.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Sakaki Y;

XX WPI; 1998-495844/42.

XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or

XX treating diseases associated with apoptosis.

XX Example 1; Page 48; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method of the

XX invention, involving the use of novel apoptosis-related DNAs and

XX proteins. The inventions can be used as diagnostic reagents for apoptosis

XX e.g. (monoclonal) antibodies for the protein, as a reagent in

XX immunohistological staining, as apoptosis inhibitors. It can also be used

XX for treatment of apoptosis-related diseases

XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2825

AAZ90649

AAZ90649 standard; DNA; 18 BP.

XX AAZ90649;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #10.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISR ) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose

XX tissue relating to obesity, particularly complications of visceral

XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,

XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the

XX proteins (AAZ90634-90636) are used in the genetic diagnosis, prevention

XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51

XX represent PCR primers amplifying the human adipose tissue genes

XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 2 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2826

AAZ90648

AAZ90648 standard; DNA; 18 BP.

XX AAZ90648;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #9.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISR ) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,  
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the  
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention  
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51  
 CC represent PCR primers amplifying the human adipose tissue genes  
 XX

Sequence 18 BP; 1 A; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16

## RESULT 2827

AA290646  
 ID AA290646 standard; DNA; 18 BP.

XX  
 AC AA290646;

XX  
 DT 13-JUN-2000 (first entry)

DE Human adipose tissue gene amplifying primer #7.

XX  
 KM Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 KM arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX  
 OS Homo sapiens.

XX  
 PN JP2000037190-A.

PD 08-FEB-2000.

PF 23-JUL-1998; 98JP-00225228.

PR 23-JUL-1998; 98JP-00225228.

XX  
 PA (NISR) JAPAN TOBACCO INC.

XX  
 DR WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX  
 PS Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,  
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the  
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention  
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51  
 CC represent PCR primers amplifying the human adipose tissue genes  
 XX

Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16

## RESULT 2828

AA290651  
 ID AA290651 standard; DNA; 18 BP.

XX  
 AC AA290651;

XX  
 DT 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #12.

XX  
 KM Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
 KM arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX  
 OS Homo sapiens.

XX  
 PN JP2000037190-A.

PD 08-FEB-2000.

PF 23-JUL-1998; 98JP-00225228.

PR 23-JUL-1998; 98JP-00225228.

XX  
 PA (NISR) JAPAN TOBACCO INC.

XX  
 DR WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX  
 PS Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose  
 CC tissue relating to obesity, particularly complications of visceral  
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,  
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the  
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention  
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51  
 CC represent PCR primers amplifying the human adipose tissue genes  
 XX

Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478  
 |||||  
 Db 2 TTTT TTTT TTTT TTTT 16

## RESULT 2829

AAA58385/C  
 ID AAA58385 standard; DNA; 18 BP.

XX  
 AC AAA58385;

XX  
 DT 01-NOV-2000 (first entry)

XX Polynucleotide # 1 used in a biomolecule detection system.

XX  
 KM Nanocysteral; biomolecule detection; nonisotopic detection system; ss.

XX  
 OS Synthetic.

XX  
 PN WO200028088-A1.

PD 18-MAY-2000.

PF 10-NOV-1999; 99WO-US026612.

PR 10-NOV-1998; 98US-0107828P.

PR 09-NOV-1999; 99US-00437076.

XX  
 PA (BIOC-) BIOCRYSTAL LTD.

XX  
 PI Barbera-Guillem E, Nelson MB, Castro S;



XX DR WPI: 2000-376593/32.

XX PT Functionalized nanocrystal carrying polynucleotide, used for detecting

PT target analyte, forms dendrimers with complementary nanocrystals to

PT amplify the fluorescent signal.

XX PS Example 3; Page 68; 72pp; English.

XX CC The present invention relates to functionalised nanocrystals for use in

CC nonisotopic detection systems for biomolecules e.g. nucleic acids,

CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands

CC attached to their surfaces with one end of the polynucleotide extending

CC outwardly from the nanocrystal. The present sequence is one such

CC polynucleotide. These nanocrystals are used with a second series of

CC nanocrystals, which have polynucleotides complementary to the first

CC polynucleotides, so that the respective complementary strands hybridise

CC to each other and form a dendrimer. This dendrimer produces a signal

CC which can then be detected e.g. fluorescence. The present sequence is

CC composed mainly of Adenine bases. This sequence may therefore be used

CC with a polynucleotide composed mainly of Thymine bases (AA58386)

XX SQ Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 18 TTTT TTTT TTTT TTTT TTTT 4

RESULT 2830

AA58386

ID AA58386 standard; DNA; 18 BP.

XX AC AA58386;

XX DT 01-NOV-2000 (first entry)

XX DE Polynucleotide # 2 used in a biomolecule detection system.

XX KM Nanocrystal; biomolecule detection; nonisotopic detection system; ss.

XX OS Synthetic.

XX PN WO200028088-A1.

XX PD 18-MAY-2000.

XX PF 10-NOV-1999; 99WO-US026612.

XX PR 10-NOV-1998; 98US-0107828P.

XX PR 09-NOV-1999; 99US-00437076.

XX PA (BIOC-) BIOCRYSTAL LTD.

XX PI Barbera-Guillem E, Nelson MB, Castro S;

XX DR WPI: 2000-376593/32.

XX PT Functionalized nanocrystal carrying polynucleotide, used for detecting

PT target analyte, forms dendrimers with complementary nanocrystals to,

PT amplify the fluorescent signal.

XX PS Example 3; Page 69; 72pp; English.

XX CC The present invention relates to functionalised nanocrystals for use in

CC nonisotopic detection systems for biomolecules e.g. nucleic acids,

CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands

CC attached to their surfaces with one end of the polynucleotide extending

CC outwardly from the nanocrystal. The present sequence is one such

CC polynucleotide. These nanocrystals are used with a second series of

CC nanocrystals, which have polynucleotides complementary to the first

CC polynucleotides, so that the respective complementary strands hybridise

CC to each other and form a dendrimer. This dendrimer produces a signal

CC which can then be detected e.g. fluorescence. The present sequence is

CC composed mainly of Thymine bases. This sequence may therefore be used

CC with a polynucleotide composed mainly of Adenine bases (AA58385)

XX SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4478

DB 4 TTTT TTTT TTTT TTTT TTTT 18

RESULT 2831

AAF2668

ID AAF2668 standard; DNA; 18 BP.

XX AC AAF2668;

XX DT 02-APR-2001 (first entry)

XX DE Human Smad7 phosphorothioate antisense oligonucleotide SEQ ID NO:11.

XX KM Human; Smad7; antisense oligonucleotide; phosphorothioate; inhibition;

KM antiinflammatory; cytostatic; infection; inflammation; tumour formation;

XX OS ss.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

FT modified\_base 1..18

FT /\*tag= a

FT /note= "phosphorothioate linkages"

XX PN US6159697-A.

XX PD 12-DEC-2000.

XX PF 09-JAN-2000; 2000US-00487444.

XX PR 09-JAN-2000; 2000US-00487444.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Cowsett LM;

XX DR WPI: 2001-070108/08.

XX PT Antisense compound capable of inhibiting the expression of human Smad7,

PT useful for preventing or delaying infection, inflammation or tumor

PT formation.

XX PS Claim 1; Col 40; 33pp; English.

XX CC The present invention describes an antisense compound (I) of up to 30

CC nucleobases in length capable of inhibiting the expression of human

CC Smad7. (I) has antiinflammatory and cytostatic, and is a modulator of

CC Smad7 expression. (I) can be useful for inhibiting the expression of

CC human Smad7 in human cells or tissues, in vitro. (I) is commonly used as

CC a research reagent and in diagnostics for example, to elucidate the

CC function of particular genes. (I) is also useful for distinguishing

CC between functions of various members of a biological pathway and for

CC research use. (I) is also utilised for diagnostics, therapeutics,

CC prophylaxis and in kits. (I) is also useful prophylactically, e.g. to

CC prevent or delay infection, inflammation or tumour formation. AAF2667 to

CC AAF26706 represent human Smad7 antisense oligonucleotides from the

CC present invention

XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7413 CAGCAGCAGCAGCAG 7427  
DB 4 CAGCAGCAGCAGCAG 18  
RESULT 2832  
AAS17036/C  
ID AAS17036 standard; DNA; 18 BP.  
XX  
XX AAS17036;  
XX  
XX 27-FEB-2002 (first entry)  
XX  
XX Human G-alpha2 reverse PCR primer.  
XX  
XX Luciferase; ss; PCR primer; protein-protein interaction;  
XX transcriptional activation protein DNA binding domain; TAP; luciferase;  
XX cancer; human immunodeficiency virus infection; antiviral;  
XX modified yeast cell; human; G-alpha2; RGS-Z.  
XX  
XX Homo sapiens.  
XX  
XX WO200181548-A1.  
XX  
XX 01-NOV-2001.  
XX  
XX 23-APR-2001; 2001WO-US013006.  
XX  
XX 24-APR-2000; 2000US-00556390.  
XX  
XX (AMHP ) AMERICAN HOME PROD CORP.  
XX  
XX Young KH, Gao J;  
XX  
XX WPI; 2002-049273/06.  
XX  
XX New yeast cell, useful for determining protein-protein interactions,  
XX expresses heterologous fusion proteins comprising peptides of peptide  
XX binding pair joined to transcriptional activation protein DNA binding  
XX domain.  
XX  
XX Example 6; Page 53; 119pp; English.  
XX  
XX The invention relates to a yeast cell comprising nucleotide sequences  
XX encoding first and second heterologous fusion proteins comprising first  
XX and second peptides (P1, P2) of a peptide binding pair joined to a  
XX transcriptional activation protein (TAP) DNA binding domain or TAP  
XX transcriptional activation domain, respectively, and a luciferase gene  
XX activated by positive transcriptional control of TAP reconstituted by  
XX binding of P1 and P2. The cell is useful for detecting the interaction of  
XX a first peptide and a second peptide of a peptide binding pair which  
XX involves culturing the cell, incubating a test sample with the yeast cell  
XX under conditions suitable to detect the selected phenotype and detecting  
XX the level of expression of the luciferase gene. The cell is also useful  
XX for determining whether a test sample interacts with a first or second  
XX peptide of a peptide binding pair. The yeast cell comprises a nucleotide  
XX The new modified yeast cells are useful in the study and discovery of  
XX peptide mimics, including ligand mimics and receptor mimics. The cell may  
XX be used for monitoring the binding of peptides by peptide binding pair  
XX which bind through extracellular interaction, and for studying numerous  
XX mammalian ligand/receptor interactions, e.g., hormone/receptor  
XX interactions. The cells are also useful in the detection of the ability  
XX of the test sample to affect the binding of a peptide binding pair for  
XX example ligand-receptor interaction. The screening methods can be used  
XX for identifying novel compounds interacting with any peptide binding pair and  
XX to discover novel compounds that disrupt that interaction, e.g., protein

CC kinases implicated in cancers can be inserted into the yeast system to  
CC screen for compounds that block the kinase-target interaction and thus  
CC may serve as unique cancer therapeutics; viral coat proteins such as  
CC human immunodeficiency virus glycoprotein and corresponding cell surface  
CC proteins such as CD4 can be inserted into the cell system to screen for  
CC compounds that disrupt this interaction and may serve as antiviral  
CC agents. The present sequence is a PCR primer used to isolate a cDNA  
CC encoding human G-alpha2. G-alpha2 is expressed in yeast cells in a  
CC construct which uses the luciferase gene as a marker for the interaction  
CC between G-alpha2 and a coexpressed RGS-Z  
XX  
XX Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2994 ATGTCCGCCACCCCT 3008  
DB 17 ATGTCCGCCACCCCT 3  
RESULT 2833  
AAA83021/C  
ID AAA83021 standard; DNA; 19 BP.  
XX  
XX AAA83021;  
XX  
XX 04-DEC-2000 (first entry)  
XX  
XX cdK6 ribozyme binding site #81.  
XX  
XX  
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotrophic; restenosis; ss.  
XX  
XX Mammalia.  
XX  
XX WO200032765-A2.  
XX  
XX 08-JUN-2000.  
XX  
XX 06-DEC-1999; 99WO-US028772.  
XX  
XX 04-DEC-1998; 98US-0110954P.  
XX  
XX (IMMU-) IMMUSOL INC.  
XX  
XX Tyltz R, Welch PJ, Barber JR, Robbins JM;  
XX  
XX WPI; 2000-412314/35.  
XX  
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
XX PCNA and Cyclin B1.  
XX  
XX Disclosure; Page 55; 109pp; English.  
XX  
XX The present invention relates to a hairpin or hammerhead ribozyme,  
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
XX Representative examples of ribozyme recognition sites are given in  
XX CC AAA82415 to AA86787. The ribozyme of the invention is useful for  
XX inhibiting restenosis by introduction of the ribozyme into cells. The  
XX ribozyme is resistant to endonuclease activity and hence is efficient in  
XX restenosis treatment  
XX  
XX Sequence 19 BP; 5 A; 3 C; 5 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1678 TTCTGCAATATGCA 1692  
|||||||

DB 19 TTGCAATATGCA 5

RESULT 2834  
AAH58183/c  
ID AAH58183 standard; DNA; 19 BP.  
XX  
AC AAH58183;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:607.  
XX  
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KW recognition site; target; ribozyme binding site; eye disease; vulnery;  
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KW antiproliferative; dermatological; keratolytic; gene therapy; viral wart;  
KW antisticking; ophthalmological; antiseborrheic; antidiabetic; vitruide;  
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
KW sickle cell retinopathy; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FN WO200130362-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US029500.  
XX  
PR 26-OCT-1999; 99US-0161532P.  
XX  
PI (IMMU-) IMMUSOL INC.  
XX  
PI Robbins JM, Tiltz R;  
XX  
DR WPI; 2001-300427/31.  
XX  
PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 116; 408pp; English.  
XX  
XX The present invention describes a method for treating a proliferative  
XX skin or eye disease and scarring. The method involves administering a  
XX ribozyme (I) which cleaves RNA encoding a cytokine involved in  
XX inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
XX dependent kinase, growth factor or a reductase, or administering a  
XX nucleic acid molecule (II) comprising a promoter operably linked to a  
XX nucleic acid segment encoding (I). (I) can have antiproliferative,  
XX dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,  
XX ophthalmological, vulnery, keratolytic and vitruide activities, and  
XX cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
XX in gene therapy. (I) and (II) are useful for treating proliferative skin  
XX diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
XX squamous or basal cell carcinoma and viral or seboreic wart. They can  
XX also be used for treating proliferative eye diseases such as diabetic  
XX retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
XX prematurity and retinal detachment, and for treating and preventing  
XX scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
XX scar. AAH57577 to AAH62099 represent sequences used in the  
XX exemplification of the present invention  
XX  
XX Sequence 19 BP; 5 A; 3 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1678 TTGCAATATGCA 1692  
DB 19 TTGCAATATGCA 5

RESULT 2835  
AAQ13458/c  
ID AAQ13458 standard; DNA; 20 BP.  
XX  
AC AAQ13458;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-NOV-1991 (first entry)  
XX  
DE Probe to mutant codon 201 (AAA) of G-protein Gi(alpha)1 subunit.  
XX  
KW Gi(alpha)1-201; point mutation; oncogenesis; PCR; tumour;  
KW adenylate cyclase activity inhibition; ss.  
XX  
OS Synthetic.  
XX  
FN WO9112343-A.  
XX  
PD 22-AUG-1991.  
XX  
PF 07-FEB-1990; 90US-00477260.  
XX  
PR 07-FEB-1990; 90US-00477260.  
XX  
PA (CETU ) CETUS CORP.  
XX  
PI McCormick FP, Lyons JF;  
XX  
DR WPI; 1991-267154/36.  
XX  
PT Method for detection of point mutation(s) in nucleic acid segments -  
PT where segments encode GTP binding protein or sub-unit and method involves  
PT amplification followed by sequence-specific probe hybridisation.  
XX  
XX Claim 18; Page 65; 69pp; English.  
XX  
XX This probe corresponds to a mutant sequence around codon 201 (AGA = Arg).  
XX This codon is a potentially oncogenic site and a group of mutant probes  
XX were synthesised based on single point mutations at codon 201. After PCR  
XX amplification of nucleic acid samples using specific primer pairs, these  
XX probes can be used to detect Gi(alpha)1 mutations associated with  
XX oncogenesis. See AAQ13431-Q13542. (Updated on 25-MAR-2003 to correct PI  
XX field.)  
XX  
XX Sequence 20 BP; 10 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 7204 GTTTCACCTTACGTT 7218  
DB 19 GTTTCACCTTACGTT 5

RESULT 2836  
AAT73291  
ID AAT73291 standard; DNA; 20 BP.  
XX  
AC AAT73291;  
XX  
DT 12-DEC-1997 (first entry)  
XX  
DE Primer 1 for pUC19 DNA amplification.  
XX  
KW primer; PCR; polymerase chain reaction; sequencing; walking;  
KW complementary extension reaction; low redundancy; universal primer; ss.  
XX

```

OS Synthetic.
XX EP767240-A2.
XX 09-APR-1997.
XX 17-SEP-1996; 96EP-00114907.
XX 18-SEP-1995; 95JP-00238141.
XX 30-JAN-1996; 96JP-00013634.
XX (HITA ) HITACHI LTD.
XX Kambara H, Okano K;
XX WPI; 1997-205424/19.
XX
XX Efficient sequencing of long DNA by fragment walking - with simultaneous
XX sequencing of restriction enzyme fragment and adjacent region of intact
XX DNA, avoids the need for cloning and requires fewer primers.
XX
XX Example 1; Page 11; 50pp; English.
XX
XX A method for DNA analysis based on a complementary extension reaction
XX using a DNA polymerase, comprises a combination of fragment walking and
XX DNA sequencing. DNA fragments are formed by digestion of DNA with a
XX restriction enzyme and the targeted DNA sequence can be determined
XX directly from the digested DNA fragments. By exploring the overlapping
XX sequence of the determined base sequence, the overall base sequence of a
XX lengthy DNA can be determined with low redundancy without cloning or
XX subcloning. In addition, the method can be done with commercially
XX available universal primers or with fewer primers than required in
XX existing methods. AAT73291-92 are primers used in determination of the
XX pUC19 sequence. Primer extension was carried out using 16 primers
XX AAT73293
XX
XX Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4470 TTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTG 15
XX
XX RESULT 2837
XX AAT73292
XX ID AAT73292 standard; DNA; 20 BP.
XX
XX AAT73292;
XX
XX 12-DEC-1997 (first entry)
XX
XX Primer 2 for pUC19 DNA amplification.
XX
XX primer; PCR; polymerase chain reaction; sequencing; walking;
XX complementary extension reaction; low redundancy; universal primer; ss.
XX
XX Synthetic.
XX EP767240-A2.
XX 09-APR-1997.
XX 17-SEP-1996; 96EP-00114907.
XX 18-SEP-1995; 95JP-00238141.
XX 30-JAN-1996; 96JP-00013634.
XX (HITA ) HITACHI LTD.
XX

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PI Kambara H, Okano K;
XX WPI; 1997-205424/19.
XX
XX Efficient sequencing of long DNA by fragment walking - with simultaneous
XX sequencing of restriction enzyme fragment and adjacent region of intact
XX DNA, avoids the need for cloning and requires fewer primers.
XX
XX Example 1; Page 11; 50pp; English.
XX
XX A method for DNA analysis based on a complementary extension reaction
XX using a DNA polymerase, comprises a combination of fragment walking and
XX DNA sequencing. DNA fragments are formed by digestion of DNA with a
XX restriction enzyme and the targeted DNA sequence can be determined
XX directly from the digested DNA fragments. By exploring the overlapping
XX sequence of the determined base sequence, the overall base sequence of a
XX lengthy DNA can be determined with low redundancy without cloning or
XX subcloning. In addition, the method can be done with commercially
XX available universal primers or with fewer primers than required in
XX existing methods. AAT73291-92 are primers used in determination of the
XX pUC19 sequence. Primer extension was carried out using 16 primers
XX AAT73293
XX
XX Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4470 TTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTG 15
XX
XX RESULT 2838
XX AAA72163
XX ID AAA72163 standard; DNA; 20 BP.
XX
XX AAA72163;
XX
XX 15-SEP-2003 (revised)
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:93.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
XX humanised antibody; complementarity determining region; CDR; human Fas;
XX Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenias;
XX hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
XX
XX Mus musculus.
XX Homo sapiens.
XX Chimeric.
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-00278301.
XX 30-SEP-1998; 98JP-00276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX
XX Preventive or treating agent for the diseases caused by an abnormality in
XX the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
XX antibody.
XX Example 15; Page 49; 139p; Japanese.

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XX The invention relates to compositions for the prevention or treatment of diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarily determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The composition of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents a humanised HFE7A-derived anti-Fas antibody heavy chain sequencing primer used in an exemplification of the invention. (Updated on 15-SEP-2003 to standardise OS field)

SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7181 GGTGGGCGATGTGTGA 7195  
|||||  
5 GGTGGGCGATGTGTGA 19

Db 5 GGTGGGCGATGTGTGA 19

RESULT 2839  
AA238528  
ID AA238528 standard; DNA; 20 BP.

XX  
AC AA238528;  
XX  
DT 22-FEB-2000 (first entry)

XX Human microtubule-associated protein 4 (MAP4) antisense oligo #63.

DE  
XX  
KW Microtubule associated protein 4; MAP4; real-time quantitative PCR; expression; microtubule assembly; function; cytoskeleton; structural; dynamic; stabilisation; lattice; overexpression; p53; oncogene; cancer; chemotherapy; tumour; drug sensitivity; antisense; therapy;  
KM hybridisation; inhibition; research; diagnostic; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX  
XX Key  
FH modified\_base  
FT 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2' methoxyethyl (2'-MOE) nucleotides"  
FT 2  
FT modified\_base  
FT /\*tag= c  
FT /mod\_base= m5c  
FT 16..20  
FT modified\_base  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2' methoxyethyl (2'-MOE) nucleotides"  
FT  
FT  
XX  
XX US5998148-A.  
PN  
XX  
XX 07-DEC-1999.  
PD  
XX  
XX 09-APR-1999; 99US-002893368.  
PF  
XX 09-APR-1999; 99US-002893368.  
PR  
XX 09-APR-1999; 99US-002893368.  
PA (ISIS-) ISIS PHARM INC.  
XX

PI Bennett CF, Ackermann EJ;  
XX  
XX WPI; 2000-052543/04.  
DR  
XX  
XX Antisense oligonucleotides for inhibiting microtubule-associated protein 4 expression, useful in treating disorders associated with microtubule protein expression.  
PT  
PT Claim 3; Col 39; 39pp; English.  
XX  
XX This sequence represents a preferred antisense oligonucleotide targeted against the gene encoding human microtubule-associated protein 4 (MAP4). Inhibition of MAP4 expression was measured by determination of MAP4 mRNA levels in a variety of cell lines via real-time quantitative PCR. The cell lines used included the bladder carcinoma cell line T-24, the human lung carcinoma cell line A549, human neonatal dermal fibroblasts and human embryonic keratinocytes. Microtubule-associated proteins comprise a group of proteins that mediate microtubule assembly and function which is required for cytoskeletal integrity. MAP4 is a member of the non-neuronal structural MAP family and is believed to affect microtubule dynamics by stabilising the microtubule lattice. MAP4 expression has been shown to be elevated in cells with mutant p53 oncogene expression, and is therefore linked to cancer chemotherapeutic drug sensitivity. These antisense molecules are useful for treating animals, particularly humans, having or being prone to a disease or condition associated with the expression of MAP4. The oligonucleotides are also useful for research and diagnostic applications  
CC  
CC  
XX  
SQ Sequence 20 BP; 7 A; 1 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3222 TGGGAGGAGGAGG 3236  
|||||  
4 TGGGAGGAGGAGG 18

Db 4 TGGGAGGAGGAGG 18

RESULT 2840  
AAA11601  
ID AAA11601 standard; DNA; 20 BP.

XX  
AC AAA11601;  
XX  
DT 08-AUG-2000 (first entry)

XX Humanised HFE7A designed heavy chain DNA primer #4.

DE  
XX  
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cadiant; dermatological; immunosuppressive; chryomimetic; antirheumatic; anti-Fas; hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; steatitis; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; primer; ss.  
KM  
XX  
XX Synthetic.  
OS  
XX  
XX EP990663-A2.  
PN  
XX  
XX 05-APR-2000.  
PD  
XX  
XX 29-SEP-1999; 99EP-00307711.  
PF  
XX 30-SEP-1998; 98JP-00276881.  
PR  
XX 30-SEP-1998; 98JP-00276882.  
XX

PA (SANTY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI; 2000-256930/23.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems.  
 XX  
 PS Example reference 15; Page 137; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymotropic,  
 CC antineoplastic, nephroprotective, antifertility, neuroprotective,  
 CC antiatherosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC primer used in the construction of a humanised anti-Fas antibody HFE7A  
 CC designed heavy chain which is used in the method described in the  
 CC invention  
 CC  
 XX  
 SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7181 GGTGGGCGATGTGTGA 7195  
 Db 5 GGTGGGCGATGTGTGA 19  
 RESULT 2841  
 ABL48723  
 ID ABL48723 standard; DNA; 20 BP.  
 AC ABL48723;  
 XX  
 XX 30-APR-2002 (first entry)  
 DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 61.  
 XX  
 KW Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;  
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;  
 KW autoimmune disease; allergy; atopy; PCR primer; ss.  
 XX  
 OS Synthetic.  
 PN JP2001342149-A.  
 PD 11-DEC-2001.  
 PF 28-MAR-2001; 2001JP-00093243.

XX  
 XX 29-MAR-2000; 2000JP-00091144.  
 PR  
 PA (SANTY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2002-145114/19.  
 XX  
 PT Drug for preventing or treating e.g. autoimmune disease or allergy,  
 PT comprises humanized anti-Fas antibody.  
 XX  
 PS Example 14 (preparatory); Page 32; 154pp; Japanese.  
 XX  
 CC The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in the Fas/Fas ligand system containing, as the  
 CC active component, an antibody having a light chain subunit and a heavy  
 CC chain subunit and an activity of combining specifically with mammalian  
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The  
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is  
 CC used for preventing and treating autoimmune diseases, allergy, atopy and  
 CC others. The present sequence is that of a PCR primer useful in the  
 CC construction of anti-Fas antibodies of the invention  
 CC  
 XX  
 SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7181 GGTGGGCGATGTGTGA 7195  
 Db 5 GGTGGGCGATGTGTGA 19  
 RESULT 2842  
 ABQ74807  
 ID ABQ74807 standard; DNA; 20 BP.  
 AC ABQ74807;  
 XX  
 XX 24-OCT-2002 (first entry)  
 DE Human TNFR2 antisense oligonucleotide SEQ ID NO:57.  
 XX  
 KW Tumour necrosis factor receptor 2; TNFR2; antisense oligonucleotide;  
 KW phosphorothioate; 2'-O-methoxyethyl; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages"  
 FT 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl nucleotides"  
 FT 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl nucleotides"  
 XX  
 XX US6410324-B1.  
 XX  
 XX 25-JUN-2002.  
 PD  
 XX 27-APR-2001; 2001US-00844634.  
 PF  
 PR 27-APR-2001; 2001US-00844634.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Watt AT;

XX DR WPI: 2002-606814/65.  
XX PT New compounds antisense to nucleic acid encoding human or mouse tumor  
PT necrosis factor receptor 2 are useful to treat disease associated with  
PT mouse tumor necrosis factor receptor 2 expression.  
XX PS Claim 3; Col 47; 69pp; English.  
XX CC The present invention describes compounds of 8-30 nucleobases antisense  
CC to a nucleic acid encoding human or mouse tumour necrosis factor receptor  
CC 2 (TNFR2). Also described is a method for inhibiting expression of human  
CC or mouse TNFR2 comprising contacting cells or tissues in vitro with one  
CC of the claimed compounds. The antisense compounds are used to treat a  
CC disease or condition associated with expression of TNFR2. The present  
CC sequence represents a human TNFR2 antisense chimeric phosphorothioate  
CC oligonucleotide, which is given in the present invention  
XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 1765 GTCATCCGCGCAGG 1779  
Db 1 GTCATCCGCGCAGG 15  
RESULT 2843  
ABL45980  
ID ABL45980 standard; DNA; 20 BP.  
XX AC ABL45980;  
XX DT 26-APR-2002 (first entry)  
XX DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 18.  
XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
KW autoimmune disease; allergy; atopic; PCR primer; ss.  
XX OS Synthetic.  
XX PN JP2001342148-A.  
XX PD 11-DEC-2001.  
XX PF 28-MAR-2001; 2001JP-00093106.  
XX PR 29-MAR-2000; 2000JP-00090918.  
XX PS (SANYO) SANKYO CO LTD.  
XX DR WPI: 2002-145113/19.  
XX PT Drug containing humanised anti-Fas antibody, used for preventing and  
PT treating autoimmune diseases, allergy, and atopy.  
XX PS Example 4 (Preparatory); Page 23; 194pp; Japanese.  
XX CC The invention relates to a preventive or treating agent for diseases  
CC caused by abnormality in Fas/Fas ligand system containing as the active  
CC component an antibody having as the light chain subunit a polypeptide  
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
CC fully defined in the specification and having an activity of combining  
CC specifically with mammalian Fas and an activity of inducing apoptosis in  
CC a cell expressing Fas. The agent has immunosuppressive and antiallergic  
CC activity and is used for preventing and treating autoimmune diseases,  
CC allergy, atopy and others. The present sequence is that of a PCR primer,  
CC useful to the invention

XX SQ Sequence 20 BP; 3 A; 3 C; 10 G; 4 T; 0 U; 0 Other;  
XX PT Query Match 0.2%; Score 15; DB 1; Length 20;  
PT Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
PT Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 7181 GGTGGCATGTGTGA 7195  
Db 5 GGTGGCATGTGTGA 19  
RESULT 2844  
ABZ85436  
ID ABZ85436 standard; DNA; 20 BP.  
XX AC ABZ85436;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human oligonucleotide sequence.  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX OS Homo sapiens.  
XX PN WO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PS (EPIC-) EPIGENESIS PHARM INC.  
XX PI NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX DR WPI: 2003-229219/22.  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX PS Claim 15; SEQ ID NO 678; 872pp; English.  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4470 TTTT TTTT TTTT TTTT G 4484  
Db 1 TTTT TTTT TTTT TTTT G 15

RESULT 2845  
AB291658/c  
ID AB291658 standard; DNA; 20 BP.  
AC AB291658;  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiaesthetic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
PI Miller S, Tang L, Shahbuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 6900; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,  
CC immunosuppressive, and cytosstatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4464 TTTT TTTT TTTT TTTT T 4478  
Db 20 TTTT TTTT TTTT TTTT T 6

RESULT 2846  
ADA66464  
ID ADA66464 standard; DNA; 20 BP.  
AC ADA66464;  
DT 20-NOV-2003 (first entry)  
XX  
DE Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 23.  
XX  
KW Cytostatic; antirheumatic; antiarthritic; gynecological;  
KW antiarteriosclerotic; transforming growth factor beta-3; TGF beta-3;  
KW hyperproliferative disorder; cancers; atherosclerosis;  
KW rheumatoid arthritis; preclampsia; fibrosis; phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "This oligonucleotide has a phosphorothioate  
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'  
FT and 3' ends, which are 5 nucleotides in length. Also all  
FT cytidine residues are 5-methylcytidines"  
XX  
PN W02003008544-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 12-JUL-2002; 2002WO-US022423.  
XX  
PR 14-JUL-2001; 2001US-00906158.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freiler SM;  
XX  
DR WPI; 2003-229569/22.  
XX  
PT Novel antisense compound which is targeted to nucleic acid encoding  
PT transforming growth factor beta-3, and inhibits expression of TGF-beta 3,  
PT useful for treating a condition associated with TGF-beta 3, e.g. cancer.  
XX  
PS Claim 3; Page 87; 154pp; English.  
XX  
CC The present invention relates to antisense oligonucleotides (ADA66459-  
CC ADA66609), which inhibit transforming growth factor (TGF) beta-3  
CC expression, which inhibit transforming growth factor (TGF) beta-3  
CC of TGF-beta3 in cells or tissues, and for treating an animal having a  
CC disease condition associated with TGF-beta3, e.g. a hyperproliferative  
CC disorder such as cancers of lung, liver, colon, oesophagus, pancreas,  
CC breast, skin or haematopoietic, atherosclerosis, rheumatoid arthritis,  
CC preclampsia and fibrosis.  
XX  
SQ Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 4290 TTGCAAGTGCATCTT 4304  
|||||  
DB 2 TTGCAAGTGCATCTT 16

RESULT 2847  
ABZ80969  
ID ABZ80969 standard; DNA; 20 BP.  
XX  
AC ABZ80969;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Herpes virus infection diagnostic primer III.  
XX  
KW Primer; PCR; diagnosis; ss.  
XX  
OS Human herpesvirus.  
XX  
PN RU2192473-C1.  
XX  
PD 10-NOV-2002.  
XX  
PF 26-JUN-2001; 2001RU-00117331.  
XX  
PR 26-JUN-2001; 2001RU-00117331.  
XX  
PA (ASMO=) AS USSR MOLECULAR GENETICS INST.  
XX  
PI Demkin VV, Kruglova AI, Nikolaeva NP;  
XX  
DR WPI; 2003-146311/14.  
XX  
PT Method of diagnosis of herpes virus infection.  
XX  
PS Claim 1; Page 5; 6pp; Russian.  
XX

CC The invention relates to a method of diagnosing herpes virus infections  
CC by two-stage polymerase chain reaction (PCR) carried out using two  
CC external primers I (ABZ80967) and II (ABZ80968) on the first stage and  
CC two internal primers I and III (this sequence) on the second stage. The  
CC method ensures determination of four types of herpes viruses in a single  
CC sample simultaneously. The method is useful in medicine, especially in  
CC immunobiology, virology and molecular biochemistry  
CC  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 GTGTCCCGTAGAGT 416  
|||||  
DB 5 GTGTCCCGTAGAGT 19

RESULT 2848  
ABZ80971  
ID ABZ80971 standard; DNA; 20 BP.  
XX  
AC ABZ80971;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Alternative Herpes virus infection diagnostic primer III.  
XX  
KW Primer; PCR; diagnosis; ss.  
XX  
OS Human herpesvirus.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 2  
FT /\*tag= a

FT /mod base= i  
FT /\*tag= i  
FT /\*note= "inosine"  
XX  
PN RU2192473-C1.  
XX  
PD 10-NOV-2002.  
XX  
PF 26-JUN-2001; 2001RU-00117331.  
XX  
PR 26-JUN-2001; 2001RU-00117331.  
XX  
PA (ASMO=) AS USSR MOLECULAR GENETICS INST.  
XX  
PI Demkin VV, Kruglova AI, Nikolaeva NP;  
XX  
DR WPI; 2003-146311/14.  
XX  
PT Method of diagnosis of herpes virus infection.  
XX  
PS Disclosure; Page 3; 6pp; Russian.  
XX

CC The invention relates to a method of diagnosing herpes virus infections  
CC by two-stage polymerase chain reaction (PCR) carried out using two  
CC external primers I (ABZ80967) and II (ABZ80968) on the first stage and  
CC two internal primers I and III (ABZ80969) on the second stage. The method  
CC ensures determination of four types of herpes viruses in a single sample  
CC simultaneously. The method is useful in medicine, especially in  
CC immunobiology, virology and molecular biochemistry. This sequence  
CC represents an alternative version of primer III with an inosine residue  
CC replacing at thymidine at position 2  
CC  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 4 T; 0 U; 1 Other;

Query Match 0.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 GTGTCCCGTAGAGT 416  
|||||  
DB 5 GTGTCCCGTAGAGT 19

RESULT 2849  
ABZ59521  
ID ABZ59521 standard; DNA; 20 BP.  
XX  
AC ABZ59521;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE Mouse src-c chimeric phosphorothioate oligonucleotide SEQ ID NO:142.  
XX  
KW Mouse; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;  
KW antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;  
KW antisense oligonucleotide; aberrant bone remodeling; breast cancer;  
KW hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;  
KW ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;  
KW Kaposi's sarcoma; infection; inflammation; tumour formation;  
KW phosphorothioate; ss.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages"  
FT 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"  
FT modified\_base 16..20

```

FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl gapmer (2'-MOE wing) "
XX
XX      WO200295053-A2.
XX
XX      28-NOV-2002.
XX
XX      16-MAY-2002; 2002WO-US015684.
XX
XX      18-MAY-2001; 2001US-00860473.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett FC, Watt AT;
XX
XX      WPI; 2003-120806/11.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding src-c,
XX      useful for diagnosing, treating or preventing diseases associated with
XX      the expression of src-c, e.g. cancer or inflammation, and in research
XX      applications.
XX
XX      Example 16; Page 92; 137pp; English.
XX
XX      The present invention describes a compound (I) that is 8-50 nucleobases
XX      in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
XX      coding region, intron region, exon region, stop codon, intron:exon
XX      junction, exon:exon junction, or 5' mRNA variant of src-c, and which
XX      specifically hybridizes with and inhibits the expression of src-c. (1)
XX      have cytostatic, antiinflammatory, osteopathic and antibacterial
XX      activities, and can be used in antisense therapy and in vaccines. The
XX      antisense compounds (I) can be used for modulating the expression of src-
XX      c and for treating diseases or conditions associated with expression of
XX      src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
XX      particularly cancer, such as breast cancer, pancreatic cancer, lung
XX      cancer, ovarian cancer, esophageal cancer, neuroblastoma, retinoblastoma
XX      or Kaposi's sarcoma. (I) are also useful for diagnosis, therapeutics,
XX      prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
XX      formation, as research reagents and kits, and in distinguishing between
XX      functions of various members of a biological pathway. The present
XX      sequence represents a mouse src-c antisense chimeric phosphorothioate
XX      oligonucleotide, which is used in an example from the present invention
XX
XX      Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      30 GAGCTGCTGCAGGCT 44
XX      |||||
XX      6 GAGCTGCTGCAGGCT 20
XX
XX      RESULT 2850
XX      ID      ADA08088 standard; DNA; 20 BP.
XX
XX      ADA08088;
XX
XX      06-NOV-2003 (first entry)
XX
XX      Human PFM5 cDNA RT-PCR primer.
XX
XX      Human; PR Family Member 5; PFM5; PFM PR domain; PFM zinc finger domain;
XX      PFM ZF domain; modulation of cell growth; cancer;
XX      cell degeneration disease; Alzheimer's disease; Parkinson's disease;
XX      insulin-dependent diabetes mellitus; IDDM; neuroprotective;
XX      antiparkinsonian; antidiabetic; cytoskeletal; RT-PCR;
XX      reverse transcriptase-PCR; primer; ss.
XX
XX      Homo sapiens.

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XX      US6586579-B1.
XX
XX      01-JUL-2003.
XX
XX      03-SEP-1999; 99US-00389956.
XX
XX      03-SEP-1999; 99US-00389956.
XX
XX      (BURN-) BURHAM INST.
XX
XX      Huang S;
XX
XX      WPI; 2003-66568/63.
XX
XX      New PR Family Member 2 oligonucleotide, useful for preparing a
XX      composition for modulating cell growth for treating cancer or diseases of
XX      cell degeneration, e.g., Alzheimer's disease or insulin-dependent
XX      diabetes mellitus.
XX
XX      Example 5; Col 32; 95pp; English.
XX
XX      The present invention relates to the isolation of human and mouse PR
XX      Family Member (PFM) proteins, and the polynucleotide sequences encoding
XX      them. Also disclosed are PFM PR and PFM zinc finger (ZF) domains, and the
XX      polynucleotide sequences encoding them. The invention also discloses PFM
XX      oligonucleotide sequences and methods for detecting a PFM polynucleotide sequence
XX      in a sample. The PFM polypeptide and polynucleotide sequences are useful
XX      for preparing a composition for modulating cell growth for treating
XX      cancer or diseases of cell degeneration, e.g. as Alzheimer's disease,
XX      Parkinson's disease or insulin-dependent diabetes mellitus (IDDM). The
XX      present sequence represents a primer used in the examples of the present
XX      invention.
XX
XX      Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 15; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e+03;
XX      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      4647 GGAATTCCTCTTTG 4661
XX      |||||
XX      6 GGAATTCCTCTTTG 20
XX
XX      RESULT 2851
XX      AA226500/c
XX      ID      AA226500 standard; DNA; 21 BP.
XX
XX      AA226500;
XX
XX      30-NOV-1999 (first entry)
XX
XX      Human polymorphic region 689.
XX
XX      Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX      cell viability; loss of heterozygosity; precancerous condition; ASI;
XX      allele specific inhibitor; somatic cell; diagnosis; prevention;
XX      atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX      dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX      graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX      Homo sapiens.
XX
XX      WO9841648-A2.
XX
XX      24-SEP-1998.
XX
XX      19-MAR-1998; 98MO-US005419.
XX
XX      20-MAR-1997; 97US-0041057P.
XX
XX      (VARI-) VARIAGENICS INC.

```

XX Housman D, Ledley FD, Stanton VP;  
 XX WPI; 1998-521232/44.  
 XX  
 PT Identifying target genes for allele-specific drugs - used for diagnosis,  
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 PT dysplastic lesions, endometriosis or graft versus host disease.  
 XX  
 PS Disclosure; Fig 7; 605pp; English.  
 XX  
 CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AA25812-226825 represent  
 CC human polymorphic sites described in the method of the invention  
 SQ  
 Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4470 TTTT TTTT TTTT TTTT G 4484  
 Db 21 TTTT TTTT TTTT TTTT G 7  
 RESULT 2852  
 AA26584/c  
 ID AA26584 standard; DNA; 21 BP.  
 AC  
 XX AA26584;  
 AC  
 DT 30-NOV-1999 (first entry)  
 DE Human polymorphic region 773.  
 XX  
 KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
 KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
 KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
 KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
 KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
 KW graft versus host disease; malignant cell removal; bone marrow; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9841648-A2.  
 XX  
 PD 24-SEP-1998.  
 XX  
 PF 19-MAR-1998; 98WO-US005419.  
 XX  
 PR 20-MAR-1997; 97US-0041057P.  
 XX  
 PA (VARI-) VARIAGENICS INC.  
 XX  
 PI Housman D, Ledley FD, Stanton VP;  
 XX WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for diagnosis,  
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 PT dysplastic lesions, endometriosis or graft versus host disease.  
 XX  
 PS Disclosure; Fig 7; 605pp; English.  
 XX  
 CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AA25812-226825 represent  
 CC human polymorphic sites described in the method of the invention  
 SQ  
 Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT T 4478  
 Db 21 TTTT TTTT TTTT TTTT T 7  
 RESULT 2853  
 AA274799/c  
 ID AA274799 standard; DNA; 21 BP.  
 AC  
 XX AA274799;  
 AC  
 DT 10-SEP-2001 (first entry)  
 DE Human biallelic marker downstream amplification primer SEQ ID NO:9155.  
 XX  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 XX  
 PR 23-NOV-1998; 98US-0109732P.  
 XX  
 PA (GIST ) GENSET.  
 XX  
 PI Cohen D, Blumenfeld M, Chumakov I;  
 XX WPI; 2000-013267/01.  
 XX  
 PT Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX

PS Claim 8; Page 2182; 2745pp; English.

XX  
CC AA265654 to AA269578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AA269579 to AA277440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX  
SQ Sequence 21 BP; 6 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5151 GGGAGGGAGGCTTC 5165  
DB 21 GGGAGGGAGGCTTC 7

RESULT 2854  
AAC73128/c  
ID AAC73128 standard; DNA; 21 BP.

XX  
AC AAC73128;  
DT 02-FEB-2001 (first entry)

XX  
SNP flanking sequence #15 used in multiplexing PCR/SBE assay.

XX  
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;  
KM polymorphic locus; single nucleotide polymorphism; ss.

XX  
OS Unidentified.

XX  
FN WO200058516-A2.

XX  
PD 05-OCT-2000.

XX  
PF 27-MAR-2000; 2000WO-US008069.

XX  
PR 26-MAR-1999; 99US-0126473P.  
PR 23-JUN-1999; 99US-0140359P.

XX  
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (AFVY-) AFFYMETRIX INC.

XX  
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;  
PI Ryder T, Sklar P;  
XX  
DR WPI; 2000-656171/63.

XX  
PT Universal array of oligonucleotide tags attached to a solid substrate  
PT along with locus-specific tagged oligonucleotides useful in genotyping  
PT using single base extension reactions.

XX  
PS Example 7; Page 49; 70pp; English.

XX  
CC The present invention relates to an oligonucleotide array comprising  
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide  
CC array is useful for genotyping a nucleic acid sample at one or more loci  
CC via single base extension (SBE) reactions. A pair of primers is used to  
CC amplify a polymorphic locus in a sample e.g. a single nucleotide  
CC polymorphism (SNP). The present sequence is one such polymorphic locus

CC used in the present invention. The amplified nucleic acid product is then  
CC used as a template in a SBE reaction with an extension primer. The SBE  
CC reaction products are used to form the oligonucleotide array. Note: This  
CC sequence includes a SNP represented by the degenerate codon in the  
CC sequence

XX  
SQ Sequence 21 BP; 4 A; 11 C; 3 G; 2 T; 0 U; 1 Other;

Query Match 0.2%; Score 15; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 GAGAGCTGCGGCGCG 77  
DB 20 GAGAGCTGCGGCGCG 4

RESULT 2855  
AAQ30432/c  
ID AAQ30432 standard; DNA; 23 BP.

XX  
AC AAQ30432;  
DT 25-MAR-2003 (revised)  
DT 07-DEC-1992 (first entry)

XX  
XX Oligomer IL6805 for forming triplex with HUMIL6 target duplex.

XX  
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
KM malignancy; hepatitis; inflammation; ss.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*tag= OTHER  
FT /mod\_base= OTHER  
FT /note= "OTHER= N4 N4 ethanocytosine"

FT misc\_feature 11..12  
FT /\*tag= d  
FT /note= "o-xylosa dimer synthon linkage"

FT misc\_feature 12..23  
FT /\*tag= c  
FT /label= inverted polarity\_region  
FT /note= "see comments"

FT modified\_base 23  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= N4 N4 ethanocytosine"

XX  
PN WO9209705-A1.

XX  
PD 11-JUN-1992.

XX  
PF 25-NOV-1991; 91WO-US008811.

XX  
PR 23-NOV-1990; 90US-00617907.  
PR 18-JAN-1991; 91US-00643382.  
PR 08-APR-1991; 91US-00683420.  
PR 17-APR-1991; 91US-00686544.  
PR 17-APR-1991; 91US-00686546.  
PR 17-APR-1991; 91US-00686547.  
PR 27-SEP-1991; 91US-00766733.

XX  
PA (GILE-) GILEAD SCI INC.

XX  
PI Freohler B, Krawczyk S, Matteucci MD, Milligan J;  
XX  
DR WPI; 1992-217083/26.

XX  
PT New oligomers contg. modified bases - which form a triplex with G-C  
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
PT herpes malignancy and inflammation.

XX Claim 12; Page 71; 77pp; English.

XX The synthetic oligomer is capable of forming a triplex at physiological  
 CC pH with a purine rich target sequence by coupling into the major groove  
 CC of the duplex. The specific target sequence of this oligomer is the human  
 CC interleukin 6 gene untranslated sequence contg. a purine rich sequence  
 CC concd. on one strand of the duplex. The oligomer, and others like it are  
 CC useful in diagnosis and therapy of diseases characterised by specific DNA  
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
 CC tumours and inflammation. The triple helices form under mild conditions  
 CC harsh assays may be carried out without subjecting the test specimen to  
 CC harsh conditions. The oligomer contains an inverted polarity region  
 CC formed from an o-xylosid dimer synthon. The linking gp. is o-xylosid  
 CC (nucleotides have the 3' positions of xylose sugars linked via the o-  
 CC xylenic ring). Two nucleotides are coupled through a xylene residue to  
 CC form the dimer synthon. This additional modifications may render the  
 CC oligomer stable to nuclease activity. The oligomer is able to inhibit  
 CC gene expression, as verified by in vitro systems. See also AA025452-25501  
 CC and AA030226-448. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;  
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4019 GAAAAAGAGAGAAAAAATAATG 4041  
 Db 23 GAAAAAAGAGAGAAAAAATAATG 1

RESULT 2856  
 AA03762  
 ID AA03762 standard; DNA; 23 BP.

XX AA03762;  
 AC 25-MAR-2003 (revised)  
 DT 09-AUG-1990 (first entry)

XX Tissue plasminogen activator analogue oligonucleotide.  
 DE Tissue plasminogen activator; tPA analogues; fibrinolytic therapy; ss.  
 KM Tissue plasminogen activator; tPA analogues; fibrinolytic therapy; ss.  
 XX Synthetic.  
 OS  
 XX DE3831714-A.  
 PN 22-MAR-1990.  
 PD 17-SEP-1988; 88DE-03831714.  
 XX 17-SEP-1988; 88DE-03831714.  
 PR 17-SEP-1988; 88DE-03831714.  
 XX (BADT) BASF AG.  
 PA Bach A, Schmidt M, Scrube KH, Baldinger V, Schwarz M;  
 PI WPI; 1990-100100/14.

XX New tissue plasminogen activator analogues - are polypeptide(s) with TPA  
 PT sequence contg. arginine-glycine-aspartic acid tripeptide units.  
 XX Example 3.6; Page 5; 17pp; German.

XX Sequence containing this oligonucleotide encodes tPA-like polypeptides  
 CC displaying the amino acid sequence of tPA in which 1-6 tripeptides are  
 CC replaced by thr tripeptide RGD (=Arg-Gly-Asp). The produced polypeptides  
 CC have plasminogen activator activity and can be used in fibrinolytic  
 CC therapy, eg after cardiac infarct. They have increased blood clot  
 CC specificity, longer half life, reduced inhibitor binding and/or greater  
 CC proteolytic activity. See also AA03754-Q03771 and DR 3830734. (Updated

CC on 25-MAR-2003 to correct PD field.)

XX Sequence 23 BP; 1 A; 13 C; 5 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;  
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3524 GACCCGTCTTCTTCGCGCCGC 3546  
 Db 1 GATGCCCTTCCTTCGCGCCGC 23

RESULT 2857  
 AA021598/c  
 ID AA021598 standard; DNA; 23 BP.

XX AA021598;  
 AC 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 16-MAY-1992 (first entry)

XX Infectious bovine rhinotracheitis virus primer oligo E748.  
 DE Herpes virus-based viral vector; foot and mouth disease; epitope;  
 KM vaccine; ss.  
 XX Bovine herpesvirus 1.  
 OS Foot-and-mouth disease virus.  
 OS virus.  
 XX EP471457-A.  
 PN 19-FEB-1992.  
 PD 22-JUL-1991; 91EP-00306646.  
 XX 24-JUL-1990; 90US-00556593.  
 PR (NOVA-) NOVAGEN INC.  
 PA (BLIL) LILLY & CO ELI.  
 XX Dimarchi RD, Kit S, Little SP, Gale C, Kit M;  
 PI WPI; 1992-058515/08.

XX Vaccine for foot and mouth disease and Herpes virus - comprising a Herpes  
 PT virus-based viral vector which expresses a foot and mouth disease virus  
 PT epitope.  
 XX Example; Page 63; 72pp; English.

XX An oligonucleotide cloning/expression cassette was synthesised for  
 CC insertion into the NcoI site of the IBRV gIII gene-contg. plasmid  
 CC pIA(gIII):30 dl. Hind III/HpaI (see AA021591). The cassette was designed  
 CC to provide cloning sites, optimal translation start signals for the  
 CC bovine growth hormone (bGH) signal sequence, the RMDV epitope sequence  
 CC and restriction nuclease sites to permit unidirectional nuclease digestion  
 CC into the IBRV gene. The resulting plasmid was then transformed with a bGH  
 CC -FMV sequence and subjected to exonuclease II digestion to remove  
 CC sequences encoding the 39 N-terminal amino acids from the IBRV gIII  
 CC gene. The final plasmid obtained has the sequences for bGH-FMV which can  
 CC be expressed from the IBRV gIII promoter. When the PstI to MluI region of  
 CC AA021592 is transferred into the pIA(gIII):30 dl HindIII/HpaI oligo  
 CC 171/172 cassette, the bGH-FMV sequence will be in the same reading frame  
 CC as the gIII protein. (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 23 BP; 4 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 23;  
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7234 CCTCTCAATCCAGCATGATGG 7256

DB 23 CCTCTCAAGTTGGGACGAGGG 1

RESULT 2858

AAQ23949

ID AAQ23949 standard; DNA; 23 BP.

XX AAQ23949;

DT 27-OCT-1992 (first entry)

DE Degenerate PCR primer DG129 based on thermostable polymerase conserved sequence.

KM Thermophilicity; polymerase chain reaction; Taq Pol I; Thermophilic africanus; thermophilic bacteria; ss.

XX Synthetic.

PN WO9206202-A.

PD 16-APR-1992.

PF 26-SEP-1991; 91WO-US007076.

PR 28-SEP-1990; 90US-00590490.

PA (CETU ) CETUS CORP.

PI Gelfand DH, Lawyer FC, Abramson RD, Greenfield L, Reichert FL;

DR WPI; 1992-150887/18.

PT Thermostable DNA polymerase from Thermophilic africanus - prepd. by purification from cells or by expression of Taq polymerase gene in host cells.

PS Example 2; Page 38; 80pp; English.

CC Chromosomal DNA from Thermophilic africanus (Taq) was PCR-amplified with degenerate primers corresponding to the amino acid sequences of conserved regions of known thermostable polymerases. DG129 is one example of a degenerate primer. See AAQ23917 for full-length Taq Pol I coding sequence

SO Sequence 23 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 4 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4687 GATCTGGTATGAGCCATG 4706

DB 4 GATCTGGATGATGATGATG 23

RESULT 2859

AAAT40331/c

ID AAAT40331 standard; DNA; 23 BP.

XX AAAT40331;

DT 06-DEC-1996 (first entry)

DE DNA cleavage substrate for generation of improved ribozymes.

KM Wild type; self-splicing group I intron; large ribosomal RNA precursor; Tetrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.

OS Synthetic.

PN WO9531551-A1.

PD 23-NOV-1995.

PF 26-APR-1995; 95WO-US005141.

PR 13-MAY-1994; 94US-00242402.

PA 01-JUL-1994; 94US-00270180.

PA (SCRI ) SCRIPPS RES INST.

PI Joyce GF;

DR WPI; 1996-010936/01.

PT Enzymatic RNA molecules having one or more point mutation(s) - improve the enzymatic performance of the molecules.

PS Example 1; Page 111; 209pp; English.

CC The sequences given in AAAT40331-32 represent sequences that were as substrate molecules in experiments for selection of improved catalytic activity of ribozymes. The evolution experiment spanned 10 successive generations and catalytic activity was deduced after each generation. The self-splicing group I intron of the invention is based on the large ribosomal RNA precursor from Tetrahymena thermophila. The biological function of this molecule is to catalyze its own excision from precursor RNA to produce mature RNA. The Tetrahymena wild type sequence was used in the design of the enzymatic RNA molecules of the invention. A number of mutations are listed in the specification which improve the enzymatic properties of this molecule, e.g. G444A, G191U, U190A and A314G. The modified enzymatic molecules may be used as medical or pharmaceutical agents for use in anti-viral agents, food products, personal care products or cleaning agents

SO Sequence 23 BP; 12 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6683 TATTTTATTATATGAGGCC 6705

DB 23 TTTATTATTATTATTAGAGGCC 1

RESULT 2860

AAAT40328/c

ID AAAT40328 standard; DNA; 23 BP.

XX AAAT40328;

DT 05-DEC-1996 (first entry)

DE Group I intron substrate.

KM Wild type; self-splicing group I intron; large ribosomal RNA precursor; Tetrahymena thermophila; catalysis; enzymatic RNA; food product; anti-viral agent; mutation; personal care product; cleaning agent; ss.

OS Synthetic.

PN WO9531551-A1.

PD 23-NOV-1995.

PF 26-APR-1995; 95WO-US005141.

PR 13-MAY-1994; 94US-00242402.

PA 01-JUL-1994; 94US-00270180.



```

CC reactive airways
XX
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;
  Query Match      0.2%; Score 15; DB 1; Length 23;
  Best Local Similarity 78.3%; Pred. No. 2.2e+03;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5699 TTGGCTTCTCTTCTCTCTCTCTC 5721
  Db 1 TTTCCTTCTCTCTCTCTCTCTC 23
  RESULT 2863
  AAV37972/c
  ID AAV37972 standard; DNA; 23 BP.
  XX
  AC AAV37972;
  XX
  DT 11-SEP-1998 (first entry)
  XX
  DE ECEPO section 2 construction oligonucleotide 9 for human EPO.
  XX
  KM Human; erythropoietin; EPO; bone marrow; reticulocyte; red blood cell;
  KM expression; CHO; chinese hamster ovary cell; diagnosis; blood disorder;
  KM ss.
  OS Synthetic.
  OS Homo sapiens.
  OS
  PN A0688723-B.
  XX
  PD 19-FEB-1998.
  XX
  PF 02-DEC-1997; 97AU-00046867.
  XX
  PR 02-DEC-1997; 97AU-00046867.
  XX
  PA (KIRI ) KIRIN AMGEN INC.
  XX
  PI Lin F;
  XX
  DR WPI; 1998-261957/24.
  XX
  PT Recombinant human erythropoietin - potentially useful for diagnosis and
  PT treatment of blood disorders.
  PT
  PS Example 11; Page 64; 100pp; English.
  XX
  CC The present sequence represents a construction oligonucleotide for ECEPO
  CC section 2 as part of the assembly of human erythropoietin (EPO), used in
  CC an example from the present invention. The present invention describes
  CC recombinant human EPO which causes bone marrow cells to increase
  CC production of reticulocytes or red blood cells, where the polypeptide is
  CC the product of expression in CHO (Chinese hamster ovary) cells of an
  CC exogenous DNA sequence encoding human EPO. EPO is potentially useful in
  CC the diagnosis and treatment of blood disorders characterised by low or
  CC defective red blood cell production
  CC
  SQ Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
  XX
  Query Match      0.2%; Score 15; DB 1; Length 23;
  Best Local Similarity 78.3%; Pred. No. 2.2e+03;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 7124 TTCTGTGACACAGTCCAGCCT 7146
  Db 23 TGCTGGCCACGACGTACAGCCT 1
  RESULT 2864
  AAV09049/c
  ID AAV09049 standard; DNA; 23 BP.

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XX
AC AAV09049;
XX
DT 25-JUN-1998 (first entry)
XX
DE Substrate for tetrahymena ribozyme L-21.
XX
KM Tetrahymena ribozyme; group I intron; amide end hydrolysis; peptidase;
KM protease; antiviral agent; gene regulator; immunogenic virus; vaccine;
KM mutation detection; ss.
XX
OS Synthetic.
OS Tetrahymena sp.
XX
PN M09802583-A1.
XX
PD 22-JAN-1998.
XX
PF 16-JUL-1997; 97MO-US012394.
XX
PR 17-JUL-1996; 96US-00682423.
XX
PA (SCRI ) SCRIPPS RBS INST.
XX
PI Joyce GF;
XX
DR WPI; 1998-110627/10.
XX
PT Catalytic RNA for site-specific cleavage of nucleic acid or hydrolysis of
PT amide bonds - and ribozyme amidase intermediates, useful e.g. as
PT peptidase(s), antiviral agents and gene regulators.
XX
XX
XX Example 1; Page 120; 215pp; English.
XX
CC This sequence is a substrate for a wild type tetrahymena ribozyme L-21
CC form. The ribozyme sequence is an example of a catalytic RNA (I) of the
CC invention, which catalyses site-specific cleavage of nucleic acid under
CC physiological conditions includes a sequence derived from a group I
CC intron. Similar catalytic RNAs (II) which catalyse hydrolysis of amide
CC ends are useful as peptidases and proteases, e.g. in wound debridement,
CC clot dissolution, in detergents or as a meat tenderiser. (I) cleave
CC single- and (partly) double-stranded nucleic acids in vitro or in vivo,
CC and are potentially useful as antiviral agents and gene regulators; also
CC to generate defective but still immunogenic viruses (for vaccines);
CC diagnostically to detect mutations in nucleic acid or to identify nucleic
CC acid binding agents; to modulate/terminate reactions initiated by DNA
CC primers; to generate truncated transcripts from DNA; to modulate
CC therapeutic/diagnostic processes using antisense sequences; in DNA
CC fingerprinting and for vector construction. (I) and (II) are produced by
CC in vitro evolution processes that provide better catalytic performance;
CC broader active temperature and pH ranges; new enzymatic activities or
CC specificities; altered recognition sites or co-factor requirement
XX
SQ Sequence 23 BP; 12 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
  Query Match      0.2%; Score 15; DB 1; Length 23;
  Best Local Similarity 78.3%; Pred. No. 2.2e+03;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 6683 TATTATTATTATATGGGCC 6705
  Db 23 TTATTATTATTATTAGGGCC 1
  RESULT 2865
  AAT99526
  ID AAT99526 standard; DNA; 23 BP.
  XX
  AC AAT99526;
  XX
  DT 21-MAY-1998 (first entry)
  XX
  DE Human ST receptor PCR primer.

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XX ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
KW metastasis; diagnosis; human; PCR; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX MO9742506-A1.
XX 13-NOV-1997.
XX 02-MAY-1997; 97WO-US007467.
XX 03-MAY-1996; 96US-0016564P.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Waldman SA, Carrithers SL;
PI WPI, 1998-006454/01.
XX Determining whether an individual has metastasised colorectal cancer
PT cells and origin of tumour cells - by detecting presence of heat-stable
PT toxin receptor on cells in a sample.
XX Claim 14; Page 54; 62pp; English.
XX Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
CC encode the extracellular domain of human heat-stable toxin (ST) receptor
CC protein (see AAW37371), a highly specific marker for metastasised
CC colorectal cancer cells. PCR using these primers provides specific and
CC sensitive detection of human ST receptor expression. A specific primer
CC pair comprises the primers given in AAT99526 and AAT99527. Claimed in
CC vitro methods for determining whether or not (i) an individual has
CC metastasised colorectal cancer cells, or (ii) an individual has
CC colorectal cancer cell comprise the steps of examining a sample of
CC extraintestinal tissue and/or body fluids or tumour cells from an
CC individual to determine whether ST receptor protein is being expressed by
CC cells in the sample. Expression is determined by immunassay or by PCR
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also
CC AAT97229)
XX
XX Sequence 23 BP; 8 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3199 AGTAGGGGCTTGAGAAAGTGGG 3221
Db 1 AATGAGGGGCTGGAATAGTAGAG 23

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PF 19-SEP-1997; 97JP-00271927.
XX 19-SEP-1997; 97JP-00271927.
XX (SHIS ) SHISEIDO CO LTD.
XX WPI, 1999-281045/24.
XX Immortalised human hair papilla cells used for evaluation of hair growth
PT agent - are prepared by transformation of human hair papilla cells with
PT gene with deleted replication initiation point.
XX Example 2; Page 7; 23pp; Japanese.
XX The specification describes the preparation of immortalized human hair
CC papilla cells (HPC). The method comprises transformation of HPC with an
CC SV40 viral Large T-antigen gene with deleted replication initiation
CC point. The immortalized HPC can be used in a screening method for a hair
CC growth agent, by culture of immortalized HPC in the presence of a
CC substance to be tested and observation of hair growth stimulating agents.
CC HPC. HPC is also used in development of hair growth stimulating agents.
CC The present sequence represents a PCR primer, which is used in the course
CC of the invention
XX
XX Sequence 23 BP; 5 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 374 ACTACGAGCTGGCATGACGCG 396
Db 1 ACTACCTGCTGGCATCAAGCG 23

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RESULT 2866
AAK34877
ID AAK34877 standard; DNA, 23 BP.
XX AAK34877;
XX 28-JUN-1999 (first entry)
XX PCR primer used to amplify FGFA.
XX Immortalised human hair papilla cell; HPC; screening; hair growth;
KW SV40 viral Large T-antigen gene; deleted replication initiation point;
KW hair growth stimulating agent; PCR primer; ss.
XX Synthetic.
OS JPI1089565-A.
XX JPI1089565-A.
XX 06-APR-1999.
XX

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RESULT 2867
AAK53824
ID AAK53824 standard; DNA, 23 BP.
XX AAK53824;
XX 05-JUL-1999 (first entry)
XX Human adenosine A1 receptor antisense oligonucleotide fragment.
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX Synthetic.
XX WO9913886-A1.
XX 25-MAR-1999.
XX 17-SEP-1998; 98WO-US019419.
XX 17-SEP-1997; 97US-0059160P.
XX 09-JUN-1998; 98US-00093972.
XX (UYEC-) UNIV EAST CAROLINA.
XX NYce JW;
XX WPI, 1999-229400/19.
XX

```

PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 XX vasoconstriction.  
 PS Disclosure, Page 42; 120pp; English.  
 XX The specification describes antisense oligonucleotides (AA52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC -end and the junction between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AA55272-74. These multiple target oligonucleotides  
 CC (specifically AA55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impaired respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX  
 SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5699 TTGGCTTCTCTTCTCTCTCTC 5721  
 DB 1 TTTTCCTCTTGTCTCTCTTC 23  
 RESULT 2868  
 AAX18455/C  
 ID AAX18455 standard; DNA; 23 BP.  
 XX  
 AC AAX18455;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE Primer for DNA encoding orphan homologue GPR12.  
 XX  
 KM Agonist identification; orphan receptor; constitutively active OR;  
 KM Graves' disease; thyroid adenoma; hypertension; cardiomyopathy;  
 KM schizophrenia; Kaposi's sarcoma; fibroblast growth factor receptor;  
 KM adenylylate cyclase constitutive activator; thyrotropin receptor;  
 KM thyrotropin stimulating hormone; beta-adrenergic receptor; PCR primer;  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX  
 PN WO9846995-A1.  
 XX  
 PD 22-OCT-1998.  
 XX  
 PF 14-APR-1998; 98WO-US007496.  
 XX  
 PR 14-APR-1997; 97US-00839449.  
 XX  
 XX (BEHA/) BEHAN D P.  
 PA (CHAL/) CHALMERS D T.  
 XX  
 PI Behan DP, Chalmers DT;  
 XX  
 DR WPI; 1999-105468/09.  
 XX  
 PT Identifying agonists of orphan receptors from their effect on the

PT constitutively active receptor - particularly therapeutically active  
 PT inverse agonists at G protein coupled receptors, without requiring  
 PT knowledge of endogenous ligand or receptor function.  
 XX  
 XX Example 4; Page 72; 114pp; English.  
 XX  
 PS This sequence is a primer for DNA encoding the orphan receptor homologue  
 CC GPR3. The invention relates to a method for the identification of  
 CC candidate compounds as agonists, including inverse or partial, of an  
 CC orphan receptor (OR), which comprises: (i) applying test compound to  
 CC constitutively active OR; and (ii) measuring its effect on OR. The method  
 CC is particularly used to identify inverse agonists of G protein-coupled  
 CC OR, i.e. potential therapeutic agents for treating conditions in which  
 CC constitutively active OR are implicated (e.g. Graves' disease, thyroid  
 CC adenoma, hypertension, cardiomyopathy, schizophrenia, major depression,  
 CC Kaposi's sarcoma and many others tabulated). It is based on  
 CC identification of agents that reduce receptor activation, rather than  
 CC compounds that antagonise the normal ligand. Once identified, (inverse)  
 CC agonists can be used to study OR function. The method does not require  
 CC knowledge of the endogenous receptor ligand or receptor function, and  
 CC identifies directly compounds that inhibit the activated receptor, i.e.  
 CC able to block both ligand-dependent and -independent activation, rather  
 CC than only the ligand-dependent process, as is the case with compounds  
 CC identified by ligand-dependent assays. It should accelerate drug  
 CC discovery at a wide range of OR and since activated receptors have a  
 CC greater response to the agents, potential drugs are more likely to be  
 CC detected  
 XX  
 SQ Sequence 23 BP; 6 A; 4 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1669 CAACCTGTGTCGCAATATGC 1691  
 DB 23 CACCAGTTCCTGCTAATAGGC 1  
 RESULT 2869  
 AAX00055  
 ID AAX00055 standard; DNA; 23 BP.  
 XX  
 AC AAX00055;  
 XX  
 DT 16-MAR-1999 (first entry)  
 XX  
 DE Human Y chromosome-specific sequence DY21 PCR primer Y21.  
 XX  
 XX Human Y chromosome; DY21; urine; detection; amplification; diagnosis;  
 KM hybridisation; kidney barrier; foetal sex; maternal; inherited disease;  
 KM cancer; pathogenic infection; paternity testing; PCR primer; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX  
 PN WO9854364-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 29-MAY-1998; 98WO-US010965.  
 XX  
 PR 30-MAY-1997; 97US-0048170P.  
 PR 03-JUN-1997; 97US-0048381P.  
 XX  
 XX (LXRB-) LXR BIOTECHNOLOGY INC.  
 PA  
 PI Lichtenstein AV, Melkonyan HS, Umansky SR;  
 XX  
 DR WPI; 1999-070223/06.  
 XX  
 XX Analysis of DNA present in urine that has crossed the kidney barrier -  
 PT useful in the determination of foetal sex, and in the diagnosis of

PT inherited disease, cancer and pathogenic infections.  
XX  
PS Claim 44; Page 34; 72pp; English.  
CC A method has been developed for the analysis of a fragment of foetal DNA  
CC that has crossed the placental and kidney barriers. The method comprises  
CC assaying for presence of foetal DNA in a urine sample from a pregnant  
CC subject. Also described are: (i) detecting any target nucleic acid  
CC sequences in a urine sample; (2) diagnosis for male foetal DNA in  
CC maternal urine; and (3) general method for detecting Y chromosome-  
CC specific nucleic acids using the primers given in AAX00055 to AAX00058.  
CC The methods are used: (i) to determine the sex of a foetus (by detecting  
CC Y-specific fragments); (ii) for diagnosing or monitoring diseases,  
CC particularly cancer and infections, also pre-natal diagnosis of inherited  
CC diseases and predisposition to disease; or (iii) to establish paternity.  
CC Analysis of urinary DNA is non-invasive and provides early indication of  
CC foetal sex or disease  
SQ  
Sequence 23 BP; 2 A; 9 C; 2 G; 10 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5692 CCACGTTTGCCTTCCTTC 5714  
DB 1 CCATTCTTGCATTCGCTTC 23  
RESULT 2870  
AAA33267  
ID AAA33267 standard; DNA; 23 BP.  
XX  
AC AAA33267;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:956.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorocholate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiaesthetic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PE 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 385; 1343pp; English.  
CC  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiaesthetic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ON reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33892) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5699 TTGCTTCTTCTTCTTCTCTC 5721  
DB 1 TTTTCTTCTTCTTCTCTCTC 23  
RESULT 2871  
AAA64522/C  
ID AAA64522 standard; DNA; 23 BP.  
XX  
AC AAA64522;  
XX  
DT 02-JAN-2001 (first entry)  
XX  
DE PCR primer IncuBR used to amplify exon 1 of human FEZ1 gene.  
XX  
KW Human; FEZ1 gene; tumour suppressor gene; 8p22; cancer; tumour growth;  
KW tumour proliferation; tubulin; microtubule; protein Bp1.gamma;  
KW tubulin polymerisation disorder; mitosis initiation; cell proliferation;  
KW cell growth; cell shape; cell rigidity; cell motility; DNA replication;  
KW tumorigenesis; tumour survival; metastasis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO2000050565-A2.  
XX  
PD 31-AUG-2000.  
XX  
PE 25-FEB-2000; 2000WO-US004950.  
XX  
PR 25-FEB-1999; 99US-0121537P.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Croce CM, Ishii H;  
XX  
DR WPI; 2000-558396/51.  
XX  
PT New polynucleotide homologous with a portion of one strand of the human  
PT FEZ1 gene, useful for alleviating abnormal cell proliferation such as  
PT cancer.  
XX  
PS Example 1; Page 45; 255pp; English.  
XX

PCR primers AAA64521-22 were used to amplify a fragment of the human FEZ1 gene. FEZ1 is a tumour suppressor gene, located at chromosome location 8p22. Decreased or no expression of FEZ1 is detected in a variety of cancer cells. Expression of FEZ1 inhibits tumor growth and proliferation. FEZ1 also interacts with tubulin, with microtubules, and with protein ERF-gamma. Post-translational phosphorylation and dephosphorylation modulates the effect of the FEZ1 protein. Inhibitors of FEZ1 gene expression are useful for inducing cells to proliferate. Compounds which modulate FEZ1 association with tubulin are useful for alleviating tubulin hyper- or hypo- polymerisation disorders, such as those associated with aberrant initiation of mitosis, modulation of the initiation and rate of cell proliferation and cell growth, modulation of cell shape, cell rigidity, cell motility, rate and stage of cellular DNA replication, intracellular distribution of organelles, metastatic potential of cell and cellular transformation from a non-cancerous to cancerous phenotype. Compounds which modulate FEZ1 binding and phosphorylation are also useful for alleviating a disorder, such as tumorigenesis, tumour survival, growth and metastasis

XX  
SQ Sequence 23 BP; 4 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 199 GCACGGCTATATGGATGGAAC 221  
DB 23 GCACGGCTATATGGATGGAAC 1

RESULT 2872  
AAZ50566/C  
ID AAZ50566 standard; DNA; 23 BP.  
XX  
AC AAZ50566;  
XX  
DT 20-JUN-2000 (first entry)  
XX  
DE PCR primer-2 to amplify human GPR12 DNA.  
XX  
KM G protein-coupled orphan receptor; GPCR; agonist; G protein;  
KM GPCR fusion protein; inverse agonist; drug; treatment; PCR primer; GPR12;  
KM G protein-coupled receptor; human; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC200006597-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 30-JUL-1999; 99WO-US017425.  
XX  
PR 31-JUL-1998; 98US-0094879P.  
PR 30-OCT-1998; 98US-0106300P.  
PR 04-DEC-1998; 98US-0110906P.  
PR 26-FEB-1999; 99US-0121851P.  
XX  
PA (AREN-) ARENA PHARM INC.  
XX  
PI Behan DP, Chalmers DT, Liaw C, Lan I, Lowitz K, Chen R;  
XX  
DR WPI; 2000-195260/17.  
XX  
PT Identification of a compound useful as a therapeutic agent, comprises  
PT identifying a compound against constitutively activated G protein-coupled  
PT orphan receptors.  
XX  
PS Example 7; Page 34; 123pp; English.  
XX  
CC The patent discloses a method of identifying agonists and inverse or  
CC partial agonists to the endogenous, constitutively activated G protein-  
CC coupled orphan receptors (GPCRs), by contacting them with a GPCR fusion  
CC protein comprising a GPCR and a G protein. Determining expression of

CC GPCRs in tissue samples can be used to identify related diseases. Inverse  
CC agonists to these receptors can be used as drugs for treating GPCR-  
CC related diseases. The present sequence is a PCR primer used to amplify a  
CC 220 bp fragment of human GPR12 (G protein-coupled receptor) DNA, to  
CC examine tissue samples for expression of these receptors

XX  
SQ Sequence 23 BP; 6 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1669 CAACCTGTTCCTGCATATATGC 1691  
DB 23 CAACCTGTTCCTGCATATATGC 1

RESULT 2873  
AAA03669  
ID AAA03669 standard; DNA; 23 BP.  
XX  
AC AAA03669;  
XX  
DT 19-MAY-2000 (first entry)  
XX  
DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:953.  
XX  
KM Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;  
KM adenosine A2a receptor; adenosine A2b receptor; adenosine A3 receptor;  
KM phosphodiesterase; cardiopulmonary failure; renal failure; ischaemia;  
KM endocytosis release; ARDS; acute respiratory distress syndrome;  
KM cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;  
KM supraventricular tachycardia; allergic rhinitis; acute inflammation;  
KM chronic obstructive pulmonary disease; ss.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WC9963938-A2.  
XX  
PD 16-DEC-1999.  
XX  
PF 08-JUN-1999; 99WO-US012775.  
XX  
PR 08-JUN-1998; 98US-0088501P.  
PR 09-JUN-1998; 98US-00093972.  
PR 09-JUN-1998; 98US-0088657P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Hill JL;  
XX  
DR WPI; 2000-116433/10.  
XX  
PT Novel composition for treating or preventing e.g. cardiopulmonary and  
PT renal injury.  
XX  
PS Claim 17; Page 38; 252pp; English.  
XX  
CC The present invention describes a pharmaceutical composition, comprising  
CC at least one agent (I) that prevents, alleviates and/or inhibits  
CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.  
CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide  
CC (Ib), containing less than 15% adenosine (A), that is antisense to target  
CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3'  
CC ends or segments between coding and non-coding sequences), or to all  
CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and  
CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at  
CC least no agonist activity at this receptor). (I) may be a mixture of (Ia  
CC and (Ib), and optionally also contains one or more surfactants. The  
CC compositions are used to prevent, alleviate and/or treat adenosine  
CC receptor-mediated cardiac, lung and/or renal damage or failure  
CC (particularly where associated with ischaemia, toxin release and/or

CC administration of drugs or imaging agents, e.g. adenosine for treating  
CC supraventricular tachycardia); (adult) respiratory distress syndrome  
CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive  
CC pulmonary disease; cardiopulmonary hypoxia associated with administration  
CC of stress-test agents, particularly where such conditions are associated  
CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to  
CC AAA03715 represent specifically claimed phosphorothioate antisense  
CC oligonucleotides for use in the composition of the present invention.  
CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other  
CC phosphorothioate oligonucleotides used in the exemplification of the  
CC present invention  
CC  
CC  
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 5699 TTGGCTTCCTTTCCCTCTCTC 5721  
Db 1 TTTTCCTTCCTTGTCTCTCTTC 23  
RESULT 2874  
AAFI9389  
ID AAFI9389 standard; DNA; 23 BP.  
AC AAFI9389;  
XX  
XX  
DT 14-MAR-2001 (first entry)  
XX  
XX Human adenosine A1 receptor polynucleotide fragment #956.  
DB  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antispasmodic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200062736-A2.  
PN  
XX 26-OCT-2000.  
PD  
XX 24-MAR-2000; 2000WO-US008020.  
PF  
XX 06-APR-1999; 99US-0127958P.  
PR  
XX (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
XX MYCE JW;  
PI  
XX WPI; 2000-679539/66.  
DR  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.  
XX  
XX Claim 14; Page 120; 1592pp; English.  
PS  
XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antispasmodic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAFI8434 to AAFI21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention  
CC  
CC  
SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;  
Query Match 0.2%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 5699 TTGGCTTCCTTTCCCTCTCTC 5721  
Db 1 TTTTCCTTCCTTGTCTCTCTTC 23  
RESULT 2875  
AAA39003/C  
ID AAA39003 standard; DNA; 23 BP.  
XX  
XX AAA39003;  
AC  
XX 30-AUG-2000 (first entry)  
DT  
XX  
XX Human orphan receptor GPR12 RT-PCR primer #2.  
DB  
XX Identification; modulator; cell surface membrane receptor; treatment;  
KW orphan receptor; antihypertoid; antidiabetic; neuroleptic; antidepressant;  
KW cytostatic; G protein-coupled receptor agonist; reverse transcriptase;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200021987-A2.  
FN  
XX 20-APR-2000.  
PD  
XX 12-OCT-1999; 99WO-US023935.  
PF  
XX 13-OCT-1998; 98US-00170496.  
PR  
XX (AREN-) ARENA PHARM INC.  
PA  
XX Behan DP, Chalmers DT;  
PI  
XX WPI; 2000-317935/27.  
DR  
XX  
XX Identifying compounds with inverse agonist activity to orphan receptors  
PT useful for treating e.g. Graves' disease, and schizophrenia, involves  
PT contacting candidate compounds with constitutively activated receptors.  
PS Example 4; Page 73; 110pp; English.  
XX  
XX The present invention describes a method for directly identifying a



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XX XX WO200181378-A2.
XX XX 01-NOV-2001.
XX XX 27-APR-2001; 2001WO-US013680.
XX XX 27-APR-2000; 2000US-0199947P.
XX XX 27-APR-2000; 2000US-0199960P.
XX XX 14-AUG-2000; 2000US-0275226P.
XX XX 18-DEC-2000; 2000US-0256399P.
XX XX 18-DEC-2000; 2000US-0256524P.
XX XX 22-DEC-2000; 2000US-0258159P.
XX XX 28-DEC-2000; 2000US-0258511P.
XX XX 28-DEC-2000; 2000US-0258828P.
XX XX 04-JAN-2001; 2001US-0259659P.
XX XX 13-MAR-2001; 2001US-00275226.
XX XX (CURA-) CURAGEN CORP.
XX XX Padigaru M, Mishra V, Spytek KA, Grosse WM, Szekeres ES;
XX XX Alsbrook JP, Burgess CE, Casman SJ, Lepley DM, Gangolli EA;
XX XX Macdougall JR, Smithson G;
XX XX WPI; 2001-611739/70.
XX XX
XX XX G-Protein coupled receptor polypeptides and NAs useful for
XX XX preventing, diagnosing and treating cardiomyopathy, atherosclerosis,
XX XX cancers and diabetes.
XX XX
XX XX Example 1G; Page 198; 242pp; English.
XX XX
XX XX The present DNA sequence is a probe which is used for determining the
XX XX expression analysis of human G-protein coupled receptor-12 (GPCR-12)
XX XX cDNA. GPCR protein and DNA may be used in the prevention, diagnosis and
XX XX treatment of diseases associated with inappropriate GPCR expression,
XX XX obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain,
XX XX atherosclerosis, neurodegenerative disorders (Alzheimer's disease,
XX XX Parkinson's disease, Huntington's disease); bulimia, immune disorder,
XX XX haematopoietic disorders, disorders related to cell signal processing and
XX XX metabolic pathway modulation, retinal disorder (photoreception),
XX XX bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm
XX XX adenocarcinoma); angina pectoris, hypotension, hypertension, asthma,
XX XX Crohn's disease, multiple sclerosis, ulcers, neurological disorders
XX XX (dementia, mental retardation, schizophrenia, anxiety); acute heart
XX XX failure, osteoporosis, myocardial infarction and urinary retention
XX XX
XX XX Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX XX
XX XX Query Match 0.2%; Score 15; DB 1; Length 23;
XX XX Best Local Similarity 100.0%; Pred. No. 2.2e+03;
XX XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
OY 267 GCAGGTGTCAGGC 281
DB 17 GCAGGTGTCAGGC 3
XX XX
XX XX RESULT 2878
XX XX AAH40410/C
XX XX ID AAH40410 standard; DNA; 23 BP.
XX XX
XX XX AAH40410;
XX XX
XX XX 14-AUG-2001 (first entry)
XX XX
XX XX SNP specific lower PCR primer SEQ ID 3206.
XX XX
XX XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX XX SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX XX Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX XX poly cystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

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XX XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX XX Homo sapiens.
XX XX WO200129262-A2.
XX XX 26-APR-2001.
XX XX
XX XX 13-OCT-2000; 2000WO-US028436.
XX XX 15-OCT-1999; 99US-0160096P.
XX XX (ORCH-) ORCHID BIOSCIENCES INC.
XX XX Picoult-Newburg L, Pohl M;
XX XX WPI; 2001-290930/30.
XX XX
XX XX New genotyping oligonucleotide, useful for detecting the presence,
XX XX absence or identity of single polynucleotide polymorphism in a nucleic
XX XX acid sample.
XX XX
XX XX Claim 1; Page 66; 83pp; English.
XX XX
XX XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX XX primer extension (SNPs) primers, and the sequences of regions flanking
XX XX sites of single nucleotide polymorphisms SNPs. The present invention
XX XX includes kits for determining the presence or absence of a SNP, using the
XX XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX XX SNP flanking sequence, the SNP primer is used as a genotyping primer.
XX XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX XX performing a single-nucleotide primer extension reaction. The
XX XX oligonucleotides are useful for determining the presence, absence or
XX XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX XX assess by association analysis the genotype of an individual or group of
XX XX individuals, having a pathological phenotypic trait suspected of being
XX XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX XX agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
XX XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX XX traits also include symptoms of or susceptibility to multifactorial
XX XX disease of which a component is or may be genetic such as autoimmune
XX XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX XX microorganism. The method is also useful in forensic investigations and
XX XX paternity analysis. The present sequence represents a PCR primer specific
XX XX for a human SNP containing DNA sequence
XX XX
XX XX Sequence 23 BP; 15 A; 4 C; 4 G; 0 T; 0 U; 0 Other;
XX XX
XX XX Query Match 0.2%; Score 15; DB 1; Length 23;
XX XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;
XX XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX XX
OY 3926 GGCCTTTTCTCTCCTTGATGCT 3948
DB 23 GGCCTTTTCTCTTGTGCTGT 1
XX XX
XX XX RESULT 2879
XX XX AAF32064/C
XX XX ID AAF32064 standard; DNA; 23 BP.
XX XX
XX XX AAF32064;
XX XX
XX XX 10-APR-2001 (first entry)
XX XX
XX XX eIF-5A PCR primer #5.
XX XX
XX XX eIF-5A; eukaryotic initiation factor 5A; senescence inhibition;
XX XX PCR primer; ss.
XX XX
XX XX Unidentified.

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XX XX MO200102592-A2.
XX PN
XX PD 11-JAN-2001.
XX PF 06-JUL-2000; 2000MO-US018364.
XX PR 06-JUL-1999; 99US-00348675.
XX PR 19-JUN-2000; 2000US-00597771.
XX PA (SENE-) SENESCO INC.
XX PI Thompson JE, Wang T, Lu DL;
XX DR WPI; 2001-061978/07.
XX PT Tomato, Arabidopsis and carnation cDNA clones encoding senescence-induced
XX PT deoxyhypusine synthase and eIF-5a, useful for inhibiting senescence in a
XX PT plant when introduced in reverse orientation into the genome of the
XX PT plant.
XX PS Claim 21; Page 51; 135pp; English.
XX CC The present sequence is a PCR primer used to isolate the coding sequences
XX CC for Arabidopsis, carnation and tomato eukaryotic initiation factor 5A
XX CC (eIF-5A; see AAF32055, AAF32056 and AAF32057). The eIF-5A coding
XX CC sequence, when introduced into a plant cell in reverse orientation,
XX CC inhibits expression of the endogenous eIF-5A gene. The eIF-5A coding
XX CC sequences are useful for altering age-related senescence and/or
XX CC environmental stress-related senescence, for inhibiting seed aging and
XX CC for increasing seed yield in a plant. In addition, the inhibition of
XX CC senescence in a plant results in increased resistance of the plant to
XX CC environmental stress-induced and/or pathogen-induced senescence,
XX CC increased plant biomass, delayed fruit softening and spoilage
XX CC
XX SQ Sequence 23 BP; 12 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3912 CATTTCACCTCTGGCTCTTT 3934
Db |||||
23 CCTTCTCTCTGATGATCTTT 1
RESULT 2880
AAF27080
ID AAF27080 standard; DNA; 23 BP.
XX
AC AAF27080;
XX
DT 06-APR-2001 (first entry)
XX
DE Human MEK1 real-time quantitative PCR primer, SEQ ID NO:2.
XX
XX Human MEK1; mitogen-activated protein kinase kinase kinase 1;
XX MEK kinase 1; MAP/ERK kinase 1; pro-apoptotic;
XX apoptosis signal regulation; programmed cell death;
XX serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
XX Jun N-terminal kinase/stress-activated protein kinase; Bcl-2 substrate;
XX NF-kappa-B-mediated transcription regulation; expression inhibition;
XX anti-sense therapy; hyperproliferative disorder; cancer; inflammation;
XX quantitative real-time PCR primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN US6168950-B1.
XX
XX PD 02-JAN-2001.
XX
XX PF 23-JUL-1999; 99US-00359756.
XX

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PR 23-JUL-1999; 99US-00359756.
XX
XX (ISIS-) ISIS PHARM INC.
XX PA
XX PI Monia BP, Cowseert LM, Gaarde W, Ward DT;
XX PR WPI; 2001-122264/13.
XX DR
XX PT New antisense compound targeting nucleic acid encoding human mitogen-
XX PT activated protein kinase kinase 1 (MEK1), useful for treating diseases
XX PT or conditions associated with MEK1 expression, or preventing
XX PT inflammation or tumor formation.
XX PS Example 14; Col 39; 35pp; English.
XX
XX CC Sequences AAF27080-AAF27081 represent human MEK1 PCR primers used in
XX CC quantitative real-time PCR with probe AAF27082 in an exemplification of
XX CC the present invention. The invention relates to antisense
XX CC oligonucleotides targeted to the human MEK1 gene, which inhibit its
XX CC expression. A series of oligonucleotides (AAF27086-AAF27125) were
XX CC designed to target different regions of the human MEK1 RNA, and were
XX CC analysed for their effect on MEK1 mRNA levels by quantitative real-time
XX CC PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as a
XX CC control. MEK1 (also known as mitogen-activated protein kinase kinase
XX CC kinase 1, MEK kinase 1 and MAP/ERK kinase 1) is a dual-specific
XX CC serine/threonine kinase which mediates cellular responses to mitogenic
XX CC stimuli, being involved in JNK/SAPK (Jun N-terminal kinase/stress-
XX CC activated protein kinase) MAP kinase cascades. MEK1 regulates signalling
XX CC events associated with apoptosis (programmed cell death) and NF-kappa-B,
XX CC both of which have been associated with the development of
XX CC hyperproliferative disorders such as cancer. Specifically, MEK1 lies
XX CC directly downstream of Bcl-2 in an apoptotic signalling cascade, and
XX CC plays a critical role in the control of NF-kappa-B-mediated transcription
XX CC at multiple points in the apoptotic cascade. The oligonucleotides of the
XX CC invention are useful for diagnosis, prevention and treatment of
XX CC conditions associated with MEK1 expression, such as inflammation, and
XX CC cancer and other hyperproliferative disorders
XX
XX SQ Sequence 23 BP; 9 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4878 GCAACTCACAAGGTTGCA 4900
Db |||||
1 GAAACTCTCAAGGTTGCA 23
RESULT 2881
ABK52683
ID ABK52683 standard; DNA; 23 BP.
XX
AC ABK52683;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human GPCR promoting insulin secretion, 5' RACE primer #1.
XX
XX Human GPCR; G protein coupled receptor; GPCR; insulin secretion; primer;
XX diabetes; antidiabetic; pancreatic beta cell; PCR;
XX intracellular cAMP concentration.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200244362-A1.
XX
XX PD 06-JUN-2002.
XX
XX PF 30-NOV-2001; 2001WO-JP010472.
XX
XX PR 01-DEC-2000; 2000JP-00367349.
XX PR 10-AUG-2001; 2001JP-00243841.
XX

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XX (YAMA) YAMANOUCHI PHARM CO LTD.  
 XX PA  
 XX P1 Ohishi T, Takasaki J, Matsumoto M, Saito T, Kamohara M, Soga T,  
 XX P1 Yoshida S, Ueda Y;  
 XX WP1; 2002-463740/49.  
 XX DR  
 XX PT Drug screening using a polypeptide which promotes pancreatic beta cell  
 XX PT insulin secretion and intracellular cyclic adenosine monophosphate  
 XX PT concentration for identification of antidiabetic agents.  
 XX PS Claim 1; Page 62; 73pp; Japanese.  
 XX CC The invention relates to screening for potential diabetes treatment  
 XX CC agents using G-protein coupled receptor (GPCR) polypeptide which promotes  
 XX CC insulin secretion by pancreas beta-cells under high glucose levels, and  
 XX CC increases intracellular cyclic adenosine monophosphate (cAMP  
 XX CC concentration. Also included are (1) screening method of cells  
 XX CC transformed by a vector containing a gene encoding the GPCR polypeptide;  
 XX CC (2) antidiabetic agents identified by the screening method; (3) drug  
 XX CC compositions containing these compounds; and (4) treatment of diabetes  
 XX CC using these drug compositions. The present sequence is a 5' RACE (rapid  
 XX CC amplification of cDNA ends) PCR primer used to isolate the human cDNA  
 XX CC encoding the GPCR  
 XX SQ Sequence 23 BP; 4 A; 5 C; 9 G; 5 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.2%; Score 15; DB 1; Length 23;  
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 OY 2215 GGGGTGCTGAAGCCAGCTACC 2237  
 Db 1 GGGCTGCTTGATGCAAGTACC 23  
 RESULT 2882  
 ABK8382/c  
 ID ABK8382 standard; DNA; 23 BP.  
 XX AC  
 XX ABK8382;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Tomato senescence-induced eIF-5A cDNA PCR primer.  
 XX KW Tomato; ss; PCR; deoxyhypusine synthase; DHS; senescence; eIF-5A; primer;  
 XX KW eukaryotic initiation factor 5A; plant; cell death; disease resistance;  
 XX KW antisense; blossom end rot; environmental stress; pathogen resistance;  
 XX KW shelf-life; perishable fruit; flower; vegetable.  
 XX OS Lycopersicon sp.  
 XX PN WO200244392-A2.  
 XX PD 06-JUN-2002.  
 XX PF 29-NOV-2001; 2001WO-US044505.  
 XX PR 29-NOV-2000; 2000US-00725019.  
 XX PA (SENE-) SENESCO TECHNOLOGIES INC.  
 XX P1 Thompson JE, Wang T, Lu DL;  
 XX DR WP1; 2002-557545/59.  
 XX PT Increasing resistance to physiological disease in plant, by integrating  
 XX PT gene or its fragment encoding senescence-induced deoxyhypusine synthase  
 XX PT or eIF5A in antisense orientation into plant genome and growing the  
 XX PT plant.

PS Example 9; Page 44; 114pp; English.  
 XX CC The invention relates to increasing resistance to physiological disease  
 XX CC in a plant, involving integrating into the plant genome a vector having  
 XX CC antisense sequences complementary to corresponding portion of one strand  
 XX CC of DNA encoding endogenous senescence-induced eIF-5A (eukaryotic  
 XX CC initiation factor 5A) gene or 3' end of endogenous senescence-induced  
 XX CC deoxyhypusine synthase (DHS), a portion of RNA sequence encoded by eIF-5A  
 XX CC gene or DHS gene, and growing the plant. Also included is a plant or its  
 XX CC progeny, where the plant is derived from a cell having inhibited or  
 XX CC reduced expression of senescence-induced DHS, senescence-induced eIF-5A,  
 XX CC or both, where the cell is produced by the method of the invention. The  
 XX CC method is useful for increasing resistance to physiological disease such  
 XX CC as blossom end rot in a plant. The method results in delayed onset of  
 XX CC senescence and improved resistance to environmental stress and pathogens,  
 XX CC thus extending the plant shelf-life and/or growth period. The method  
 XX CC delays deterioration and spoilage of perishable fruits, flowers,  
 XX CC vegetables, and plants, increases the shelf-life of perishable fruits,  
 XX CC flowers, vegetables, and plants, and renders their tissues more stress-  
 XX CC tolerant and pathogen resistant. The present sequence is a PCR primer  
 XX CC used to isolate their full length the tomato senescence-induced eIF-5A  
 XX CC cDNA  
 XX SQ Sequence 23 BP; 12 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.2%; Score 15; DB 1; Length 23;  
 XX Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 OY 3912 CATTTTCACGCTTGCTCTT 3934  
 Db 23 CTTTCTCTCTAGGATCTTT 1  
 RESULT 2883  
 ABK95525/c  
 ID ABK95525 standard; DNA; 23 BP.  
 XX AC  
 XX ABK95525;  
 XX DT 24-SEP-2002 (first entry)  
 XX DE Novel G-protein coupled receptor probe #14.  
 XX KW G protein coupled receptor; GPCR; olfactory receptor;  
 XX KW cell signal processing disorder; metabolic pathway modulation;  
 XX KW cardiomyopathy; atherosclerosis; diabetes; developmental disease;  
 XX KW immune disease; taste disorder; scent detectability disorder; obesity;  
 XX KW Burkitt's lymphoma; corticosteroid-induced disease; infectious disease; pain;  
 XX KW signal transduction pathway disorder; metabolic pathway disorder;  
 XX KW renal disease; metabolic disorder; cancer; Parkinson's disease;  
 XX KW acute heart failure; urinary retention; osteoporosis; Crohn's disease;  
 XX KW ulcer; allergy; neurological disorder; genetic disorder; transplantation;  
 XX KW fertility; pancreatitis; Hyperthyroidism; Endometriosis;  
 XX KW forensic biology; transgenic animal; probe; ss.  
 XX OS Synthetic.  
 XX PN WO200240539-A2.  
 XX PD 23-MAY-2002.  
 XX PF 16-OCT-2001; 2001WO-US032256.  
 XX PR 16-OCT-2000; 2000US-0240704P.  
 XX PR 26-OCT-2000; 2000US-0243497P.  
 XX PR 31-OCT-2000; 2000US-0244542P.  
 XX PR 03-NOV-2000; 2000US-0245464P.  
 XX PR 12-DEC-2000; 2000US-0255017P.  
 XX PR 17-JAN-2001; 2001US-0262159P.  
 XX PR 22-JAN-2001; 2001US-0263216P.  
 XX PR 22-JAN-2001; 2001US-0263340P.  
 XX PR 25-JAN-2001; 2001US-0264118P.

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PR 12-FEB-2001; 2001US-0268225P.
PR 15-FEB-2001; 2001US-0269031P.
PR 27-JUL-2001; 2001US-0308203P.
XX
XX
XX (CURA-) CURAGEN CORP.
PI Kikuda R, Spytek KA, Casman SJ, Zernusen BD, Li L, Tchernev VT;
PI Colman SD, Ballinger RA, Padigaru M, Wolenc AR, Shenoy SG;
PI Edinger SR, Gerlach V, Gangoll EA, Macdonall JR, Smithson G;
PI Peyman JA, Stone DJ, Gunther E, Ellerman K, Grose WM, Alsobrook JP;
PI Lepley DM, Burgess CE;
XX
XX WPI; 2002-500205/53.
XX
XX
XX Novel G protein coupled receptor especially olfactory receptor
PT polypeptides and nucleic acids for diagnosing and treating
PT atherosclerosis, cardiomyopathy and diabetes.
XX
XX
XX Example 2; Page 223; 309pp; English.
XX
XX The invention describes an isolated G protein coupled receptor X (GPCR1-
CC 12) polypeptide, especially an olfactory receptor. GPCR polypeptides are
CC useful for identifying an agent that binds to the polypeptide and for
CC identifying a candidate substance or ligand molecules interacting with an
CC olfactory receptor polypeptide. The polypeptide, (I) and (II) are also
CC useful for treating diseases and disorders related to cell signal
CC processing and metabolic pathway modulation e.g. cardiomyopathy,
CC atherosclerosis and diabetes, and developmental diseases, immune
CC diseases, taste and scent detectability disorders, Burkitt's lymphoma,
CC corticosteroid disease, signal transduction pathway disorders,
CC metabolic pathway disorders, retinal diseases, metabolic disorders,
CC obesity, infectious disease, pain, cancer, Parkinson's disease, acute
CC heart failure, urinary retention, osteoporosis, Crohn's disease, ulcers,
CC allergies, neurological disorders, genetic disorders, transplantation,
CC fertility, Pancreatitis, Hyperthyroidism and Endometriosis. GPCR
CC sequences are also useful for identifying a cell or tissue type in a
CC biological sample, to amplify DNA sequences from very small biological
CC samples such as tissues e.g. hair or skin or body fluids in forensic
CC biology. Cells comprising (I) are useful for producing non-human
CC transgenic animals for studying the function and/or activity of GPCR
CC protein and for identifying and/or evaluating modulators of GPCR protein
CC activity. This sequence represents a probe used to detect DNA encoding a
CC novel G-protein coupled receptor produced from real time quantitative (RTQ)
CC -PCR
XX
XX Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 267 GCAGGTGTTCCAGGC 281
DB 17 GCAGGTGTTCCAGGC 3

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PN WO200218649-A1.
XX
XX 07-MAR-2002.
XX
XX 24-AUG-2001; 2001WO-US026452.
XX
XX 25-AUG-2000; 2000US-0228057P.
XX
XX (LOVE-) LOVEFACE RESPIRATORY RES INST.
XX
XX Belinsky SA, Palmsano WA;
XX
XX WPI; 2002-269531/31.
XX
XX
XX Nested, two-stage polymerase chain reaction for amplifying gene in cancer
PT e.g. of lung, comprises expanding copies of gene by amplification method
PT and using the product in a second amplification to detect gene
PT inactivation.
XX
XX
XX Example 2; Page 21; 55pp; English.
XX
XX The invention relates to a nested, two-stage polymerase chain reaction
CC (PCR) for amplifying a gene that is altered in a particular cancer. The
CC method comprises expanding copies of a gene by amplification method and
CC using the product in a second methylation-specific amplification to
CC detect gene inactivation. The method is useful for amplifying the gene
CC that may be altered in a particular cancer (preferably lung cancer, other
CC cancers which include head and neck, leukemia, colorectal, prostate and
CC bladder) thereby permitting cancer detection and monitoring by detecting
CC gene inactivation in biological fluid such as sputum and blood. The
CC method finds application in the area of chemoprevention, where markers
CC are needed to identify high-risk subjects and to evaluate efficacy of
CC preventive agents. The method is further useful for identifying
CC individuals who subsequently could be enrolled in prevention intervention
CC studies using dietary supplements that are designed to impede or reverse
CC this premalignant state, and for monitoring the efficacy of the
CC interventions, by determining whether the previously detected methylation
CC biomarker persists or disappears during the course of the interventions,
CC which include immunological modulation, antisense treatment, gene therapy
CC and alkylating treatments. The method is useful for detecting the
CC aberrant methylation of the p16 gene, death-associated protein kinase
CC gene, O-6-methylguanine DNA methyltransferase gene (MGMT), RAS-associated
CC family 1 (RASAP1) gene or other gene promoters. The present sequence is
CC a PCR primer used for amplifying RASAP1 gene
XX
XX Sequence 23 BP; 14 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3167 GTTAGCTTGGCTTGATGACTTT 3189
DB 23 GTTAGCTTGGCTTGATGACTT 1

```

```

XX 23-JUL-2001; 2001WO-US023311.
PF
XX
XX 21-JUL-2000; 2000US-0220057P.
PR
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY.
PA
XX Farr SB, Pickett GG, Neft RE, Dunn RT,
PI WPI; 2002-217063/27.
XX
XX Identifying toxicologically relevant canine gene to determine
PT toxicological responses of agents, by obtaining and comparing gene
PT expression profiles of untreated canine cells and canine cells treated
PT with an agent.
XX
XX Example 5; Page 53; 140pp; English.
PS
XX This invention relates to identifying a toxicologically relevant canine
CC gene and the generation of an array of toxicologically relevant canine
CC genes. The gene array is useful for obtaining a gene expression profile,
CC by exposing a population of cells to an agent, obtaining cDNA from the
CC population of cells, labeling the cDNA, and contacting the cDNA with the
CC gene array. The relevant gene is useful for making and using arrays to
CC determine toxicological responses to various agents, and also useful for
CC identifying novel gene sequences and novel canine genes. The method for
CC analyzing toxicological responses using the canine gene array is rapid
CC and efficient. The present sequence is related to the canine gene array
CC
SQ Sequence 23 BP; 2 A; 11 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4735 GGGCAGCTGAGAGAGAGGTC 4757
DB 23 GGGCAGCTGAGAGAGAGGTC 1

RESULT 2886
ABK67730
ID ABK67730 standard; DNA; 23 BP.
XX
XX ABK67730;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Novel transglutaminase TGz associated PCR primer #17.
DE
XX Transglutaminase; TGM; transamidation; autoimmune diseases;
KM Addison's disease; AI haemolytic anaemia; AI thrombocytopenic purpura;
KM AI thyroid disease; atrophic gastritis; pernicious anaemia;
KM Chron's disease; colitis ulcerosa; Goodpasture syndrome; Iga nephropathy;
KM IgG glomerulonephritis; myasthenia gravis; partial lipodystrophy;
KM polymyositis; primary biliary cirrhosis; recurrent pericarditis;
KM progressive systemic sclerosis; recurrent pericarditis;
KM Sjogren's syndrome; relapsing polychondritis; arthritis; rheumatism;
KM sarcoidosis; SLE; splenic atrophy; diabetes; Wegener granulomatosis;
KM ulcerative colitis; vasculitis; vitiligo; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200222830-A2.
FN
XX
XX 21-MAR-2002.
PD
XX
XX 14-SEP-2001; 2001WO-GB004120.
PF
XX 15-SEP-2000; 2000GB-00022768.
PR
XX 16-MAY-2001; 2001GB-00011995.
XX
XX (UYCA-) UNIV COLLEGE CARDIFF.
PA

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XX Aeschlimann DP, Grenard PM;
PI
XX
XX WPI; 2002-329954/36.
DR
XX
XX Nucleic acids which encode novel transglutaminase enzymes TG-Z and TG-Y
PT which can be used in diagnostic methods of autoimmune diseases.
PT
XX
XX Disclosure; Page 26; 67pp; English.
PS
XX
XX The invention relates to nucleic acids which encode novel polypeptides
CC having transglutaminase activity. The compositions of polypeptides are
CC useful for transamidation reactions on peptides and polypeptides.
CC Detection of the polypeptides with transglutaminase activity are useful
CC in a diagnostic method in a subject or in cells derived from a subject
CC having an autoimmune disease. The method for detecting transglutaminase
CC proteins may be used to diagnose autoimmune diseases which include
CC Addison's disease, AI haemolytic anaemia, AI thrombocytopenic purpura, AI
CC thyroid diseases, atrophic gastritis, pernicious anaemia, Chron's
CC disease, colitis ulcerosa, Goodpasture syndrome, Iga nephropathy or IgG
CC glomerulonephritis, myasthenia gravis, partial lipodystrophy,
CC polymyositis, primary biliary cirrhosis, primary sclerosing cholangitis,
CC progressive systemic sclerosis, recurrent pericarditis, relapsing
CC polychondritis, rheumatoid arthritis, rheumatism, sarcoidosis, Sjogren's
CC syndrome, SLE, splenic atrophy, type I (insulin-dependent) diabetes
CC mellitus, Wegener granulomatosis, ulcerative colitis, vasculitis (both
CC systemic and cutaneous) and vitiligo. This sequence represents a primer
CC used in the study of transglutaminase genes in which DNA, amino acid
CC sequences and chromosomal locations of novel transglutaminases are
CC determined
CC
SQ Sequence 23 BP; 7 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4731 TGGAGCCAGCTGAGAGAGAG 4753
DB 1 TGAAGCTCAGCCGAGGTAGAG 23

RESULT 2887
ABZ95083
ID ABZ95083 standard; DNA; 23 BP.
XX
XX ABZ95083;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human adenosine A1 receptor antisense fragment no.946.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
FN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Tang L, Shahabuddin S;

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XX WPI; 2003-229219/22.  
 DR 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ublquinone.  
 XX  
 PS Disclosure; SEQ ID NO 10325; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ublquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cyostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ublquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 23 BP; 0 A; 8 C; 1 G; 14 T; 0 U; 0 Other;  
 Query Match 0.24; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5699 TTTGCTTCTTCTTCTTCTTCTC 5721  
 DB 1 TTTCTCTTCTTCTTCTTCTTCTC 23  
 RESULT 2888  
 ABX93429  
 ID ABX93429 standard; DNA; 23 BP.  
 XX  
 AC ABX93429;  
 XX  
 DT 27-MAY-2003 (first entry)  
 XX  
 DE Y chromosome specific sequence DY21, PCR primer Y21.  
 XX  
 KW Transplanted material monitoring; urine sample analysis; kidney barrier;  
 KW nucleic acid detection; nucleic acid modification detection;  
 KW specific foetal nucleic acid; cancer; diabetes; arteriosclerosis;  
 KW obesity; autoimmune disease; chromosomal abnormality; genetic disease;  
 KW haemophilia; Alzheimer's disease; Huntington's disease; cystic fibrosis;  
 KW pathogen infection; genetic predisposition; cancer treatment monitoring;  
 KW foetus sex determination; foetal genetic disease; paternity;  
 KW amniocentesis; Y chromosome specific sequence; DY21; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6492144-B1.  
 XX  
 PD 10-DEC-2002.  
 XX  
 PF 03-AUG-2000; 2000US-00634732.  
 XX  
 PR 30-MAY-1997; 97US-0058170P.  
 PR 03-JUN-1997; 97US-0048381P.  
 PR 29-MAY-1998; 98WO-US010965.  
 PR 04-FEB-2000; 2000US-00230704.

PR 03-JUL-2000; 2000US-00609162.  
 XX  
 XX (DIAG-) DIAGEN CORP.  
 XX  
 PT Unanaky SR, Lichtenbein AV, Melkonyan HS;  
 XX  
 DR WPI; 2003-340405/32.  
 XX  
 PT Monitoring transplanted material in a patient, by analyzing urine samples  
 PT for nucleic acids from cell genomes of the transplanted material that are  
 PT different from nucleic acids of recipient and have crossed the kidney  
 PT barrier.  
 XX  
 PS Example 3; Col 29; 32pp; English.  
 XX  
 CC The invention describes a method of monitoring (M) transplanted material  
 CC in a patient, involving providing a urine sample suspected of containing  
 CC nucleic acid of the transplanted material, where the transplanted  
 CC material is located outside the urinary tract, and analyzing the urine  
 CC sample for nucleic acids from the cell genome of the transplanted  
 CC material that are different from nucleic acids of the recipient and have  
 CC crossed the kidney barrier. (M) is useful for detecting the presence of  
 CC specific nucleic acids as well as nucleic acid modifications and  
 CC alterations, for detecting specific foetal nucleic acids that contain  
 CC modified nucleotides, for diagnosis of diseases such as cancer, diabetes,  
 CC arteriosclerosis, obesity and various autoimmune diseases or chromosomal  
 CC abnormality, genetic diseases (such as haemophilia, Alzheimer's disease,  
 CC Huntington's disease, cystic fibrosis) and pathogen infections, for  
 CC detecting genetic predisposition to various diseases, for monitoring  
 CC cancer treatment, for analysing specific nucleic acids in urine to track  
 CC the success of transplanted cells, tissue and organs, for determination  
 CC of foetus sex and the identification of foetal genetic diseases, such as  
 CC those inherited from the father for various purposes, including  
 CC determination of paternity, or for diagnosis of diseases caused by clonal  
 CC expansion of cells containing DNA modifications accompanied by death of  
 CC at least one subset of the cells bearing DNA modifications. (M) is a  
 CC safe, and simple non-invasive test, an excellent alternative to  
 CC amniocentesis, less expensive and more cost-effective. This sequence  
 CC represents a primer used to amplify fragments of the Y chromosome  
 CC specific DY21 sequence  
 XX  
 SQ Sequence 23 BP; 2 A; 9 C; 2 G; 10 T; 0 U; 0 Other;  
 Query Match 0.24; Score 15; DB 1; Length 23;  
 Best Local Similarity 78.3%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5692 CCACTGTTTGCCTTCTTCTTCC 5714  
 DB 1 CCACTCTTTCATTCGCTTCC 23  
 RESULT 2889  
 ABV74137  
 ID ABV74137 standard; DNA; 23 BP.  
 XX  
 AC ABV74137;  
 XX  
 DT 23-JAN-2003 (first entry)  
 XX  
 DE Oligonucleotide used in cDNA library array.  
 XX  
 KW G-protein coupled receptor; odourant; receptor; olfaction; array;  
 KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "5' polylinker"  
 FT misc\_feature 16..21

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FT      /*tag= b
FT      /note= "each N represents A, C, G or T"
FT      22. .23
FT      misc_feature
FT      /tag= C
FT      /note= "NN represents every possible dinucleotide
FT      combination"
XX      WO200277200-A2.
XX
XX      03-OCT-2002.
XX
XX      26-MAR-2002; 2002WO-US009559.
XX
XX      27-MAR-2001; 2001US-0279168P.
XX      31-JAN-2002; 2002US-035392P.
XX
XX      (INSC-) INSCENT INC.
XX
XX      Woods D, Dimltratos S;
XX
XX      WPI; 2003-029930/02.
XX
XX      Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX      receptors, useful for isolating odorant binding proteins or pesticide
XX      alternatives, by analyzing sequences from a male- and female-specific
XX      nucleic acid library.
XX
XX      Disclosure; Fig 5; 83pp; English.
XX
XX      The present sequence is that of an oligonucleotide used in a method
XX      designed to rapidly array and normalize a complex cDNA library obtained
XX      from a target species. Clones are arrayed into multi-well plates. Each
XX      well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
XX      capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
XX      which allows an anchored oligonucleotide in each well to selectively
XX      hybridise only to those cDNA clones with a complementary 5' end. The
XX      unique 3' key sequences are designed to give a comprehensive level of
XX      degeneracy since they are diverse and numerous enough to ensure that
XX      every possible cDNA sequence can be bound by an individual, specific
XX      oligonucleotide in a single well. The cDNA library is heated to denature
XX      the clones into single stranded DNA, and an aliquot is added to every
XX      well. The anchored oligonucleotide serves as the 3' primer in PCR, and
XX      the common 5' region present in every cDNA clone serves as the 5' priming
XX      site. Denaturing and washing leave anchored cDNA in each well. The
XX      library is now arrayed and normalised. The method was used to identify
XX      and isolate clones encoding G-protein coupled receptors, especially
XX      odorant receptors, and active effectors involved in the olfactory
XX      pathway of invertebrates and vertebrates, e.g. odorant binding proteins,
XX      or other olfactory or neuronal proteins. The identified receptors and
XX      proteins are useful for identifying compounds that reduce a target
XX      animal's sensitivity to odours, for manufacturing compounds or devices
XX      that mask odours, or trapping invertebrates with odourants.
XX      Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
XX      with desirable effects on specific species, for the development of pest
XX      monitoring systems or non-toxic, species-specific pesticide alternatives,
XX      for controlling insect feeding and breeding behaviour, detecting the
XX      presence of small air-borne molecules, etc
XX
XX      Sequence 23 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 8 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4464 TTTT TTTT TTTT TTTT 4478
DB      1 TTTT TTTT TTTT TTTT 15
RESULT 2890
AB221707
ID      AB221707 standard; DNA; 23 BP.
XX
```

```
AC      AB221707;
XX
XX      27-FEB-2003 (first entry)
XX
XX      RBM15-MKL1 fusion protein PCR primer RBM15-1118F SEQ ID NO:23.
DE
XX
XX      Human; RBM15; RNA binding motif protein 15; megakaryoblastic leukemia 1;
XX      MKL1; fusion protein; acute megakaryoblastic leukaemia; AMKL; cytostatic;
XX      t(1;22) chromosomal rearrangement; gene therapy; chromosome 22q13;
XX      chromosome 1p13; PCR primer; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      WO200288309-A2.
XX
XX      07-NOV-2002.
XX
XX      23-APR-2002; 2002WO-US012797.
XX
XX      27-APR-2001; 2001US-0286910P.
XX
XX      (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX      (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
XX      Morris SW, Ma Z, Hitzler JK;
XX
XX      WPI; 2003-103455/09.
XX
XX      New RNA-binding motif protein-15 (RBM15)-megakaryoblastic leukemia-1
XX      (MKL1), MKL1-RBM15-S and MKL1-RBM15-S+AE fusion proteins, useful for
XX      identifying agents useful for treating patients with acute
XX      megakaryoblastic leukemia.
XX
XX      Example 1; Page 108; 109pp; English.
XX
XX      The present invention describes an RNA-binding motif protein-15 (RBM15)-
XX      megakaryoblastic leukemia-1 (MKL1) fusion protein, a MKL1-RBM15-S fusion
XX      protein, and a MKL1-RBM15-S+AE fusion protein associated with acute
XX      megakaryoblastic leukaemia (AMKL). Also described: (1) an antibody that
XX      specifically binds to the RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE
XX      fusion proteins; (2) a non-human transgenic animal that has been altered
XX      to express a gene encoding a RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE
XX      fusion protein; (3) identifying an agent capable of binding to a RBM15-
XX      MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE fusion protein; (4) detecting the
XX      t(1;22) chromosomal rearrangement associated with AMKL; and (5) screening
XX      for agents capable of (selectively) inhibiting the activity of a fusion
XX      protein arising from the t(1;22) chromosomal rearrangement associated
XX      with AMKL. The fusion proteins have cyrostatic activity and can be used
XX      in gene therapy. The RBM15-MKL1, MKL1-RBM15-S, or MKL1-RBM15-S+AE fusion
XX      proteins and nucleotide molecules are useful for designing and preparing
XX      agents that specifically inhibit the expression of the RBM15-MKL1 or MKL1-
XX      RBM15 genes in cells for therapeutic and other purposes. The transgenic
XX      animals are useful for identifying and testing carcinogenic or
XX      therapeutic compositions. The methods are also useful for detecting the
XX      t(1;22) chromosomal rearrangement associated with AMKL, or for
XX      identifying agents useful for treating patients with AMKL. The antibodies
XX      can be used to selectively kill cells expressing RBM15-MKL1, MKL1-RBM15-
XX      S, or MKL1-RBM15-S+AE fusion protein. RBM15 is located to chromosome
XX      1p13, and MKL1 is located to chromosome 22q13. The present sequence
XX      represents a PCR primer which is used in the generation of a fusion
XX      protein in an example from the present invention
XX
XX      Sequence 23 BP; 8 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      5953 CAAGCTTACTAGAGAGACGA 5975
DB      1 CATGCTTACTAGAGAGACGA 23
```





```

ID  ABV77669 standard; DNA; 24 BP.
XX
AC  ABV77669;
XX
DT  03-FEB-2003 (first entry)
XX
DE  Human zinc finger protein 9.79 PCR primer #1.
XX
XX  Human; zinc finger protein 9.79; cancer; HIV infection; cytoskeletal;
XX  anti-HIV; PCR; primer; ss.
XX
OS  Homo sapiens.
XX
PN  CN1343710-A.
XX
PD  10-APR-2002.
XX
PF  19-SEP-2000; 2000CN-00125246.
XX
PR  19-SEP-2000; 2000CN-00125246.
XX
PA  (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI  Mao Y, Xie Y;
XX
DR  WPI; 2002-548879/59.
XX
PT  A novel human zinc finger protein 9.79 polypeptide, useful for treating
XX  several diseases e.g. cancer and HIV infection.
XX
PS  Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC  The present invention relates to human zinc finger protein 9.79 (see
XX  APP59011). The zinc finger protein is useful for treating several
XX  diseases e.g. cancer and HIV infection. The present sequence is a PCR
XX  primer, which was used in an example from the invention
XX
SQ  Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match      0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  4014 AATGAGAAAAAGAGAGAAAAA 4036
DB  24 AATGAGAAAAAGAGAGAAAAA 2

RESULT 2896
ABA98547/C
ID  ABA98547 standard; DNA; 24 BP.
XX
AC  ABA98547;
XX
DT  30-APR-2002 (first entry)
XX
DE  Insulin-like growth factor binding protein 16.17 PCR primer #1.
XX
XX  Insulin-like growth factor; binding protein; cytoskeletal; gene therapy;
XX  cancer; PCR primer; ss.
XX
OS  Unidentified.
XX
PN  WO200212301-A1.
XX
PD  14-FEB-2002.
XX
PF  11-JUN-2001; 2001WO-CN000947.
XX
PR  14-JUN-2000; 2000CN-00116509.
XX
PA  (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX

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PI  Mao Y, Xie Y;
XX
XX  WPI; 2002-172131/22.
XX
XX  Insulin-like growth factor binding protein 16.17 and encoding
XX  polynucleotide, used in diagnosis and treatment of cancer.
XX
PS  Example 2; Page 12; 37pp; Chinese.
XX
CC  The present invention relates to insulin-like growth factor binding
XX  protein 16.17 (see AM48365). The binding protein and its coding sequence
XX  are useful for the diagnosis and treatment of cancer. The present
XX  sequence is a PCR primer, which was used in an example from the invention
XX
SQ  Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;

Query Match      0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  4011 TAAATGAGAAAAAGAGAGAAA 4033
DB  24 TCAAAAAAGAAAAAGAGAGAAA 2

RESULT 2897
ABV75621/C
ID  ABV75621 standard; DNA; 24 BP.
XX
AC  ABV75621;
XX
DT  23-JAN-2003 (first entry)
XX
DE  Argininoacyl tRNA synthetase 12.87 PCR primer 1.
XX
XX  Argininoacyl tRNA synthetase 12.87; malignant tumour; inflammation;
XX  immunological disease; haemopathy; human immunodeficiency virus; HIV;
XX  enzyme; PCR; primer; ss.
XX
OS  Unidentified.
XX
PN  CN1347985-A.
XX
PD  08-MAY-2002.
XX
PF  11-OCT-2000; 2000CN-00125646.
XX
PR  11-OCT-2000; 2000CN-00125646.
XX
PA  (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI  Mao Y, Xie Y;
XX
DR  WPI; 2002-548992/59.
XX
XX  New polypeptide argininoacyl tRNA synthetase 12.87 and encoding
XX  polynucleotide; useful for treating malignant tumors, inflammations,
XX  immunological diseases, hemopathy and human immunodeficiency virus
XX  infection.
XX
PS  Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC  The invention relates to a novel polypeptide, argininoacyl tRNA
XX  synthetase 12.87, and the polynucleotide encoding it. The polypeptide is
XX  useful for treating various diseases, such as malignant tumours,
XX  inflammations, immunological diseases, haemopathy and human
XX  immunodeficiency virus (HIV) infection. The invention also discloses the
XX  antagonist resisting the polypeptide and its treatment effect, and
XX  application of the polynucleotide. The present sequence represents a PCR
XX  primer used to amplify the argininoacyl tRNA synthetase 12.87 gene of the
XX  invention
XX
SQ  Sequence 24 BP; 6 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

```



Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

2340 TCACACCGCGCTTCTGTGCTG 2362  
23 TCACACCTGCTCTCTCATGCTG 1

RESULT 2898  
AAZ95163  
ID AAZ95163 standard; DNA; 24 BP.  
XX  
AC AAZ95163;  
XX  
DT 05-JUN-2000 (first entry)  
XX  
DE Forward primer #9 used to sequence UGT2B7 polymorphic fragments.  
XX  
KM UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;  
KM drug interaction; detect; human; single nucleotide polymorphism; primer;  
KM ss.  
XX  
OS Synthetic.  
XX  
PM WO200006776-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 22-JUL-1999; 99WO-US016675.  
XX  
PR 28-JUL-1998; 98US-0094391P.  
XX  
PA (AXYS-) AXYS PHARM INC.  
XX  
PI Galvin M, Miller A, Penny L, Riedy M;  
XX  
DR WPI; 2000-195321/17.  
XX  
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for  
PT genotyping individuals to predict rate of metabolism of substrates and  
PT for identifying potential drug interactions.  
XX  
PS Example 2; Page 22; 72pp; English.  
XX  
CC This sequence represents a primer used to sequence polymorphic fragments  
CC of the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene. UDP-  
CC glucuronosyltransferases (UGTs) are a family of enzymes that catalyze the  
CC glucuronic acid conjugation of a wide range of endogenous and exogenous  
CC substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms  
CC in the liver. Alteration of the expression or function of UGTs may effect  
CC drug metabolism. The invention relates to non-chromosomal nucleic acid  
CC molecules, which comprise human UGT2B sequence polymorphisms (see  
CC AA95051-295110). Probes which detect the UGT2B locus polymorphisms can  
CC be used to detect altered UGT2B metabolism of a substrate in an  
CC individual. The nucleic acid molecules comprising a human UGT2B sequence  
CC polymorphism can be used in screening assays for genotyping individuals,  
CC also to predict their rate of metabolism of UGT2B substrate, potential  
CC drug-drug interactions and adverse side effects. The polymorphisms can be  
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic  
CC linkage related to phenotypic variation in activity or expression of  
CC UGT2B protein. The polymorphism containing nucleic acid molecules may  
CC also be used for generating genetically modified non-human animals and  
CC for obtaining site specific gene modification in cell lines  
XX  
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4023 AAAGAGAAAACAAATGTTAT 4045

Db 1 AAAGAGAAAACAAATGTTT 23

RESULT 2899  
AAD46030  
ID AAD46030 standard; DNA; 24 BP.  
XX  
AC AAD46030;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human UGT2B7 DNA sequencing forward primer #9.  
XX  
KM Human; UDP-glucuronosyl transferase; UGT; UGT2B7; toxicity; cancer;  
KM therapy; epirubicin; cytostatic; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PM WO200259375-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 25-JAN-2002; 2002WO-US002083.  
XX  
PR 26-JAN-2001; 2001US-0264534P.  
XX  
PA (UYCH-) UNIV CHICAGO.  
XX  
PI Ratain MJ, Innocenti F, Das S, Iyer L, Sawyer M;  
XX  
DR WPI; 2002-691534/74.  
XX  
PT Determining the dose of a UGT2B7-glucuronidated drug for treating cancer,  
PT comprises determining the level of UGT2B7 activity or expression in a  
PT patient.  
XX  
PS Disclosure; Page 53; 160pp; English.  
XX  
CC The invention relates to an UDP-glucuronosyl transferase (UGT) enzyme,  
CC UGT2B7. The invention also relates to compositions and methods for  
CC optimizing UGT2B7 substrate dosings and for predicting UGT2B7 substrate  
CC toxicity. The method is useful in determining the dose of a UGT2B7-  
CC glucuronidated drug that may be used in treating cancer patients. It is  
CC also useful in determining side effects associated with epirubicin  
CC reducing or eliminating side effects associated with epirubicin  
CC treatment, and in ways of increasing the efficacy of dosage regimens. The  
CC present sequence is a primer used for sequencing human UGT2B7 DNA  
XX  
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4023 AAAGAGAAAACAAATGTTAT 4045

Db 1 AAAGAGAAAACAAATGTTT 23

RESULT 2900  
ABK9281  
ID ABK9281 standard; RNA; 24 BP.  
XX  
AC ABK9281;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #11.  
DE Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.  
XX  
OS Synthetic.

XX US2002064771-A1.  
PN 30-MAY-2002.  
XX 06-APR-2001; 2001US-00828034.  
XX 07-APR-2000; 2000US-0195852P.  
XX (ZHON/) ZHONG W.  
XX (HONG/) HONG Z.  
XX (FERR/) FERRARI E.  
XX Zhong W, Hong Z, Ferrari E;  
PI WPI; 2002-582330/62.  
XX Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3  
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,  
PT and template and primer which do not form a stable duplex in the absence  
PT of HCV NS5B.  
XX Example; Page 6; 17pp; English.  
XX The invention relates to a replicase complex comprising a hepatitis C  
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a  
CC complementary nucleic acid primer which is annealed to the 3' terminus of  
CC the template, where the template is at least three nucleotides and the  
CC primer is two or three nucleotides, and the template and primer do not  
CC form a stable duplex in solution in the absence of the HCV NS5B protein.  
CC The complex is useful for detecting HCV replicase activity and permits  
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen  
CC and evaluate antiviral inhibitors and to improve the specificity and  
CC efficiency of the inhibitors. The complex is also useful in the development  
CC of a reliable system for determining kinetic and thermodynamic constants  
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of  
CC mechanistic inhibitors for mis-incorporation or chain termination.  
CC Specifically, the short RNA template and primer pairs are useful in  
CC screening assays which are used for determining kinetic, thermodynamic  
CC and mechanistic properties of NS5B replication and ultimately in the  
CC development of inhibitors of NS5B. Newly identified inhibitors in the  
CC replicase activity may be used for developing anti-HCV pharmaceuticals.  
CC Sequences ABR92971-ABR92986 represent HCV NS5B replicase RNA synthesis  
CC templates  
XX  
XX Sequence 24 BP; 0 A; 18 C; 6 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5774 GCCGGCTGCTGCTGCTGCC 5796  
DB 1 GCCCGCCGCCGCCGCCGCCGCC 23  
RESULT 2901  
ABR57119  
ID ABR57119 standard; DNA; 24 BP.  
XX ABR57119;  
XX 30-JAN-2003 (first entry)  
XX Huma shear protein 8.91 RT-PCR primer #1.  
XX Human; ss; shear protein 8.91; tumour; haemopathy; HIV; PCR; primer;  
KW human immunodeficiency virus infection; immunological disease;  
KM inflammation; RT-PCR; reverse transcriptase PCR.  
XX Homo sapiens.  
XX OS  
XX CN1352095-A.  
XX PN

XX 05-JUN-2002.  
XX 06-NOV-2000; 2000CN-00127213.  
XX 06-NOV-2000; 2000CN-00127213.  
XX 06-NOV-2000; 2000CN-00127213.  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX Mao Y, Xie Y;  
PI WPI; 2002-644454/70.  
XX New human shear protein 8.91 polypeptide for treating malignant tumors,  
PT hemopathy, human immunodeficiency virus infection, immunological diseases  
PT and various inflammations.  
XX Example 2; Page 16 (disclosure); 32pp; Chinese.  
XX The present invention discloses a new kind of polypeptide, human shear  
CC protein 8.91, polynucleotides encoding the polypeptide and producing the  
CC polypeptide by recombinant DNA technology. The present invention also  
CC discloses applying the polypeptide in treating various diseases, such as  
CC malignant tumours, haemopathy, human immunodeficiency virus (HIV)  
CC infection, immunological diseases and various inflammations. The present  
CC invention also discloses the antagonist resisting the polypeptide and its  
CC treatment effect. The present invention also discloses application of the  
CC polynucleotides encoding human shear protein 8.91. The present sequence  
CC is a reverse transcriptase (RT)-PCR primer used to isolate nucleic acids  
CC encoding human shear protein 8.91  
XX  
XX Sequence 24 BP; 3 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 15; DB 1; Length 24;  
Best Local Similarity 78.3%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 4459 TGGACATTTTTTTTTTTTTTTT 4481  
DB 2 TGTAAATTTTTTTCTTTCTTT 24  
RESULT 2902  
AAX84260/c  
ID AAX84260 standard; DNA; 25 BP.  
XX AAX84260;  
XX 08-SEP-1999 (first entry)  
XX PCR primer for human Nck associated protein 1 coding sequence.  
XX Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
KW therapy; PCR primer; ss.  
XX Synthetic.  
XX OS Homo sapiens.  
XX W09931239-A1.  
XX 24-JUN-1999.  
XX 14-DEC-1998; 98WO-JP005646.  
XX 15-DEC-1997; 97JP-00363183.  
XX (KYOW) KYOWA HAKKO KOGYO KK.  
PA (SAKA/) SAKAKI Y.  
XX Sakaki Y;  
PI WPI; 1999-395181/33.  
XX DR  
XX

cc gene in the cell, where the level of expression of the marker gene is dependent on the occurrence of the replication error. The method is used

Db 1 GTGTTTTTTTTTCTCTCTCTTT 23

5313 GTGTTCTCTCCTTTTCTCTTTT 5335

Db

1 GTGTTTCTCTCTCTT 23

```
RESULT 2905
AA173048/c
ID AA173048 standard; DNA; 26 BP.
XX
XX
AC AA173048;
XX
XX
DT 24-OCT-2002 (first entry)
XX
XX
DE Scaffold oligonucleotide.
XX
XX
KM Molecular scaffold; fluorophore; fluorescence; energy transfer;
KM emission wavelength; excitation wavelength; multiple; single nucleotide;
KM polymorphism; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO200222883-A1.
XX
XX
PD 21-MAR-2002.
XX
XX
PF 11-SEP-2001; 2001WO-US028967.
XX
XX
PR 11-SEP-2000; 2000US-00658077.
XX
XX
PR 31-JUL-2001; 2001US-0309156P.
XX
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX
PI Ju J, Li Z, Tong A, Russo JJ;
XX
XX
DR WPI; 2002-575156/61.
XX
XX
PT Composition of matter useful for multi-component analyses, comprises
PT multiple fluorophores bound to molecular scaffold at preset positions to
PT permit fluorescence energy transfer between two fluorophores.
XX
XX
PS Disclosure; Page 43; 113pp; English.
XX
XX
CC This sequence represents a molecular scaffold which may be used in a
CC composition of matter comprising multiple fluorophores. The fluorophores
CC are bound to the molecular scaffold at separate predetermined positions,
CC to permit fluorescence energy transfer between two fluorophores. The
CC fluorophores are characterized by maximum emission wavelength of one
CC being greater than the minimum excitation wavelength of the other. The
CC composition is useful for determining whether a preselected nucleotide
CC residue is present at a predetermined position within a nucleic acid. It
CC is also useful in multicomponent analysis including multiplex biological
CC analysis, and identifying multiple single nucleotide polymorphisms. The
CC presence of a number of given nucleotide residues is determined
CC simultaneously by the composition of the invention
XX
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 15; DB 1; Length 26;
Best Local Similarity 78.3%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4017 GAGAAAAAGAGAGAAAAACAAA 4039
Db 26 GAAAAAAAAAAAAAAAAAAAAA 4
RESULT 2906
AA520672/c
ID AA520672 standard; DNA; 26 BP.
XX
XX
AC AA520672;
XX
XX
DT 09-APR-2002 (first entry)
XX
XX
DE Human zalphall ligand sequencing primer ZC7764b.
XX
XX
KM Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
```

```
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KM immunostimulant; cytostatic; human; sequencing primer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN US6307024-B1.
XX
XX
PD 23-OCT-2001.
XX
XX
PF 09-MAR-2000; 2000US-00522217.
XX
XX
PR 09-MAR-1999; 99US-0123547P.
XX
XX
PR 11-MAR-1999; 99US-0123904P.
XX
XX
PR 01-JUL-1999; 99US-0142013P.
XX
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
XX
PI Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX
DR WPI; 2002-040208/05.
XX
XX
PT New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX
PS Example 7; Col 139; 105pp; English.
XX
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-1Gm antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall ligand gene,
CC and in gene therapy. Zalphall ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence cDNA clones in the isolation of
CC human zalphall ligand
XX
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 15; DB 1; Length 26;
Best Local Similarity 78.3%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4017 GAGAAAAAGAGAGAAAAACAAA 4039
Db 26 GAAAAAAAAAAAAAAAAAAAAA 4
RESULT 2907
ABX93461/c
ID ABX93461 standard; DNA; 26 BP.
XX
XX
AC ABX93461;
XX
XX
DT 27-MAY-2003 (first entry)
XX
XX
DE L5147-specific polynucleotide sequencing related universal primer #1.
XX
XX
DE L5147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KM primer; EST clone; expressed sequence tag clone.
XX
XX
OS Synthetic.
```

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XX US2002188114-A1.
XX
XX 12-DEC-2002.
XX
XX 05-JUN-1998; 98US-00092296.
XX
XX 05-JUN-1997; 97US-0048810P.
XX
XX (BIL/) BILTINGEL P.
XX (COHE/) COHEN M.
XX (COLP/) COLPITTS T L.
XX (FRIE/) FRIEDMAN P N.
XX (KLAS/) KLAAS M R.
XX (RUS/) RUSSELL J C.
XX (STRO/) STROUPE S.
XX
XX Billengel P, Cohen M, Colpitts TL, Friedman PN, Klaas MR;
XX Russell JC, Stroupe S;
XX WPI; 2003-341045/32.
XX
XX New LS147 polypeptide, useful for preparing a composition for treating
XX e.g., lung cancer.
XX
XX Example 2; Page 39; 47pp; English.
XX
XX The invention describes a purified polypeptide or its fragment derived
XX from the LS147 gene capable of selectively hybridising to the nucleic
XX acid of the gene and has at least 50% identity with the polynucleotide.
XX The LS147 polypeptide is useful for preparing a composition for treating
XX cancer, e.g. lung cancer using gene therapy. This sequence represents a
XX universal primer used to sequence LS147 expressed sequence tag (EST) -
XX clones
XX
XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 15; DB 1; Length 26;
XX Best Local Similarity 78.3%; Pred. No. 2.4e+03;
XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 4017 GAGGAAAAAGAGGAAAAACAAA 4039
XX |||||
XX 26 GAAAAA
XX
XX RESULT 2908
XX ABX12469/c
XX ID ABX12469 standard; DNA; 27 BP.
XX
XX ABX12469;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dt26V.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; PCR; primer; ss.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-1B003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX

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PI Tuvemo HT, Frisk GE, Yin H;
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Example 5; Page 44; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a primer used to determine the
XX genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain
XX VD2921
XX
XX Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
XX
XX
XX Query Match 0.2%; Score 15; DB 1; Length 27;
XX Best Local Similarity 70.4%; Pred. No. 2.5e+03;
XX Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
XX
XX 4011 TAAATGAGGAAAAAGAGGAAAAACA 4037
XX :|||
XX 27 BAAAAA
XX
XX RESULT 2909
XX ABN83378
XX ID ABN83378 standard; DNA; 29 BP.
XX
XX ABN83378;
XX
XX 15-AUG-2002 (first entry)
XX
XX Mononucleotide repeat locus BAT25 probe #1.
XX
XX Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 29 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "labelled with Fluorescein"
XX
XX EP1207210-A1.
XX
XX 22-MAY-2002.
XX
XX 13-NOV-2001; 2001EP-00126930.
XX
XX 15-NOV-2000; 2000EP-00124897.
XX
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Dietmaier W;
XX
XX WPI; 2002-437469/47.
XX
XX Analyzing repeat sequences in DNA using a probe which hybridizes to
XX adjacent repetitive and non-repetitive regions and determining hybrid
XX melting point is useful to detect microsatellite instability such as in
XX

```

PT hereditary cancer.  
 XX  
 PS Claim 16; Page 7; 19pp; English.  
 XX  
 CC The present invention relates to a method for analyzing a target nucleic acid consisting of repetitive and non-repetitive sequences. The method comprises hybridizing a polynucleotide probe comprising a segment complementary to a non-repetitive region and a segment complementary to an adjacent repetitive region, where the second segment consists of a defined number of repeats, and determining the melting point temperature of the hybrid. The method is used to analyse microsatellites, especially microsatellite instability, particularly as a means for detecting hereditary tumours. Alternatively, the method is used to identify an individual in a population. The present sequence is a probe for mononucleotide repeat locus BAT5, and was used to illustrate the invention  
 CC  
 SQ Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 29;  
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 4018 AGAAAAAGAGAGAAAAACAAT 4040  
 Db 5 AAAAAAAAAAAAAAAAAAAAAAT 27  
 RESULT 2910  
 AAS63441  
 ID AAS63441 standard; DNA; 30 BP.  
 XX  
 AC AAS63441;  
 XX  
 DT 29-JAN-2002 (first entry)  
 XX  
 DE Oligonucleotide-nanoparticle probe #63.  
 XX  
 KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;  
 KM nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;  
 KW ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200173123-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 28-MAR-2001; 2001WO-US010071.  
 XX  
 PR 28-MAR-2000; 2000US-0192699P.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 26-JUN-2000; 2000US-00603830.  
 PR 26-JUN-2000; 2000US-0213906P.  
 PR 08-DEC-2000; 2000US-0254392P.  
 PR 11-DEC-2000; 2000US-0255235P.  
 PR 12-JAN-2001; 2001US-00760500.  
 PR 28-MAR-2001; 2001US-00820279.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;  
 PI Taton TA, Park S, Li Z;  
 XX  
 DR WPI; 2001-656926/75.  
 XX  
 PT Detecting and separating nucleic acid, useful e.g. for diagnosis,  
 PT complementary reaction with nanoparticles that carry oligonucleotides  
 PT complementary to parts of the target.  
 XX  
 PS Example 24; Fig 44; 404pp; English.  
 XX  
 CC The invention relates to a method for detection of nucleic acid (1)

CC having at least 2 portions, comprising treatment with nanoparticles that  
 CC carry oligonucleotides complementary to at least 2 parts of (1), where  
 CC detectable change caused by hybridisation of the oligonucleotide to (1)  
 CC is observed. The method is used to detect (or to separate) specific (1),  
 CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic  
 CC analysis etc., and generally to detect analytes other than (1). The  
 CC oligonucleotide-derivatised nanoparticles are also useful for preparing  
 CC nanostructures useful, for example, as biochips, biofilters, mechanical  
 CC devices, separation membranes, chemical sensors, in computers, and for  
 CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be  
 CC produced, allowing their direct use (as probes) in polymerase chain  
 CC reaction, i.e. they survive multiple heating/cooling cycles so do not  
 CC need to be added after amplification. (1) are detected by simple colour  
 CC change, without the need for special equipment, making possible rapid  
 CC field testing for e.g. pathogens. AAS63374-AAS63448 represent  
 CC oligonucleotide-nanoparticle probes, and related sequences, used in the  
 CC method of the invention  
 CC  
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 15; DB 1; Length 30;  
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3278 AAGAGAAAAATGAAACGAGACC 3300  
 Db 5 AAAAAAAAAAAAAAAAAAGCAGACC 27  
 RESULT 2911  
 AAS10385  
 ID AAS10385 standard; DNA; 30 BP.  
 XX  
 AC AAS10385;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Oligonucleotide-cyclic disulphide linker, c1 #2.  
 XX  
 KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
 KM DNA isolation; genetic disease; bacterial disease; viral disease;  
 KM forensic science; paternity testing; gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200151665-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US001190.  
 XX  
 PR 13-JAN-2000; 2000US-0176409P.  
 PR 26-APR-2000; 2000US-0200161P.  
 PR 26-JUN-2000; 2000US-00603830.  
 PR 12-JAN-2001; 2001US-00760500.  
 XX  
 PA (NANO-) NANOSPHERE INC.  
 XX  
 PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghanian R;  
 PI Taton TA, Li Z;  
 XX  
 DR WPI; 2001-451868/48.  
 XX  
 PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or  
 PT viral diseases, by contacting the nucleic acid with oligonucleotides  
 PT attached to nanoparticles and having sequences complementary a portion of  
 PT the nucleic acid.

XX Example 24; Fig 44; 323pp; English.

XX The sequence represents a cyclic disulphide linked oligonucleotide which  
 CC may be coupled with colloidal gold particles (nanoparticles) and used to  
 CC demonstrate the method of the invention. The invention relates to  
 CC isolating or detecting a nucleic acid of interest, in a mixture of  
 CC nucleic acids, by binding it to 2 or more complementary nucleotides which  
 CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.  
 CC colloidal gold) are used to both isolate and detect (e.g. by linking the  
 CC particle to a fluorescent probe) the resultant complex. The methods are  
 CC useful for detecting nucleic acids, natural or synthetic, and modified or  
 CC unmodified. The methods may also be applied in the diagnosis of genetic,  
 CC bacterial and viral diseases, in forensics, in DNA sequencing, for  
 CC paternity testing, for cell line authentication, and for monitoring gene  
 CC therapy. The methods are further useful in research and analytical  
 CC laboratories in DNA sequencing, in the field to detect the presence of  
 CC specific pathogens, for quick identification of an infection to assist in  
 CC drug prescription, and in homes and health centres for inexpensive first-  
 CC line screening. The methods, which are based on observing colour change  
 CC with the naked eye, are cheap, fast, simple, robust (reagents are  
 CC stable), do not require specialised or expensive equipment, and little or  
 CC no instrumentation is required

XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 30;  
 XX Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAAAATGAAACGAGCC 3300  
 DB 5 AAAAAAAAAAAAAAAAAAGCAGACC 27

RESULT 2912

ABK65048  
 ID ABK65048 standard; DNA; 30 BP.

XX AC ABK65048;

XX 02-JUL-2002 (first entry)

XX Nanoparticle-oligonucleotide #68.

XX Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;  
 KM ss.

XX Synthetic.

XX WO200218643-A2.

XX 07-MAR-2002.

XX 10-AUG-2001; 2001WO-US025237.

XX 11-AUG-2000; 2000US-0224631P.

XX 08-DEC-2000; 2000US-0254392P.

XX 11-DEC-2000; 2000US-0255235P.

XX 12-JAN-2001; 2001US-00760500.

XX 28-MAR-2001; 2001US-00820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Garimella V, Li Z, Park S;  
 XX WPI; 2002-256024/30.

XX Detecting nucleic acid, useful for diagnosis of genetic, viral or  
 PT bacterial diseases, comprises hybridizing nanoparticles with attached  
 PT oligonucleotides to nucleic acid and detecting change brought about by  
 PT hybridization.

XX Example 24; Fig 44; 412pp; English.

XX The invention relates to a method of detecting a nucleic acid (NA) having  
 CC at least 2 portions comprising: (a) providing nanoparticles (NP) with  
 CC attached oligonucleotides (OGN), where OGN has a sequence complementary  
 CC to the sequence of NA; (b) contacting NA and NP under conditions  
 CC effective to allow hybridisation of OGN with NA; and (c) observing a  
 CC detectable change brought about by hybridisation of OGN with NA. The  
 CC method is useful for detecting a nucleic acid, separating a selected  
 CC nucleic acid from others and methods of nanofabrication. Detecting  
 CC analytes such as nucleic acids and proteins are useful for the diagnosis  
 CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use  
 CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.  
 CC In particular assays using OGN-NP conjugates prepared using linkers  
 CC comprising a steroid residue attached to a cyclic disulphide have been  
 CC found to be approximately 10 times more sensitive than assays employing  
 CC conjugates prepared using alkanethiols or acyclic disulphides as the  
 CC linker. The OGN-NP conjugates are stable allowing them to be used  
 CC directly in PCR solutions. Therefore conjugates added as probes to a DNA  
 CC target to be PCR amplified can be carried through the 30 or 40 heating  
 CC cooling cycles of the PCR and are still able to detect the amplicons  
 CC without opening the tubes and causing contamination. ABK64981-ABK65055  
 CC represent nanoparticle-oligonucleotides of the invention

XX Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 15; DB 1; Length 30;  
 XX Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 XX Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAAAATGAAACGAGCC 3300  
 DB 5 AAAAAAAAAAAAAAAAAAGCAGACC 27

RESULT 2913

ABS64686  
 ID ABS64686 standard; DNA; 30 BP.

XX AC ABS64686;

XX 15-NOV-2002 (first entry)

XX Nucleic acid detection method associated polynucleotide #68.

XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;  
 KM nanoparticle; viral RNA detection; bacterial DNA detection;  
 KW fungal DNA detection; nanoprobe conjugate; ss.

XX Synthetic.

XX WO200246472-A2.

XX 13-JUN-2002.

XX 07-DEC-2001; 2001WO-US046418.

XX 08-DEC-2000; 2000US-0254392P.

XX 08-DEC-2000; 2000US-0254418P.

XX 11-DEC-2000; 2000US-0255235P.

XX 11-DEC-2000; 2000US-0255236P.

XX 12-JAN-2001; 2001US-00760500.

XX 28-MAR-2001; 2001US-00820279.

XX 09-APR-2001; 2001US-0282640P.

XX 10-AUG-2001; 2001US-00927777.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
 PI Taton TA, Garimella V, Li Z, Park S;  
 XX WPI; 2002-608256/65.

XX Detecting nucleic acid having two portions, by providing nanoparticles  
 PT having oligonucleotides attached to it, contacting nucleic acid and  
 PT nanoparticles to allow hybridization, and observing detectable change.  
 XX  
 XX  
 XX Example 24; Fig 44; 442pp; English.

CC The invention describes a method of detecting (M1) a nucleic acid having  
 CC two portions, involving providing nanoparticles having oligonucleotides  
 CC attached to it, which has a sequence complementary to sequence of two  
 CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to  
 CC allow hybridization of oligonucleotides with two or more portions of  
 CC nucleic acid, and observing a detectable change brought about by  
 CC hybridization. (M1), nanoparticles (I), nanoparticle-oligonucleotide  
 CC conjugates (II) and the aggregate probe are useful for detecting two or  
 CC more nucleic acids (from a biological source) having at least two  
 CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated  
 CC with a disease, synthetic, or structurally-modified natural or synthetic  
 CC RNA or DNA, or a product of a polymerase chain reaction amplification.  
 CC (II) is useful for preparing a nanoprobe conjugate for detecting an  
 CC analyte, and for detecting a nucleic acid bound to an electrode surface.  
 CC (I) and (II) are useful for fabrication, and for separating a selected  
 CC nucleic acid having two portions from other nucleic acids. (I), (II) and  
 CC the aggregate probe are useful for detecting an analyte (especially  
 CC polyvalent analyte) in a sample. This sequence represents a  
 CC polynucleotide used to demonstrate the method of the invention  
 CC  
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 30;  
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAATGAAACCGAGCC 3300  
 |||||  
 Db 5 AAAAAAAAAAAAAAAAAAGCAGACC 27

## RESULT 2914

AA61658  
 ID AAL61658 standard; DNA; 30 BP.

AC AAL61658;

DT 22-SEP-2003 (first entry)

DE Oligonucleotide #19 used in the nucleic acid detection method.

XX Nucleic acid detection; fabrication; ss.

XX Unidentified.

XX WO2003035829-A2.

XX 01-MAY-2003.

XX 08-OCT-2002; 2002MO-US032088.

XX 09-OCT-2001; 2001US-0327864P.

XX 07-DEC-2001; 2001US-00008978.

XX (NANO-) NANOSPHERE INC.

XX Park S, Tacon TA, Mirkin CA;

XX WPI; 2003-430409/40.

XX Detecting nucleic acid having two portions, by providing nanoparticles  
 PT having oligonucleotides attached to it, contacting nucleic acid and  
 PT nanoparticles to allow hybridization, and observing detectable change.  
 XX  
 XX Example 24; Fig 44; 467pp; English.

CC The invention relates to a method of detecting a nucleic acid having two  
 CC portions. The method involves providing nanoparticles having  
 CC oligonucleotides attached to it which has a sequence complementary to  
 CC sequence of two portions of nucleic acid, contacting nucleic acid and  
 CC nanoparticles to allow hybridization of oligonucleotides with two or more  
 CC portions of nucleic acid and observing a detectable change brought about  
 CC by hybridization. The method and aggregate probes are useful for  
 CC detecting two or more nucleic acids (from a biological source) having at  
 CC least two portions such as viral RNA, bacterial or fungal DNA, a gene  
 CC associated with a disease, synthetic or structurally modified natural or  
 CC synthetic RNA or DNA, or a product of a polymerase chain reaction  
 CC amplification. The invention is useful for preparing a nanoprobe  
 CC conjugate for detecting an analyte and for detecting a nucleic acid bound  
 CC to an electrode surface. It is also useful for fabrication and for  
 CC separating a selected nucleic acid having two portions from other nucleic  
 CC acids. The present sequence is an oligo used to illustrate the method of  
 CC the invention  
 CC  
 SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 15; DB 1; Length 30;  
 Best Local Similarity 78.3%; Pred. No. 2.7e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3278 AAGAGAGAAATGAAACCGAGCC 3300  
 |||||  
 Db 5 AAAAAAAAAAAAAAAAAAGCAGACC 27

## RESULT 2915

AAQ30395  
 ID AAQ30395 standard; DNA; 18 BP.

AC AAQ30395;

DT 25-MAR-2003 (revised)

DT 07-DEC-1992 (first entry)

XX Oligomer LAP312 for forming triplex with HUMINT02 target duplex.

XX Human leukocyte adhesion protein; P150.95 alpha subunit gene;

XX herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis;

XX inflammation; ss.

XX Synthetic.

PH Key Location/Qualifiers

FT modified\_base 2

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT modified\_base 3

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT misc\_feature 9..10

FT /\*tag= i

FT /note= "o-xyloso dimer synthon linkage"

FT modified\_base 9

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT misc\_feature 10..18

FT /\*tag= h

FT /label= inverted\_polarity\_region

FT /note= "see comments"

FT modified\_base 10

FT /\*tag= d

FT /mod\_base= OTHER

FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

FT modified\_base 13

FT /\*tag= e

FT /mod\_base= OTHER



```

FT modified_base /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 15 /tag= f
FT /mod_base= OTHER
FT modified_base /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT 17 /*tag= g
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US008811.
XX
XX 23-NOV-1990; 90US-00617907.
XX 18-JAN-1991; 91US-00643382.
XX 08-APR-1991; 91US-00683420.
XX 17-APR-1991; 91US-00686544.
XX 17-APR-1991; 91US-00686546.
XX 17-APR-1991; 91US-00686547.
XX 27-SEP-1991; 91US-00766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with G-C
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX herpes malignancy and inflammation.
XX
XX Claim 12; Page 70; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at physiological
XX pH with a purine rich target sequence by coupling into the major groove
XX of the duplex. The specific target sequence of this oligomer is the human
XX leukocyte adhesion protein p150, 95 alpha subunit gene (HUMINT02)
XX beginning at nucleotide 677 contg. a purine rich sequence concd. on one
XX strand of the duplex. The oligomer, and others like it are useful in
XX diagnosis and therapy of diseases characterized by specific DNA duplex
XX targets, e.g. HIV, hepatitis B, herpes, malignant tumours and
XX inflammation. The triple helices form under mild conditions thus assays
XX may be carried out without subjecting the test specimen to harsh
XX conditions. The oligomer contains an inverted polarity region formed from
XX an o-xylosa dimer synthon. The linking gp. is o-xylosa (nucleotides have
XX the 3' positions of xylose sugars linked via the o-xylosa ring). Two
XX nucleotides are coupled through a xylose residue to form the dimer
XX synthon. This additional modifications may render the oligomer stable to
XX nuclease activity. The oligomer is able to inhibit gene expression, as
XX verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 7 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6682 TTAATTTTAAATTAATAT 6699
XX | | | | | | | | | | | | | | | |
XX 1 TAAATTTTAAATTAATAT 18
XX
XX RESULT 2916
XX AAQ38707 standard; RNA; 18 BP.
XX
XX AC AAQ38707;
XX
XX 25-MAR-2003 (revised)
XX

```

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DT 15-JUL-1993 (first entry)
XX
XX First chimeric primer for adding poly A tails.
XX
XX oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;
XX treatment; diagnosis; testing; assay; Candida; papillomavirus;
XX cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;
XX liver disease; human immunodeficiency virus; herpes simplex virus; HSV;
XX human immunodeficiency virus; HIV; AIDS; Influenza virus;
XX genetic disease; genetic abnormalities.
XX
XX Synthetic.
XX
XX WO9305182-A1.
XX
XX 18-MAR-1993.
XX
XX 04-SEP-1992; 92WO-US007489.
XX
XX 05-SEP-1991; 91US-00755485.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bruce TW;
XX
XX WPI; 1993-101001/12.
XX
XX Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule
XX - for use in therapeutics, diagnostics and research reagents.
XX
XX Disclosure; Page 27; 61pp; English.
XX
XX This sequence was used as a PCR primer in order to add a polyA tail to
XX the 3' end of the highest specific activity selected oligonucleotide in
XX order to form a first strand. The primer is comprised of a 5' known
XX sequence and a 3' polynucleotide portion corresp. to the polynucleotide
XX tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4460 GGAAGCTTTTCTTTTCTTTT 4477
XX | | | | | | | | | | | | | | | |
XX 1 GGAAGCTTTTCTTTTCTTTT 18
XX
XX RESULT 2917
XX AAQ92177
XX ID AAQ92177 standard; DNA; 18 BP.
XX
XX AC AAQ92177;
XX
XX 12-JAN-1996 (first entry)
XX
XX p53 detection probe, (codon 273 CGT to TGT).
XX
XX Primer; polymerase chain reaction; amplify; mutant; K-ras; PCR;
XX flanking region; amplification; probe; detection; sputum; diagnosis;
XX benign; malignant; neoplasm; lung; lung cancer; head; neck; ss.
XX
XX Synthetic.
XX
XX WO9513397-A1.
XX
XX 18-MAY-1995.
XX
XX 10-NOV-1994; 94WO-US012947.
XX
XX 12-NOV-1993; 93US-00152313.
XX

```

PA (UYUO ) UNIV JOHNS HOPKINS SCHOOL MED.  
 XX  
 PI Sidrensky D;  
 XX  
 XX MPI; 1995-194114/25.  
 DR  
 XX  
 PT Detecting target nucleic acid in mammalian sputum - particularly for  
 PT diagnosis of lung neoplasia involving mutation(s) in the K-ras oncogene  
 PT or p53 tumour suppressor.  
 XX  
 PS Example 1; Page 34; 122pp; English.  
 XX  
 CC The sequences given in AAQ92112-211 are probes which were used in the  
 CC detection of a mutant p53 gene sequence. The DNA to be detected is  
 CC amplified using PCR and then these probes which are pref. labeled using  
 CC 32-P gamma-ATP are used to detect the mutant sequences. The primers and  
 CC probes given in AAQ92098-219 are used in the method of the invention for  
 CC detecting mammalian target DNA in sputum samples. Analysis of the target  
 CC DNA is used to diagnose benign or malignant neoplasms of the lung. It is  
 CC also useful for screening people at high risk or for monitoring progress  
 CC of treatment of lung neoplasms. The method is based on the discovery that  
 CC mutant target DNA associated with lung cancer is present at detectable  
 CC levels in sputum. Cells shed into sputum from head and neck cancers may  
 CC also be detected  
 CC  
 SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 7309 TTGAGATTGTTGTTG 7326  
 Db 1 TTGAGCTGTGTTGTTG 18  
 XX  
 RESULT 2918  
 AAQ83415  
 ID AAQ83415 standard; DNA; 18 BP.  
 XX  
 AC AAQ83415;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-SEP-1995 (first entry)  
 XX  
 DE c-fos antisense oligonucleotide.  
 XX  
 XX c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasia; antisense;  
 KM phosphorothioate; ss.  
 KM  
 XX Synthetic.  
 OS  
 XX  
 PN WO9502051-A2.  
 PN  
 PD 19-JAN-1995.  
 PD  
 XX  
 PP 06-JUL-1994; 94MO-EP002218.  
 PP  
 XX 10-JUL-1993; 93EP-00111059.  
 PR  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;  
 XX  
 XX MPI; 1995-066896/09.  
 DR  
 XX  
 PT Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and  
 PT treating neuronal injury, degeneration, cell death and/or neoplasms.  
 XX  
 XX Claim 2; Page 61; 86pp; English.  
 PS  
 XX Antisense nucleic acid hybridising with an area of the mRNA and/or DNA  
 CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a

CC causal role in neuronal injury, degeneration, cell death and/ or  
 CC neoplasms, can be used to prevent and treat such conditions. c-jun  
 CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B  
 CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-  
 CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.  
 CC Preferably the antisense sequences are phosphorothioate oligonucleotides  
 CC since these are not destroyed as fast by endogenous factors as naturally  
 CC occurring molecules. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 18 BP; 2 A; 7 C; 0 G; 9 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4299 CATCTTTTCCCTCCCT 4316  
 Db 1 CATCTTATTCCTTCCCT 18  
 XX  
 RESULT 2919  
 AAT96107  
 ID AAT96107 standard; DNA; 18 BP.  
 XX  
 AC AAT96107;  
 XX  
 DT 31-MAR-1998 (first entry)  
 DT  
 XX  
 DE First chimeric primer.  
 XX  
 KM Determination; oligonucleotide; specific activity; therapy;  
 KM target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;  
 KM chimeric; primer; ss.  
 KM  
 XX Synthetic.  
 OS  
 XX  
 PN US5686242-A.  
 PN  
 PD 11-NOV-1997.  
 PD  
 XX  
 PP 27-OCT-1994; 94US-00330000.  
 PP  
 XX  
 PR 05-SEP-1991; 91US-00755485.  
 PR 04-SEP-1992; 92WO-US007489.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Lima WF, Bruice TW;  
 PI  
 DR MPI; 1997-558135/51.  
 DR  
 XX  
 PT Determination of oligo-nucleotide with specific activity for target bio-  
 PT molecule - using set of randomised oligo-nucleotide(s).  
 XX  
 PS Disclosure; Col 27-28; 22pp; English.  
 PS  
 XX  
 CC The present sequence was used in the development of a method of  
 CC determining an oligonucleotide having specific activity for a target  
 CC biomolecule. The method comprises assaying a set of randomised  
 CC oligonucleotides for activity against a target biomolecule, separating  
 CC active from inactive oligonucleotides and recovering, amplifying and  
 CC determining the nucleic acid sequence of the active oligonucleotides. The  
 CC oligonucleotides can be used for therapeutic, diagnostic and research  
 CC purposes  
 CC  
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4460 GGACTTTTCTTTTCTTT 4477  
 ||| ||||| ||||| |||||

Db 1 GGATGTTTTTTTTTTTTT 18

RESULT 2920

AAK63294/c

XX AAK63294 standard; RNA; 18 BP.

XX AAK63294;

XX 16-JUL-1999 (first entry)

XX Delta-9 desaturase halpin ribozyme substrate SEQ ID NO:1169.

XX Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;

XX granule bound starch synthase; hammerhead ribozyme; halpin ribozyme;

XX modulation; gene expression; transgenic plant; cleavage; canola plant;

XX caffeine synthesis; coffee plant; nicotine production; tobacco;

XX fruit ripening; flower pigmentation; lignin production; ss.

XX Zea mays.

XX WO9710328-A2.

XX 20-MAR-1997.

XX 12-JUL-1996; 96WO-US011689.

XX 13-JUL-1995; 95US-0001135P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (DOMC) DOWELANCO.

XX Zwack MG, Edington BE, Mcswigen JA, Merlo PAO, Guo L, Skokut TA;

XX Young SA, Folkerts O, Merlo DJ;

XX WPI; 1997-202224/18.

XX Ribozyyme which modulates plant gene expression - preferably modulates

XX expression of DELTA-9 desaturase or granule bound starch synthase in

XX maize or canola.

XX Claim 40; Page 93; 155pp; English.

XX The present invention describes an enzymatic nucleic acid molecule (I)

XX with RNA cleaving activity, which modulates the expression of a plant

XX gene. Also described is a gene comprising a cDNA sequence encoding maize

XX Delta-9 desaturase. (I) can be used to modulate expression of a gene,

XX preferably Delta-9 desaturase or a granule bound starch synthase (GBS)

XX gene, in a plant (preferably a maize or canola plant). (I) can be used to

XX modulate caffeine synthesis in a coffee plant, nicotine production in a

XX tobacco plant, fruit ripening processes in an apple, tomato, pear, plum

XX or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or

XX marigold plant or lignin production in a tobacco, aspen, poplar or pine

XX plant

XX Sequence 18 BP; 2 A; 10 C; 6 G; 0 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 65 GCTGCGGCGGCGGCGG 82

XX 18 GCTGCTGCGGCGGCGG 1

RESULT 2921

AAK8679

XX AAK8679 standard; DNA; 18 BP.

XX 10-SEP-1999 (first entry)

XX Human chromosome 18q YAC clone primer.

XX Human chromosome 18q; mood disorder; polymorphic marker; detection;

XX identification; trinucleotide repeat expansion; schizophrenia;

XX anxiety disorder; adjustment disorder; personality disorder;

XX nucleotide triplet repeat; ss.

XX Synthetic.

XX Homo sapiens.

XX WO932643-A2.

XX 01-JUL-1999.

XX 17-DEC-1998; 98WO-EP008543.

XX 18-DEC-1997; 97GB-00026804.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOC.

XX Van Broeckhoven C, Raeymaekers P, Del-Favero J;

XX WPI; 1999-418934/35.

XX Detecting nucleotide triplet repeats in human chromosome 18q.

XX Disclosure; Page 56; 87pp; English.

XX The present invention describes detecting nucleotide triplet repeats in a

XX region of human chromosome 18q disposed between polymorphic markers

XX D18S68 and D18S979 to identify a human gene associated with a mood

XX disorder or related disorder. AAX88542 to AAX88705 represents human

XX chromosome 18q YAC clones and primers corresponding to them, used in the

XX exemplification of the present invention. YAC clones comprising a portion

XX of the region of human chromosome 18q between markers D18S68 and D18S979

XX are used to identify at least one human gene associated with a mood

XX disorder or related disorder. The mood disorder or related disorder, is

XX chosen from the Diagnostic and Statistical Manual of Mental Disorders,

XX version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4,

XX 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1,

XX 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3),

XX adjustment disorders (309.XX) and personality disorders (codes 301.XX).

XX Probes derived from genes associated with the mood disorder or related

XX disorder can be used to detect pathological mutations or genetic

XX variations in patients. The methods, probes and antibodies can be used to

XX determine the susceptibility of an individual to a mood disorder or

XX related disorder. The nucleic acids and proteins of the human gene can be

XX used to treat mood disorders and related disorders

XX Sequence 18 BP; 2 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX 5795 CTTGCTGCTGCTGCTG 5812

XX 1 CTTGCTGCTGCTGCTG 18

XX RESULT 2922

AAZ35875

XX AAZ35875 standard; DNA; 18 BP.

XX AAZ35875;

XX 03-FEB-2000 (first entry)

XX Human sentrin phosphorothioate antisense oligonucleotide SEQ ID NO:17.

XX Human; sentrin; antisense oligonucleotide; phosphorothioate; inhibition;

XX modulation; expression; diagnosis; ss.

```

XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX US5985664-A.
XX
XX 16-NOV-1999.
XX
XX 17-DEC-1998; 98US-00213768.
XX
XX 17-DEC-1998; 98US-00213768.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowser LM;
XX
XX WPI; 2000-022284/02.
XX
XX Antisense compound which modulates human sentrin expression, useful for
XX treating diseases associated with sentrin expression.
XX
XX Claim 3; Col 38; 28pp; English.
XX
XX The present invention describes an antisense compound (I) 8-30
XX nucleotides long targeted to a nucleic acid molecule encoding human
XX sentrin. The antisense compound comprises a phosphorothioate antisense
XX oligonucleotide which inhibits expression of human sentrin. (I) is useful
XX for inhibiting expression of sentrin in human cells or tissues in vitro,
XX for treating humans or other animals suspected of having or being prone
XX to a disease associated with sentrin expression. (I) can also be used for
XX research or diagnostic purposes. The present sequence represents a human
XX sentrin phosphorothioate antisense oligonucleotide from the present
XX invention
XX
XX Sequence 18 BP; 4 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 328 CTGGCCCAATTACTTTGAG 345
XX |||||
XX 1 CTGTCCAMTGACTTTGAG 18
XX
XX RESULT 2923
XX AA265529
XX ID AA265529 standard; DNA; 18 BP.
XX
XX AC AA265529;
XX
XX 30-MAR-2000 (first entry)
XX
XX Immunosuppressant inhibitor oligonucleotide TGF-beta1-98-17.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
XX glomerulonephritis; acute respiratory distress syndrome; se;
XX atherosclerosis.
XX
XX Unidentified.
XX
XX WO9963975-A2.
XX
XX 16-DEC-1999.
XX
XX

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PF 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX
XX 25-JUL-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGEN IDEC GSK BIONOLEKULARE DIAGNOSTIK.
XX
XX Schlingsenstepen K, Schlingsenstepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
XX adversely affects the immune response, for treating cancers and
XX infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
XX used in the invention. The invention relates to a composition which
XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.
XX transforming growth factor TGF-beta, vascular endothelial growth factor
XX VEGF, interleukin-10, IL-10, prostaglandin E2 PGE2, or their receptors)
XX that adversely affects the immune response. The composition also includes
XX at least one stimulant that positively affects the immune response. This
XX oligonucleotide is an example of an inhibitor that is used in the
XX composition. The composition is used as an immunostimulant for the
XX treatment of neoplasms and infections, particularly hyperproliferation;
XX leukemias; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
XX most of which are directed against TGFbeta or VEGF, are inhibitors of
XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
XX colitis, diabetes, glomerulonephritis, acute respiratory distress
XX syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 18 BP; 1 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 CTGGCAGCTGCGCGGCG 19
XX |||||
XX 1 CCGGCAGCGCGCGCGCG 18
XX
XX RESULT 2924
XX AA259187/c
XX ID AA259187 standard; DNA; 18 BP.
XX
XX AC AA259187;
XX
XX 15-SEP-2003 (revised)
XX
XX 20-APR-2000 (first entry)
XX
XX Reverse primer for construct MWPsp-MWPmp5 DNA.
XX
XX Fusion protein; Bacillus; cell wall protein; promoter; cleavage site;
XX TEV protease; PCR primer; se.
XX
XX Brevibacillus brevis.
XX
XX JF11341991-A.
XX
XX 14-DEC-1999.
XX
XX 30-MAR-1999; 99JP-00089488.
XX
XX 31-MAR-1998; 98JP-00087339.
XX
XX (ITOH-) ITOHAM FOODS INC.
XX

```

PA (UDAK/) UDAKA S.  
XX Sato S, Higashikuni N, Kudo T, Kondo M;  
XX WPI; 2000-101697/09.  
DR A DNA coding a new fused protein and preparation of a useful peptide  
XX through its expression.  
PT Example 3; Page 10; 43pp; Japanese.  
XX  
XX The invention relates to a DNA construct encoding a fusion protein  
CC comprising a Bacillus species cell wall protein fused to a cleavage  
CC peptide and a heterologous protein. The fusion construct is placed  
CC downstream of a Bacillus species promoter sequence. This sequence  
CC represents a PCR primer for the MWp5-MWpms part of the construct MWp5-  
CC MWpms-Mec-Proinsulin, which comprises the Bacillus brevis middle wall  
CC protein mw5 linked to the human proinsulin protein. (Updated on 15-SEP-  
CC 2003 to standardise OS field)  
XX  
SQ Sequence 18 BP; 0 A; 6 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7415 GCAGCAGCAGCAGCAGCA 7432  
DB 18 GCAGCAGAGAGAGCAGCA 1  
RESULT 2925  
AAZ48498  
ID AAZ48498 standard; DNA; 18 BP.  
XX  
AC AAZ48498;  
XX  
XX 31-MAR-2000 (first entry)  
DT  
XX Human TNFRI mRNA inhibiting antisense oligo ISIS# 18891.  
DE  
XX Tumour necrosis factor receptor type 1; TNFRI; antisense; infection;  
KW inflammation; tumour formation; TNFRI; anticancer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US6007995-A.  
XX  
XX 28-DEC-1999.  
PD  
XX 26-JUN-1998; 98US-00106038.  
PE  
XX 26-JUN-1998; 98US-00106038.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Baker BF, Cowseert LM;  
PI WPI; 2000-105333/09.  
DR  
XX Antisense inhibition of tumor necrosis factor type 1 expression for  
PT diagnosis, treatment and prevention of disease, particularly tumors.  
XX  
XX Example 10; Col 24; 34pp; English.  
PS  
XX The invention provides antisense compounds targeted to human tumour  
CC necrosis factor receptor type 1 (TNFRI) RNA. These antisense compounds  
CC can be used in a method of inhibiting the expression of TNFRI human cells  
CC or tissues. The antisense compounds specifically hybridize with one or  
CC more nucleic acids encoding TNFRI modulating the function of nucleic acid  
CC molecules encoding TNFRI, ultimately modulating the amount of TNFRI  
CC produced. The antisense compounds and method are useful as research

CC reagents and diagnostics, and in the treatment and prophylaxis of  
CC infection, inflammation or tumour formation. Sequences AAZ48482-555  
CC represent antisense oligos used for inhibition of the human TNFRI mRNA  
XX  
SQ Sequence 18 BP; 5 A; 7 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7410 CATCAGCAGCAGCAGCAG 7427  
DB 1 CACGAGCGGCGCAGCAGCAG 18  
RESULT 2926  
AAZ71698/C  
ID AAZ71698 standard; DNA; 18 BP.  
XX  
AC AAZ71698;  
XX  
XX 10-SEP-2001 (first entry)  
DT  
XX Human biallelic marker upstream amplification primer SEQ ID NO:6054.  
DE  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
PN WO9954500-A2.  
XX  
XX 28-OCT-1999.  
PD  
XX 21-APR-1999; 99WO-1B000822.  
PE  
XX 21-APR-1998; 98US-0082614P.  
PR  
XX 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
XX Cohen D, Blumenfeld M, Chumakov I;  
PI WPI; 2000-013267/01.  
DR  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
PS Claim 8; Page 1521; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention  
XX  
SQ Sequence 18 BP; 10 A; 0 C; 8 G; 0 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5704 CTTCCTTTCTCTCTC 5721  
 18 CTTCCTTTCTCTCTC 1

RESULT 2927

AAZ76847/c  
 ID AAZ76847 standard; DNA; 18 BP.

XX AAZ76847;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:11203.

XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.

XX Homo sapiens.

XX WO954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST ) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

XX Claim 9; Page 2619; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention

XX Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred.No.1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2341 CACACCCGCTTTCTGT 2358  
 18 CACACACCCCTTTCTGT 1

RESULT 2928

AAZ8678  
 ID AAZ8678 standard; DNA; 18 BP.

XX AAZ8678;

XX 11-MAY-2000 (first entry)

XX Chimeric primer #1.

XX Primer; detection; diagnosis; ss.

XX Unidentified.

XX US6022691-A.

XX 08-FEB-2000.

XX 07-NOV-1997; 97US-00965908.

XX 05-SEP-1991; 91US-00755485.

XX 04-SEP-1992; 92WO-US007489.

XX 27-OCT-1994; 94US-00330000.

XX (ISIS-) ISIS PHARM INC.

XX Lima WF, Bruce TW;

XX WPI; 2000-170669/15.

XX Assay for a chemical or drug in a sample comprises detecting binding of an oligonucleotide selected from a set of randomized oligonucleotides.

XX Disclosure; Col 27-28; 20pp; English.

XX This invention describes a novel method (1) for specifically detecting a chemical or drug in a sample comprising contacting the sample with an

CC oligonucleotide having specific activity for a target biomolecule and detecting the presence or absence of binding where the presence of

CC binding indicates the presence of the chemical or drug in the sample. The oligonucleotide is identified by: (a) assaying a prepared set of

CC randomized oligonucleotides for activity against a target biomolecule; (b) separating active from inactive oligonucleotides; (c) recovering the

CC active oligonucleotides; and (d) characterizing the recovered oligonucleotides by microanalytical structure determination. The method

XX can be used for diagnostic or research purposes

XX Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 18;

XX Best Local Similarity 88.9%; Pred.No.1.8e+03;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GGACTTTTTTTTTTTT 4477  
 1 GGATGTTTTTTTTTTT 18

RESULT 2929

AAA30403/c  
 ID AAA30403 standard; DNA; 18 BP.

XX AAA30403;

XX 21-AUG-2000 (first entry)

XX Human NF-kappa-B p65 subunit antisense oligodeoxynucleotide ISIS# 23770.

XX Human: anti-inflammatory; cytostatic; antimicrobial; infection;

XX antisense inhibition; inflammation; transcription factor; apoptosis;

XX cancer; ss.

XX Homo sapiens.

```

FH Key      Location/Qualifiers
FT modified_base 1..18
FT /+tag= a
FT /note= "all or some internucleoside bonds are
FT phosphorothioate and optionally some sugars may be 2'
FT methoxyethyl"
XX
XX US6069008-A.
XX
XX 30-MAY-2000.
XX
XX 25-NOV-1998; 98US-00199859.
XX
XX 25-NOV-1998; 98US-00199859.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowseert LM, Monia BP;
XX
XX WPI, 2000-410858/35.
XX
XX Antisense compounds which inhibit the expression of the human NF-kappa-B
XX p65 subunit (p65) useful for treating diseases associated with p65
XX expression and as prophylaxis to prevent of delay infection, inflammation
XX or tumor formation.
XX
XX Example 15; Col 41; 33pp; English.
XX
XX The present sequence is one of a number of oligonucleotides designed to
XX target different regions of the human NF-kappa-B p65 subunit, which is a
XX member of the Rel/NF-kappa-B family of transcription factors. Rel/NF-
XX kappa-B proteins are involved in a diverse set of signaling pathways
XX involving stress, apoptosis, cancer, growth, infection and inflammation.
XX Antisense oligonucleotides are able to inhibit expression of the p65
XX subunit and may therefore be used in the treatment of disorders
XX associated with NF-kappa-B p65 subunit expression. They may be used as a
XX prophylaxis to prevent or delay infection, inflammation or tumor
XX formation. Antisense compounds may also be used for research and
XX diagnostics because they hybridize to nucleic acids encoding NF-kappa-B
XX p65 subunit. The effect of antisense oligonucleotides on NF-kappa-B p65
XX subunit mRNA levels was measured using real-time quantitative PCR and
XX Northern blot analysis. Antisense oligonucleotides were synthesised on an
XX automated DNA synthesiser
XX
XX Sequence 18 BP; 6 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2124 TGAAGACTTGTCTACAT 2141
XX ||||| ||||| |||||
XX 18 TGAAGACTTGTCTACAT 1
XX
XX RESULT 2930
XX AAA8376
XX ID AAA8376 standard; DNA; 18 BP.
XX
XX AAA8376;
XX
XX 21-AUG-2000 (first entry)
XX
XX Human Ets-2 phosphorothioate antisense oligonucleotide, SEQ ID NO:35.
XX
XX Ets-2; human; transcription factor; chromosome 21q22.3; cancer; invasion;
XX metastasis; skeletal abnormality; Down's syndrome; expression inhibition;
XX phosphorothioate; antisense; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN US6054316-A.
XX

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PD 25-APR-2000.
XX
XX 25-JUN-1999; 99US-00344579.
XX
XX 25-JUN-1999; 99US-00344579.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowseert LM;
XX
XX WPI, 2000-338495/29.
XX
XX Antisense compound, 8-30 nucleobases in length, inhibiting the expression
XX Ets-2 is useful for treating cancer and detecting Ets-2 expression.
XX
XX Claim 3; Col 39; 31pp; English.
XX
XX Sequences AAA8349-A3838 represent antisense oligonucleotides targeted
XX to the human Ets-2 gene, which inhibit its expression. The antisense
XX oligonucleotides were designed to target different regions of the human
XX Ets-2 RNA, and were analysed for their effect on Ets-2 mRNA levels by
XX quantitative real-time PCR. The Ets-domain transcription factors are a
XX family of proteins which are involved in controlling key cellular events
XX such as proliferation, differentiation and development. The Ets domain is
XX a DNA-binding domain shared by all members of this family. Through this
XX motif, Ets family members bind to the promoter regions of various genes
XX at a GCA consensus sequence, thereby acting as either repressors or
XX activators of the gene. All but one Ets family protein bind to DNA as a
XX monomer. Ets-2 has been implicated in the regulation of cellular
XX proliferation and differentiation. The Ets-2 gene is located at
XX chromosome 21q22.3, which is within a region known to undergo
XX translocations associated with malignancies. Ets-2 has been found to be
XX upregulated in several cancers, including lymphoblastic leukaemia. It may
XX also play a role in the cancer phenotype, as it activates the tyrosine
XX kinase plasmogen activator (uPA) promoter and the promoters of
XX metalloproteinases in response to epidermal growth factor (EGF)
XX stimulation. High levels of uPA and metalloproteinases are associated
XX with tumor invasion and metastasis in breast cancers. As the Ets-2 gene
XX is located on chromosome 21, which is triplicated in Down's syndrome, it
XX is also thought to be responsible for the skeletal abnormalities present
XX in this condition. The antisense oligonucleotides of the invention are
XX useful for the treatment or prophylaxis of conditions associated with Ets
XX -2 expression, especially cancer
XX
XX Sequence 18 BP; 3 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 7231 ATCCCTCTCAAGTCCAGC 7248
XX ||||| ||||| |||||
XX 1 ATCCGCTCTCAAGTCCAGC 18
XX
XX RESULT 2931
XX AAD17190/c
XX ID AAD17190 standard; DNA; 18 BP.
XX
XX AAD17190;
XX
XX 29-NOV-2001 (first entry)
XX
XX S. noursei PKS-encoding MYSC DNA amplifying PCR antisense primer ERD2.
XX
XX Polyketide synthase; PKS; macrocyclic; mycristin; PKS gene cluster;
XX antifungal; antibiotic; enoylreductase; ER; PCR primer; ss.
XX
XX Streptomyces noursei.
XX
XX OS
XX PN WO200159126-A2.
XX
XX 16-AUG-2001.
XX

```

XX 08-FEB-2001; 2001WO-GB000509.  
 XX  
 PF 08-FEB-2000; 2000GB-00002840.  
 XX  
 PR 10-APR-2000; 2000GB-00008786.  
 PR 14-APR-2000; 2000GB-00009387.  
 XX  
 PA (UYNO-) UNIV NORGES TEKNIISK NATURVITENSKAPRELIGE.  
 PA (SNTF-) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIELEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKV/) SEKUROVA O N.  
 PA (FJAE/) FJAEVRIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALT/) VALTA S.  
 XX  
 PI ZOTCHEV SB, SEKUROVA ON, FJAEVRIK E, BRAUTASET T, STROM AR,  
 PI VALTA S, ELLINGSEN TE, SLETTA H, GULLIKSEN O;  
 XX  
 DR WPI; 2001-557614/62.  
 XX  
 PT New mystatin polyketide synthase polynucleotides and polypeptides, useful  
 PT as antibiotics and antifungals.  
 XX  
 PS Example 2; Page 69; 266pp; English.  
 XX  
 CC The present invention relates to the cloning and sequencing of the gene  
 CC cluster encoding a modular type I polyketide synthase (PKS) enzyme  
 CC involved in the biosynthesis of the macrocyclic antibiotic mystatin. The  
 CC mystatin PKS is useful as antifungal antibiotics. The present sequence is  
 CC a PCR primer which is used for the amplification of the DNA fragment  
 CC representing the coding sequence for the C-terminal part of the  
 CC enoylreductase (ER) domain in module 5 of Streptomyces noursei PKS-  
 CC encoding Nysc  
 CC  
 XX  
 SQ Sequence 18 BP; 4 A; 10 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5542 GGTGTCGATCGCAATGG 5559  
 DB 18 GGTGTCGATCGCGCTGG 1  
 RESULT 2932  
 ID AAA46048 standard; DNA; 18 BP.  
 XX  
 AC AAA46048;  
 XX  
 OS  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synthetic oligonucleotide 23.  
 XX  
 KW Synthetic oligonucleotide; dinucleotide repeat; cytosine; apoptosis;  
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;  
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;  
 KW lymphoma; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 PN MO200144465-A2.  
 XX  
 PD 21-JUN-2001.  
 XX  
 PF 12-DEC-2000; 2000WO-CA001467.  
 PF 13-DEC-1999; 99US-0170325P.  
 PR

PR 29-AUG-2000; 2000US-0228925P.  
 XX  
 PA (BION-) BIONICHE LIFE SCI INC.  
 XX  
 PI Phillips MC, Pilon MC;  
 XX  
 DR WPI; 2001-398150/42.  
 XX  
 PT Composition comprising synthetic oligonucleotides which comprise multiple  
 PT repeats of dinucleotides such as GT, TG useful for treating cancer by  
 PT inducing cell cycle arrest, inhibiting proliferation, activating  
 PT caspases.  
 XX  
 PS Example 19; Page 32; 77pp; English.  
 XX  
 CC The present sequence is that of a synthetic oligonucleotide useful to the  
 CC invention. The invention relates to a composition, comprising a 2 to 20  
 CC base 3',-OH, 5'-OH synthetic oligonucleotide which comprises multiple  
 CC repeats of dinucleotides such as GT, TG, etc., according to specific  
 CC formula and having cytosine activity. The oligonucleotide compositions  
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,  
 CC activation of caspases and induction of apoptosis or production of  
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour  
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having  
 CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma  
 CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,  
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis  
 CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(Ink4B), p16(Ink4), drug  
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor  
 CC  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 15 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3623 GGGTGGGGTGGGAGAG 3640  
 DB 1 GGGTGGGGTGGGAGAG 18  
 RESULT 2933  
 ID ABA91529 standard; DNA; 18 BP.  
 XX  
 AC ABA91529;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.  
 XX  
 KW DNA-RNA hybrid; RNase H; nucleic acid detection; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_RNA 8..9  
 FT /\*tag= a  
 FT /label= RNA  
 XX  
 PN WO200206531-A2.  
 XX  
 PD 24-JAN-2002.  
 XX  
 XX 12-JUL-2001; 2001WO-US022166.  
 XX  
 XX 14-JUL-2000; 2000US-00616761.  
 PR 30-MAR-2001; 2001US-00823647.  
 XX  
 PA (GENE-) APPLIED GENE TECHNOLOGIES INC.  
 PA  
 PI Dataagupta N;  
 XX



```
XX WPI; 2002-171819/22.
XX
XX Probes for detecting target nucleotide sequence in sample, has sequence
XX that forms hairpin structure having a double-stranded segment and single-
XX stranded loop collectively forming region complementary to target
XX sequence.
XX
XX Example 4; Page 49; 72pp; English.
XX
XX The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
XX AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
XX to assess the minimum number of ribonucleotides in DNA-RNA chimeric
XX oligonucleotides required for RNase H cleavage. Each oligonucleotide of
XX the set had a different number of ribonucleotides, 2 in the present case.
XX The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
XX (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
XX minutes. The results showed that 4 ribonucleotides were the minimum
XX number for RNA cleavage. The invention provides probes for nucleic acid
XX hybridisation. The probes form a hairpin structure comprising a double-
XX stranded stem and a single-stranded loop, and are capable of both
XX intramolecular and intermolecular hybridisation. The double-stranded stem
XX may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
XX RNase H cleavage. When the probe hybridises with a target DNA, the RNA
XX strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
XX can be removed. Arrays and methods for nucleic acid hybridisation using
XX the probes are provided
XX
XX Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4481
XX ||||| ||||| ||||| |||||
XX 1 TTTT TTTT AATTTT TTTT 18
XX
XX Db
XX
XX RESULT 2934
XX ABL40838
XX ID ABL40838 standard; DNA; 18 BP.
XX
XX ABL40838;
XX
XX 03-JUL-2002 (first entry)
XX
XX P. putida exdB and exdD genes amplifying RT-PCR primer.
XX
XX exdB; exdD; tonB; antibiotic; toluene; pHBA; aromatic compound; parabene;
XX para-hydroxybenzoic acid; RT-PCR; primer; ss.
XX
XX Pseudomonas putida.
XX
XX WO200229034-A2.
XX
XX 11-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US031180.
XX
XX 30-SEP-2000; 2000US-0236879P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Ramos JL, Ben-Bassat A, Godoy P, Ramos-Gonzales MI, Duque E;
XX WPI; 2002-340103/37.
XX
XX Novel isolated nucleic acid of the tonB operon from Pseudomonas, useful
XX for producing transformed bacterial strains which are more sensitive to
XX antibiotics, and toluene.
XX
XX Disclosure; Page 80; 81pp; English.
```

```
XX The invention relates to a novel gene cluster comprising the exdB, exdD
XX and tonB genes from P. putida. These genes are useful for producing
XX bacterial cells more sensitive to antibiotics, toluene, pHBA (para-
XX hydroxybenzoic acid), aromatic compounds, parabenes, and aromatic amino
XX acids. Methods are also provided to identify pHBA tolerant genes, and
XX pHBA tolerant strains, useful for producing pHBA. The present sequence
XX represents a primer for RT-PCR amplification of P. putida exdB and exdD
XX mRNA
XX
XX Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 7419 CAGCAGCAGCAGCAGCAGC 7436
XX ||||| ||||| ||||| |||||
XX 1 CAGCAGCAGCAGCAGCAGC 18
XX
XX Db
XX
XX RESULT 2935
XX AAS62957
XX ID AAS62957 standard; DNA; 18 BP.
XX
XX AAS62957;
XX
XX 29-JAN-2002 (first entry)
XX
XX Esophageal adenocarcinoma diagnostic oligonucleotide #56.
XX
XX Human; cancer; gastrointestinal adenocarcinoma;
XX esophageal adenocarcinoma; gastrointestinal dysplasia;
XX esophageal dysplasia; gastrointestinal metaplasia; diagnostic;
XX Cpg-island methylation; esophageal metaplasia; PCR primer;
XX Barrett's intestinal tissue; loss of heterozygosity; ss.
XX
XX Homo sapiens.
XX
XX WO200175172-A1.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001WO-US010658.
XX
XX 31-MAR-2000; 2000US-0193839P.
XX
XX (USC-) UNIV SOUTHERN CALIFORNIA.
XX
XX Laird P, Bads C;
XX WPI; 2002-010805/01.
XX
XX Diagnosing cancer or cancer-related conditions, e.g., gastrointestinal
XX and esophageal adenocarcinoma, comprises performing methylation assay of
XX a tissue sample obtained from a test tissue or region to be diagnosed.
XX
XX Claim 3; Page 32; 80pp; English.
XX
XX The invention relates to a method of diagnosing cancer or cancer-related
XX conditions from tissue samples. The method comprises obtaining a sample
XX from test tissue or region to be diagnosed, performing a methylation
XX assay of the sample, where the assay determines methylation state of
XX genomic Cpg sequences, and making a diagnostic or prognostic prediction
XX of the cancer based at least in part upon the methylation state of the
XX genomic Cpg sequences. The method is useful for diagnosing cancer or
XX cancer-related conditions such as gastrointestinal or esophageal
XX adenocarcinoma, gastrointestinal or esophageal dysplasia,
XX gastrointestinal or esophageal metaplasia, Barrett's intestinal tissue,
XX pre-cancerous conditions in normal esophageal squamous mucosa, or their
XX combinations, from tissue samples. Preferably, the cancer diagnosed is
XX esophageal adenocarcinoma, and making a diagnostic or prognostic
XX prediction of the cancer, based upon the methylation state of the genomic
```

CC Cpg sequences provides for classification of the adenocarcinoma by grade  
CC or stage. The method provides an opportunity for early intervention, in  
CC patients identified with cancer, or an elevated risk for developing  
CC cancer. Cpg-island methylation can easily be detected in a field of  
CC normal cell contamination as a gain of signal, unlike loss of gene  
CC expression (e.g., loss of heterozygosity (LOH) and deletion analysis),  
CC which is difficult to resolve in a sample with contaminating normal  
CC cells. AAS62902-AAS62966 represent oligonucleotide sequences used in  
CC diagnosis of esophageal adenocarcinoma as described in the method of the  
CC invention  
CC  
XX  
SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
QY  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 2194 GGCATCATCTTCTACCGA 2211  
1 GGCCTCATCTTCTCCCGA 18  
RESULT 2936  
ABLT43181  
ID ABL43181 standard; DNA; 18 BP.  
XX  
AC ABL43181;  
XX  
DT 11-APR-2002 (first entry)  
XX  
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:225.  
XX  
KW Human: chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
KW PCR primer; 88.  
XX  
OS Homo sapiens.  
XX  
PN JF2001321190-A.  
XX  
PD 20-NOV-2001.  
XX  
PE 12-MAR-2001; 2001JP-00068285.  
XX  
PR 10-MAR-2000; 2000JP-00066716.  
XX  
PA (RIKA ) RIKAGAKU KENKYUSHO.  
PA (GENO-) GENOTEX YG.  
XX  
DR WPI; 2002-144136/19.  
XX  
PT Arraying genome clones.  
XX  
PS Claim 4; Page 9; 528pp; Japanese.  
XX  
CC The present invention describes a method of arraying genome clones. The  
CC method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each wells of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634

CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
XX  
SQ Sequence 18 BP; 5 A; 1 C; 11 G; 1 T; 0 U; 0 Other;  
QY  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 6870 GGCAGGAGAGAGGCTGG 6887  
1 GGGAGAGAGAGAGGCTGG 18  
RESULT 2937  
ABT04994  
ID ABT04994 standard; DNA; 18 BP.  
XX  
AC ABT04994;  
XX  
DT 11-OCT-2002 (first entry)  
XX  
DE TNFR1 expression modulation related antisense oligo SEQ ID No 24.  
XX  
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;  
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;  
KW human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200248168-A1.  
XX  
PD 20-JUN-2002.  
XX  
PE 22-OCT-2001; 2001WO-US051224.  
XX  
PR 24-OCT-2000; 2000US-00695451.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Baker BF, Cowseert LM, Zhang H, Dean NM;  
XX  
DR WPI; 2002-583481/62.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding tumor  
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having  
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.  
XX  
PS Example 10; Page 44; 121pp; English.  
XX  
CC The invention relates to an antisense compound 8 to 30 nucleotides in  
CC length targeted to nucleic acid molecule encoding tumour necrosis factor  
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of  
CC TNFR1. The antisense compound is useful for inhibiting the expression of  
CC TNFR1 in cells or tissues. The antisense compound is also useful for  
CC treating an animal (preferably human) having a disease or condition  
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver  
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting  
CC the expression of TNFR1. The antisense compound is useful for  
CC diagnostics, therapeutic, prophylaxis and as research reagents and kits.  
CC This polynucleotide sequence represents a human oligonucleotide relating  
CC to the TNFR1 of the invention  
XX  
SQ Sequence 18 BP; 5 A; 7 C; 6 G; 0 T; 0 U; 0 Other;  
QY  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 7410 CATCAGAGCAGCAGCAG 7427  
1 CACCAGCGGAGCAGCAG 18



AC AB211030;  
 XX  
 DT 16-JUN-2003 (first entry)  
 XX  
 DE Haematopoietic cell proliferation disorder related oligonucleotide #1170.  
 XX  
 XX Human; haematopoietic cell proliferation disorder; cytostatic;  
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KW cytosine methylation state; probe; primer; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0200277272-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002MO-EP003401.  
 XX  
 PR 26-MAR-2001; 2001US-0278333P.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
 PI Lewin A, Lipbacher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
 PI Schwope I, Ziebarth H;  
 XX  
 DR WPI; 2003-018942/01.  
 XX  
 PT Detecting and differentiating between hematopoietic cell proliferative  
 PT disorders, comprising contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX  
 PS Claim 15; Page 77; 117pp; English.  
 XX  
 CC The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. AB209861 to AB21118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the  
 CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferative disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 SQ Sequence 18 BP; 4 A; 11 C; 0 G; 3 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 Db 3210 TGAGAAAGTGGGTGGGAG 3227  
 XX |||||  
 XX 18 TGGGTAAAGTGGGTGGGAG 1  
 XX  
 RESULT 2941  
 XX AB281757  
 XX ID AB281757 standard; DNA; 18 BP.

XX  
 AC AB281757;  
 XX  
 DT 11-JUN-2003 (first entry)  
 XX  
 DE Huntington's disease exon 1 triplet repeat sequence.  
 XX  
 XX Huntington's disease; noctropic; anticonvulsant; huntingtin; human;  
 KM gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN W02003013437-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 07-AUG-2002; 2002MO-US025352.  
 XX  
 PR 07-AUG-2001; 2001US-0310757P.  
 PR 08-AUG-2001; 2001US-0310770P.  
 PR 08-AUG-2001; 2001US-0310889P.  
 PR 04-DEC-2001; 2001US-0337219P.  
 XX  
 XX (UYDE ) UNITV DELAWARE.  
 XX  
 PA Kmliec EB, Parekh-Olmedo H;  
 XX  
 PI WPI; 2003-256478/25.  
 XX  
 DR WPI; 2003-256478/25.  
 XX  
 PT New single stranded oligonucleotides comprising a DNA domain having at  
 PT least one mismatch with respect to the genetic sequence of the  
 PT Huntington's disease gene to be altered, useful for treating or  
 PT preventing Huntington's disease.  
 XX  
 PS Example 1; Page 57; 133pp; English.  
 XX  
 CC The present sequence is an example of a poly-glutamine triplet repeat  
 CC region found in exon 1 of the Huntington's disease (HD) gene. The  
 CC invention is based on the discovery that oligonucleotides can be designed  
 CC to target sequence alterations to the triplet repeat region of the HD  
 CC gene. Preferred oligonucleotides are single-stranded, have at least one  
 CC mismatch with respect to the HD gene region to be altered, and have  
 CC chemical modifications, or are chimeric RNA/DNA oligonucleotides. They  
 CC can be used for the treatment or prevention of HD  
 XX  
 SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 Db 7407 CAACATCAGCAGCAGCAG 7424  
 XX |||||  
 XX 1 CAACATCAGCAGCAGCAG 18  
 XX  
 RESULT 2942  
 XX ADA27361  
 XX ID ADA27361 standard; DNA; 18 BP.  
 XX  
 AC ADA27361;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human microsatellite repeat M2\_3\_8.  
 XX  
 XX de; HLA-related research; HLA class II-associated disease;  
 KM transplantation matching; recombination hot spot identification;  
 KM linkage disequilibrium study; human; microsatellite.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN US2003108940-A1.

```
XX 12-JUN-2003.
PD 06-DEC-2002; 2002US-00314405.
PF 15-NOV-2000; 2000US-00713616.
XX (INOK/) INOKO H.
XX Inoko H, Tamiya G, Matsuzaka Y;
DR WPI; 2003-616782/58.
XX
PT New oligonucleotide primer capable of specifically hybridizing to a DNA
PT having the sequence of the flanking regions of a microsatellite (e.g.
PT M249), useful for HLA-related research, e.g. transplantation matching.
XX
PS Example 2; Page 5; 20pp; English.
XX
CC The invention relates to an oligonucleotide primer capable of
CC specifically hybridizing to a DNA having the sequence of the flanking
CC regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
CC 11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-4-25, M2-4-26, M2-2-
CC 29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-2-36, M2-5-11, M2-2-
CC 46, and M2-2-48. The primer is useful for determining the number of
CC repeat units of the microsatellite cited above. The primer is useful in
CC HLA-related research, such as genetic mapping of HLA class II-associated
CC diseases, transplantation matching, population genetics, and
CC identification of recombination hot spots as well as linkage
CC disequilibrium studies. The present sequence represents the human
CC microsatellite repeat M2_3_8.
XX
SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 65 GCTGCGGGGCGGCGCG 82
DB 1 GCGGCGGCGCGCGCGCG 18
RESULT 2943
ADBS4474
ID ADBS4474 standard; DNA; 18 BP.
AC ADBS4474;
XX
DT 04-DEC-2003 (first entry)
DE Hybridisation oligonucleotide 12 used to analyse genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated Cpg dinucleotide;
KW cytosatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
KW probe.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
PF 27-FEB-2003; 2003WO-EP002035.
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Leeche R;
XX
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.
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XX Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 36; Page 27; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated Cpg
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the hybridisation
CC oligonucleotide of the invention which was used to analyse the genomic
CC DNA region.
XX
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6672 TTGGGGACGTTATTTT 6689
DB 1 TTGGGGAGTGTATTGTT 18
RESULT 2944
ADCS69952
ID ADC69952 standard; DNA; 18 BP.
AC ADC69952;
XX
DT 18-DEC-2003 (first entry)
DE Primer oligo used for analysing Cpg islands in genomic DNA (SeqID 441).
XX
KW PCR; primer; ss; lung cell proliferative disorder; Cpg dinucleotide;
KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
KW cytosine methylation state.
XX
OS Unidentified.
XX
PN WO2003052135-A2.
XX
PD 26-JUN-2003.
PF 10-DEC-2002; 2002WO-EP014026.
PR 14-DEC-2001; 2001DE-01061625.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Field UK, Genc B, Liloglou T, Lipscher E, Maier S;
XX
PI Nimrich I;
XX
DR WPI; 2003-533029/50.
XX
PT Detecting and differentiating cytosine methylation state of genomic DNA,
PT useful for diagnosing, treating prognosticating and/or monitoring lung
PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT carcinoma.
XX
PS Claim 15; SEQ ID NO 441; 58pp; English.
```

CC This invention relates to a novel method for detecting and  
CC differentiating between lung cell proliferative disorders associated with  
CC at least one gene and/or their regulatory regions. Specifically, it  
CC refers to a method comprising contacting a target nucleic acid in a  
CC biological sample with at least one reagent, wherein the reagent is able  
CC to distinguish between methylated and non-methylated CpG dinucleotides  
CC present in the target DNA. As such, it is possible to further  
CC differentiate and diagnose medical conditions including adenocarcinoma  
CC and squamous cell carcinoma, and their respective adjacent lung tissue.  
CC The present invention describes cytosolic oligomers and PNA-oligomers  
CC that are useful as probes for determining the cytosine methylation state  
CC or single nucleotide polymorphisms (SNPs) of the target sequence. This  
CC oligonucleotide sequence is a primer oligomer used for the analysis of  
CC CpG positions within genomic DNA, used in an exemplification of the  
CC invention.

XX  
SQ Sequence 18 BP; 2 A; 0 C; 7 G; 9 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6672 TTGGGCGACGTATTATT 6689  
Db 1 TTGGGCGACGTATTATT 18

RESULT 2945  
ADE43413/C  
ID ADE43413 standard; DNA; 18 BP.  
XX  
AC ADE43413;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human SNCG sequencing primer, SEQ ID 18.  
XX  
KM Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;  
KM Alzheimer's disease; neuroprotective; nootropic; gene therapy;  
KM Chromosome 10; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003054143-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 25-OCT-2002; 2002WO-US034679.  
XX  
PR 25-OCT-2001; 2001US-0339525P.  
PR 08-NOV-2001; 2001US-0336929P.  
PR 08-NOV-2001; 2001US-0338010P.  
PR 09-NOV-2001; 2001US-0338363P.  
PR 04-DEC-2001; 2001US-0337052P.  
PR 28-MAR-2002; 2002US-0368919P.  
XX  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
XX  
PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzl RE, Bertram L;  
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;  
XX  
XX WPI; 2003-559131/52.  
XX  
PT Determining a predisposition for or the occurrence of neurodegenerative  
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid  
PT the presence or absence of an allelic variant of one or more polymorphic  
PT regions.  
XX  
XX Example 2; Page 265; 848bp; English.  
XX  
XX The present invention relates to a method (M1) for determining a  
XX predisposition for or the occurrence of neurodegenerative disease in a

CC subject. The method comprises detecting in a target nucleic acid obtained  
CC from the subject the presence or absence of an allelic variant of one or  
CC more polymorphic regions of one or more genes selected from uPA  
CC (urokinase plasminogen activator), SNCG (gamma-ynuclein), IDE (insulin-  
CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid  
CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the  
CC presence of at least one of the allelic variant of one or more  
CC polymorphic regions is indicative of a predisposition for or the  
CC occurrence of neurodegenerative disease. The genes are all located on  
CC chromosome 10. M1 is useful for determining a predisposition for or the  
CC occurrence of, and for treating neurodegenerative disease, particularly  
CC Alzheimer's disease. The present sequence is a PCR primer, which was used  
CC in the method of the invention.

XX  
SQ Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6860 CTTCTCCCTGGGAGGGA 6877  
Db 18 CTTCTCTCTGGGAGGGA 1

RESULT 2946  
AAN92724  
ID AAN92724 standard; DNA; 19 BP.  
XX  
AC AAN92724;  
XX  
DT 31-OCT-2002 (revised)  
DT 14-MAY-1990 (first entry)  
XX  
XX Probe fixed via 400nt poly-dT linker to a nylon filter to identify target  
DE Beta-thalassemia allele.  
XX  
KM Probe; fixed; oligo-nucleotide; hybridisation; ss.  
XX  
OS Synthetic.  
XX  
PN WO8911548-A.  
XX  
PD 30-NOV-1989.  
XX  
PF 18-MAY-1989; 89WO-US002170.  
XX  
PR 20-MAY-1988; 88US-00197000.  
PR 04-MAY-1989; 89US-00347495.  
XX  
PA (CETU) CETUS CORP.  
XX  
XX Saliki RK, Erlich HA;  
XX  
XX WPI; 1989-370739/50.  
XX  
PT Assay reagent contg. oligo-nucleotide probe attached via spacer - each  
PT probe having hybridisation region complementary to specific analyte  
PT sequence, e.g. for diagnosis of genetic disease.  
XX  
XX Example; Page 29; 47bp; English.  
XX  
CC Probe fixed to a filter allows simultaneous non radioactive detection of  
CC 50 or more specific nucleotide sequences in a single test sample.  
CC (Updated on 31-OCT-2002 to add missing OS field.)  
XX  
SQ Sequence 19 BP; 5 A; 2 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6716 CAGATGTAAGTGAAT 6733



DR WPI; 1993-382240/48.  
 XX Detection method of gene without using radio-isotope - by hybridisation  
 PT of nucleic acid probe which is single strand having complementary  
 XX sequence of gene and single strand denatured sample DNA.  
 PS Disclosure; Page 21; 26pp; Japanese.  
 XX  
 CC The sequences (AA053077-Q53136) are used in the invention to detect  
 CC specific genes without the use of radio-isotopes. Detection is carried  
 CC out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic  
 CC acid probe, complementary to the target sequence. Hybridisation occurs on  
 CC the surface of an electrode or optical fibre and detection is visualised  
 CC by the addition of an entity that recognises (ds) hybridised DNA and is  
 CC electrochemically / photochemically active  
 XX  
 SQ Sequence 19 BP; 3 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 510 CACTGTCAAGCACTGCC 527  
 Db 19 CCCTGTCAAGCACTGCC 2  
 RESULT 2950  
 ID AAA85905  
 XX AAA85905 standard; DNA; 19 BP.  
 AC  
 XX AAA85905;  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Cdc 25 hs ribozyme binding site #13.  
 XX  
 KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 OS Mammalia.  
 XX  
 PN WO200032765-A2.  
 PD 08-JUN-2000.  
 XX  
 PF 06-DEC-1999; 99WO-US028772.  
 XX  
 PR 04-DEC-1998; 98US-0110954P.  
 XX  
 PA (IMMU-) IMMUSOL INC.  
 PI Tiltz R, Welch PJ, Barber JR, Robbins JM;  
 XX  
 DR WPI; 2000-412314/35.  
 XX  
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 PT PCNA and Cyclin B1.  
 XX  
 PS Disclosure; Page 99; 109pp; English.  
 XX  
 CC The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 XX  
 SQ Sequence 19 BP; 3 A; 8 C; 1 G; 7 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Query Match 0.2%; Score 14.8; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1215 TACCTACCTTCCCTTGA 1232  
 Db 1 TACCTCTTTTCCCTTGA 18  
 RESULT 2951  
 ID AAA82490/C  
 XX AAA82490 standard; DNA; 19 BP.  
 AC  
 XX AAA82490;  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE cdk1 ribozyme binding site #76.  
 XX  
 KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 OS Mammalia.  
 XX  
 PN WO200032765-A2.  
 PD 08-JUN-2000.  
 XX  
 PF 06-DEC-1999; 99WO-US028772.  
 XX  
 PR 04-DEC-1998; 98US-0110954P.  
 XX  
 PA (IMMU-) IMMUSOL INC.  
 PI Tiltz R, Welch PJ, Barber JR, Robbins JM;  
 XX  
 DR WPI; 2000-412314/35.  
 XX  
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
 PT PCNA and Cyclin B1.  
 XX  
 PS Disclosure; Page 47; 109pp; English.  
 XX  
 CC The present invention relates to a hairpin or hammerhead ribozyme,  
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in  
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for  
 CC inhibiting restenosis by introduction of the ribozyme into cells. The  
 CC ribozyme is resistant to endonuclease activity and hence is efficient in  
 CC restenosis treatment  
 XX  
 SQ Sequence 19 BP; 9 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 6736 CTTCCTTTTAAATCTG 6753  
 Db 19 CTTCCTTTTAAATCTG 2  
 RESULT 2952  
 ID AAA85904  
 XX AAA85904 standard; DNA; 19 BP.  
 AC  
 XX AAA85904;  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Cdc 25 hs ribozyme binding site #12.  
 XX  
 KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.



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XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DR
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PT PCNA and Cyclin B1.
XX PS Disclosure; Page 99; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX CC Representative examples of ribozyme recognition sites are given in
XX CC AA82415 to AA86787. The ribozyme of the invention is useful for
XX CC inhibiting restenosis by introduction of the ribozyme into cells. The
XX CC ribozyme is resistant to endonuclease activity and hence is efficient in
XX CC restenosis treatment
XX SQ Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1215 TACCTACCTTCCCTAGA 1232
Db 2 TACCTCTTCCCTAGA 19

RESULT 2953
AAZ71461
ID AAZ71461 standard; DNA; 19 BP.
XX AC AAZ71461;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:5817.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;

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XX DR WPI; 2000-013267/01.
XX PT Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX PS Claim 8; Page 1471; 2745pp; English.
XX CC AA265654 to AA269578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AA269579 to AAZ77440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterisation of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence Listing from the
XX CC present invention
XX SQ Sequence 19 BP; 0 A; 7 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5702 GCCTTCTTTCCTTC 5719
Db 1 GCCTTCTTTCCTTC 18

RESULT 2954
AAC65640/C
ID AAC65640 standard; DNA; 19 BP.
XX AC AAC65640;
XX DT 16-FEB-2001 (first entry)
XX DE Human AFLP primer E51.
XX KW Human; AFLP; polymorphic loci; SNP; single nucleotide polymorphism;
XX KW amplification fragment length polymorphism; genetic marker; primer; ss.
XX OS Homo sapiens.
XX PN WO200061801-A2.
XX PD 19-OCT-2000.
XX PF 10-APR-2000; 2000WO-NL000235.
XX PR 09-APR-1999; 99EP-00201112.
XX PA (KEYG-) KEYGENE NV.
XX PI Kuiper MTR, Witsenboer H;
XX DR WPI; 2000-679499/66.
XX PF Detecting and analyzing genotypes of polymorphic loci amplified in a
XX PT mixture of amplified restriction fragments, particularly amplification
XX PT fragment length polymorphism fragments using primer extension techniques.
XX PS Example 1; Page 17; 28pp; English.
XX CC This invention describes a novel method for determining (D) genotypes of
XX CC polymorphic loci amplified in a restriction fragment mixture (M), using
XX CC an oligonucleotide sequence (OS) complementary to part of target

```

CC restriction fragment (TF), and located adjacent to polymorphism to be  
 CC detected. The method involves hybridization of TP and OS, adding labeled  
 CC nucleotide (N) or its analog (A) to (M), to extend OS, and detecting the  
 CC hybrid and/or of OS with (N) or (A). The method is useful for detecting  
 CC single nucleotide polymorphisms in constant amplification fragment length  
 CC polymorphism-fragments. The method is useful for detecting single  
 CC nucleotide polymorphisms (SNPs) located in constant amplification  
 CC fragment length polymorphism (AFLP) fragments such that useful non-  
 CC polymorphic bands, which ordinarily do not provide any useful information  
 CC when conventional AFLP-finger printing is used, are made. SNPs are also  
 CC informative as genetic markers

SO Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1826 TGGGAATGGCTACGCAGT 1843  
 19 TGGGAATTGTTACGCAGT 2

RESULT 2955  
 AAS42915  
 ID AAS42915 standard; DNA; 19 BP.  
 AC AAS42915;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human G Protein-Coupled Receptor (GPCR) PCR primer #49.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;  
 KW attention deficit disorder; anxiety; depression; bipolar disorder; ss;  
 KW neurological disorder; Huntington's disease; dementia; obesity; anorexia;  
 KW metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;  
 KW type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;  
 KW cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;  
 KW viral infection; immunostimulant; neuroleptic; nootropic; tranquilizer;  
 KW antidepressant; anorectic; PCR primer; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200162797-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-US005676.  
 XX  
 PR 23-FEB-2000; 2000US-0184247P.  
 PR 23-FEB-2000; 2000US-0184303P.  
 PR 23-FEB-2000; 2000US-0184304P.  
 PR 23-FEB-2000; 2000US-0184305P.  
 PR 23-FEB-2000; 2000US-0184397P.  
 PR 02-MAR-2000; 2000US-0186457P.  
 PR 03-MAR-2000; 2000US-0186810P.  
 PR 09-MAR-2000; 2000US-0188064P.  
 PR 13-MAR-2000; 2000US-0188880P.  
 PR 03-APR-2000; 2000US-0194344P.  
 PR 23-JUN-2000; 2000US-0213861P.  
 PR 11-JUL-2000; 2000US-0217369P.  
 PR 11-JUL-2000; 2000US-0217370P.  
 PR 14-JUL-2000; 2000US-0218337P.  
 PR 20-JUL-2000; 2000US-0218492P.  
 XX  
 PA (PHMA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Vogel I G, Wood LS, Parodi LA, Lind P;  
 XX  
 DR WPI; 2001-570628/64.  
 XX  
 PT New isolated nucleic acid encoding a new G-protein coupled receptor

PT polypeptide for detecting receptor modulators that can treat mental  
 PT disorders, such as schizophrenia, anxiety, depression, or obesity.  
 XX  
 PS Example 5; Page 124; 279pp; English.  
 XX  
 CC Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for  
 CC cDNA molecules encoding human G-protein coupled receptor (GPCR)  
 CC polypeptides. The protein and DNA sequences of the invention can be used  
 CC to identify compounds which bind to GPCR polypeptides and in screening  
 CC for compounds that modulate GPCR activity. By screening a human subject  
 CC for the presence of mutations in GPCR DNA, a GPCR-related disorder or a  
 CC genetic predisposition can be diagnosed. The sequences can also be used  
 CC for treatment and prevention of mental disorders such as schizophrenia,  
 CC attention deficit disorder, anxiety, depression, dementia and bipolar  
 CC disorder, neurological disorders such as Huntington's disease,  
 CC Parkinson's disease and Tourette's syndrome, metabolic disorders such as  
 CC obesity, anorexia and type 2 diabetes, cardiovascular disorders such as  
 CC thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,  
 CC viral infections caused by HIV and cancers

SO Sequence 19 BP; 7 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 3638 AGGAGGTAGTGGGAG 3655  
 1 AGCAGGTAGTGGGAG 18

RESULT 2956  
 AAC83562  
 ID AAC83562 standard; DNA; 19 BP.  
 AC AAC83562;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE DNA synthesis method linker/primer sequence SEQ ID NO: 1.  
 XX  
 KW DNA synthesis; directional complementary DNA library; linker; PCR primer;  
 KW ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6143531-A.  
 XX  
 PD 07-NOV-2000.  
 XX  
 PF 22-JUL-1997; 97US-00899029.  
 XX  
 PR 19-SEP-1988; 88US-00246567.  
 PR 02-MAY-1991; 91US-00700066.  
 PR 23-NOV-1992; 92US-00981931.  
 PR 02-SEP-1993; 93US-00116049.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Hansen CJ, Huse WD;  
 XX  
 DR WPI; 2001-006435/01.  
 XX  
 PT Double stranded DNA synthesis with specific orientation comprises  
 PT synthesizing a first strand of DNA complementary to a selected DNA or RNA  
 PT template and synthesizing second strand complementary to first one.  
 XX  
 PS Example 1; Fig 1; 14pp; English.  
 XX  
 CC The present invention describes an improved method of DNA synthesis which  
 CC provides double stranded DNA where the predetermined orientation of the  
 CC sequence is preserved. This can be used in the construction of  
 CC complementary DNA and directional DNA libraries



CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention

XX  
SQ Sequence 19 BP; 9 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6736 CTTCCTCTTAATCTG 6753  
Db 19 CTTCCTTTTGAATCTG 2

RESULT 2959  
AAH61066  
ID AAH61066 standard; DNA; 19 BP.  
XX  
AC AAH61066;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cdc25 hs ribozyme binding site SEQ ID NO:3490.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KM recognition site; target; ribozyme binding site; eye disease; vulnery;  
KM proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KM cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KM matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KM antiproliferative; dermatological; antiseborrheic; antidiabetic; vitruide;  
KM anti-itching; ophthalmological; keratolytic; gene therapy; viral wart;  
KM atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KM basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
KM sickle cell retinopathy; ss.

OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200130362-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US029500.  
XX  
PR 26-OCT-1999; 99US-0161532P.  
XX  
PA (IMMU-) IMMUSOL INC.  
XX  
PI Robbins JM, Tiltz R;  
XX  
DR WPI; 2001-300427/31.  
XX  
PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX  
PS Example 1, Page 325; 408pp; English.

XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,  
CC ophthalmological, vulnery, keratolytic and vitruide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention

XX  
SQ Sequence 19 BP; 3 A; 9 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1215 TACCTACCTCCCTAGA 1232  
Db 2 TACCTCCTTCCCTAGA 19

RESULT 2960  
AAS09985  
ID AAS09985 standard; DNA; 19 BP.  
XX  
AC AAS09985;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE PCR primer P4 used in RT-PCR-SSCP of PAX2 exon 8.

XX PAX2; mouse; PCR primer; nervous system; excretory system;  
XX optic nerve coloboma; renal hyperplasia; apoptosis; chemotherapy;  
KM radiation therapy; cancer; prostate; ovary; bladder; kidney;  
KM cystic kidney disease; ss.

XX  
OS Mus musculus.  
XX  
PN WO200146405-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 21-DEC-2000; 2000MO-CA001545.  
XX  
PR 22-DEC-1999; 99US-0171443P.  
XX  
PR 24-JUL-2000; 2000US-0220161P.  
XX  
PA (UYMC-) UNITV MCGILL.  
XX  
PI (UYOT-) UNITV OTAGO.  
XX  
PI Goodyer P, Eccles RM, Torban E;  
XX  
DR WPI; 2001-441672/47.

XX  
PT Modulating resistance to apoptosis, rescuing cells from apoptosis,  
PT enhancing resistance of normal tissues to apoptotic cell death induced by  
PT chemo- or radiation therapy in patients by using PAX-2 function  
PT modulators.

XX  
PS Disclosure; Page 23; 45pp; English.

XX The sequence represents PCR primer P4 used in reverse transcription PCR  
CC single strand conformation polymorphism (RT-PCR-SSCP) of PAX2 exon 8.  
CC PAX2 is a transcription factor involved in the development of the nervous  
CC and excretory systems and mutations of PAX2 have been associated with  
CC optic nerve colobomas and renal hyperplasia. These mutations are  
CC associated with increased apoptosis. The method of the invention involves  
CC modulating resistance to apoptosis, rescuing cells from apoptosis, and  
CC enhancing resistance of normal tissues to apoptotic cell death induced by  
CC chemotherapy or radiation therapy. This is achieved by administering to a  
CC patient, a nucleic acid (I) encoding a molecule which selectively  
CC inhibits and/or prevents the function of the PAX2 gene. The method can be  
CC used to modulate resistance to apoptosis of cancer cells (prostate,  
CC ovarian, bladder, kidney cancer cells and/or cystic kidney diseases) or  
CC cystic kidney cells in a patient in which PAX2 is expressed at higher  
CC level than in a healthy patient, for rescuing cells from apoptosis in a

CC patient, and for enhancing resistance of normal tissues to apoptotic cell  
 CC death induced by chemotherapy or radiation therapy. (1) is also useful  
 CC for treating cancer in a cystic kidney disease in a patient  
 XX  
 SQ Sequence 19 BP; 3 A; 1 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2872 AGGAGGAGTGGGTAG 2889  
 ||| |||||  
 Db 2 AGGGTGGAGTGGGTAG 19

RESULT 2961  
 ABL88900  
 ID ABL88900 standard; DNA; 19 BP.  
 XX  
 AC ABL88900;

DT 22-MAY-2002 (first entry)

DE HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO.122.

KM Binding molecule; HIV-1; human immunodeficiency virus type 1;  
 KM reverse transcriptase; binding group; ss.

OS Human immunodeficiency virus 1.  
 OS Synthetic.

XX EP1174518-A1.

XX 23-JAN-2002.

XX 20-JUL-2000; 2000EP-00202611.

XX 20-JUL-2000; 2000EP-00202611.

XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.

PI Loukachov VV, Van Gemen B, Goudamlt J;

XX WPI; 2002-156696/21.

PT Collection of binding groups for determining or typing samples,  
 PT especially clinical samples, has groups capable to identify essentially  
 PT all members of the family of nucleic acids of relatively high  
 PT significance.

XX Disclosure; Page 36; 16pp; English.

CC The present invention describes a collection of binding groups for a  
 CC family of nucleic acids comprising members of relative high and relative  
 CC low significance, where the binding groups are selected to be capable to  
 CC identify, alone or in combination, essentially all members of the family  
 CC of nucleic acids of relatively high significance. The collection of  
 CC binding groups is useful for typing of nucleic acid in a clinical sample,  
 CC by contacting the nucleic acid with the collection and determining  
 CC whether one or more binding groups bound to the nucleic acid of the  
 CC sample. This method is useful for determining whether the sample  
 CC comprises at least a part of a member of relatively high significance  
 CC of a family of nucleic acids. The collection of binding groups is useful for  
 CC diagnosing the severity of a disease caused by a pathogen containing a  
 CC member of a family of nucleic acids. ABL88779 to ABL89321 represent  
 CC oligonucleotide sequences used in the exemplification of the present  
 CC invention

XX Sequence 19 BP; 12 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6170 CATTAAGAAAAGATG 6187  
 |||||  
 Db 2 CATTAAGAAAAGATG 19

RESULT 2962  
 ABA97625/C  
 ID ABA97625 standard; DNA; 19 BP.  
 XX  
 AC ABA97625;

DT 11-APR-2002 (first entry)

XX Probe d.

XX ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

XX JP2001286300-A.

XX 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

XX 24-AUG-1999; 99JP-00236666.

XX 30-AUG-1999; 99JP-00242693.

XX 01-FEB-2000; 2000JP-00028896.

XX (BIOT-) BIOINDUSTRI KYOKAI SH.

XX (KANK-) KANKYO ENG KK.

XX (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.

XX WPI; 2002-134193/18.

XX Example 5; Page 17; 34pp; Japanese.

CC This invention relates to a method for measuring nucleic acids using a  
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
 CC decreases the fluorescence of the fluorochrome when hybridised with a  
 CC target nucleic acid, the decrease in the fluorescence is measured. The  
 CC method can be used for measuring a target nucleic acid  
 CC  
 SQ Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6682 TTATTTTATTTATAT 6699  
 |||||  
 Db 19 TTTTATTTTATTTATAT 2

RESULT 2963  
 AAL51775/C  
 ID AAL51775 standard; DNA; 19 BP.

XX AAL51775;

DT 24-APR-2003 (first entry)

XX TNF alpha PCR primer #2.

XX Screening; G protein-coupled receptor; cholesterol metabolism; ss;

XX inflammatory disease; transplantation rejection; immune insufficiency;  
 XX infection; PCR; primer; TNF alpha.

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OS Unidentified.
XX
XX WO200284286-A1.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-JP003613.
XX
XX 12-APR-2001; 2001JP-00114203.
XX 14-JUN-2001; 2001JP-00180562.
XX 16-JUL-2001; 2001JP-00214922.
XX 27-DEC-2001; 2001JP-00397767.
XX 22-FEB-2002; 2002JP-00045728.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Fujii R, Kawamata Y, Miwa M, Hosoya M,
XX
XX WPI; 2003-075569/07.
XX
XX Screening method for agonists or antagonists to alter binding properties
XX of novel G protein-coupled receptor protein in controlling cholesterol
XX metabolism, used to diagnose and treat inflammatory diseases or
XX infections.
XX
XX Disclosure; Page 174; 186pp; Japanese.
XX
XX The invention comprises a method for screening for compounds that are
XX capable of changing the binding properties of a G protein-coupled
XX receptor protein. The method of the invention is useful for screening
XX agonists or antagonists to alter binding properties of novel G protein-
XX coupled receptor proteins in controlling cholesterol metabolism. The
XX method of the invention is useful in the diagnosis and treatment of
XX inflammatory diseases, excessive immune reaction after transplantation,
XX immune insufficiency and infections. The present DNA sequence represents
XX a TNF alpha PCR primer
XX
XX Sequence 19 BP; 2 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1269 GAAGCTGACGACGACCA 1286
XX 18 GAAGCTGACGACCA 1
XX
XX RESULT 2964
XX ADA25292/c
XX ID ADA25292 standard; RNA; 19 BP.
XX
XX ADA25292;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human PKC-alpha short interfering nucleic acid target SEQ ID NO:23.
XX
XX short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
XX RNA interference; cytostatic; vasotrophic; nephrotropic; modulation;
XX inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
XX prostate cancer; glioblastoma; proliferative disease; restenosis;
XX polycystic kidney disease; human; ribozyme; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070983-A1.
XX
XX 28-AUG-2003.
XX
XX 11-FEB-2003; 2003WO-US004034.
XX

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PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0366782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 03-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 18-SEP-2002; 2002US-0411707P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mewswigen J, Beigelman L;
XX
XX WPI; 2003-679891/64.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer and restenosis, downregulates expression of the
XX protein kinase C-alpha gene.
XX
XX Example 3; Page 118; 143pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
XX that downregulates expression of a protein kinase C-alpha (PKC-alpha)
XX gene by RNA interference. Also described: (1) a siNA that modulates
XX expression and/or activity of genes for other isoforms of PKC or genes
XX involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
XX siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
XX express siNA. The siNA sequences have cytostatic, vasotropic and
XX nephrotropic activities, and can be used in the modulation (inhibition)
XX of expression of the PKC-alpha gene by RNA interference. The siNA can be
XX used to modulate expression of PKC-alpha genes. They are potentially
XX useful in treating a variety of cancers including e.g. breast cancer,
XX cancers of the head and neck, ovarian cancer, lung cancer, prostate
XX cancer, and glioblastoma and for treating other proliferative diseases
XX and conditions, such as restenosis and polycystic kidney disease. The
XX siNA may also be useful for diagnosis, drug screening, target
XX identification and validation, genetic engineering, studying gene
XX function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
XX The present sequence represents a human PKC-alpha siNA target, which is
XX used in the exemplification of the present invention.
XX
XX Sequence 19 BP; 6 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 1.9e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3937 TCCCTTGATGCTAAGTC 3954
XX 19 TCCCTTGATGATAGTC 2
XX
XX RESULT 2965
XX ADA25417
XX ID ADA25417 standard; RNA; 19 BP.
XX
XX ADA25417;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human PKC-alpha short interfering nucleic acid SEQ ID NO:148.
XX
XX short interfering nucleic acid; siNA; protein kinase C alpha; PKC-alpha;
XX RNA interference; cytostatic; vasotrophic; nephrotropic; modulation;
XX inhibition; cancer; breast cancer; ovarian cancer; lung cancer;
XX prostate cancer; glioblastoma; proliferative disease; restenosis;
XX polycystic kidney disease; human; ribozyme; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO2003070983-A1.
XX

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PD 28-AUG-2003.
XX
XX 11-FEB-2003; 2003WO-US004034.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 18-SEP-2002; 2002US-0411707P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswigen J, Beigelman L;
XX
XX WPI; 2003-679891/64.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of cancer and restenosis, downregulates expression of the
XX protein kinase C-alpha gene.
XX
XX Example 3; Page 118; 143pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
XX that downregulates expression of a protein kinase C-alpha (PKC-alpha)
XX gene by RNA interference. Also described: (1) a siNA that modulates
XX expression and/or activity of genes for other isoforms of PKC or genes
XX involved in the PKC pathway; (2) kits for in vitro or in vivo delivery of
XX siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that
XX express siNA. The siNA sequences have cytostatic, vasotropic and
XX nephroretropic activities, and can be used in the modulation (inhibition)
XX of expression of the PKC-alpha gene by RNA interference. The siNA can be
XX used to modulate expression of PKC-alpha genes. They are potentially
XX useful in treating a variety of cancers including e.g. breast cancer,
XX cancers of the head and neck, ovarian cancer, lung cancer, prostate
XX cancer, and glioblastoma and for treating other proliferative diseases
XX and conditions, such as restenosis and polycystic kidney disease. The
XX siNA may also be useful for diagnosis, drug screening, target
XX identification and validation, genetic engineering, studying gene
XX function, and for gene mapping (e.g. of single-nucleotide polymorphisms).
XX The present sequence represents a human PKC-alpha siNA, which is used in
XX the exemplification of the present invention.
XX
XX Sequence 19 BP; 4 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 61.1%; Pred. No. 1.9e+03;
XX Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3937 TCCCTTGATGCTCAAGTC 3954
XX :|||:|||||:|
XX 1 UCCCUUGAGUAGUAAAGUC 18
XX
XX RESULT 2966
XX ADE27307
XX ID ADE27307 standard; RNA; 19 BP.
XX
XX AC ADE27307;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:251.
XX
XX short interfering nucleic acid; siNA, downregulation; inhibition; SCD;
XX stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
XX antiatherosclerotic; cytostatic; virucide; obesity; diabetes;
XX atherosclerosis; cancer; viral infection; drug screening;
XX genetic engineering; pharmacogenomic; gene mapping; ss.
XX
XX Synthetic.
XX

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XX
XX WPI; 2003-679891/64.
XX
XX Mcswigen J, Beigelman L, Thompson J;
XX
XX WPI; 2003-721687/68.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
XX diagnosis of obesity or diabetes, downregulates expression of the
XX stearoyl-CoA desaturase gene.
XX
XX Example 3; SEQ ID NO 251; 139pp; English.
XX
XX The present invention describes a short interfering nucleic acid (siNA)
XX that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
XX by RNA interference. Also described: (1) modulating expression of SCD
XX genes in cells, tissue explants or organisms by introduction of siNA; (2)
XX kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
XX complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
XX siNAs have anorectic, antidiabetic, antiatherosclerotic, cytostatic and
XX virucide activities. The siNAs can be used to modulate expression of SCD
XX genes, in cells, tissue explants or organisms, e.g. for treating obesity;
XX diabetes (types I and II); atherosclerosis; cancer and viral infections.
XX CC They can also be used for drug screening; diagnosis; target
XX identification and validation; genetic engineering; pharmacogenomics;
XX studying gene function and gene mapping (e.g. of single-nucleotide
XX polymorphisms). The present sequence represents an SCD siNA, which is
XX used in the exemplification of the present invention.
XX
XX Sequence 19 BP; 1 A; 0 C; 3 G; 0 T; 15 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 5.6%; Pred. No. 1.9e+03;
XX Matches 1; Conservative 15; Mismatches 2; Indels 0; Gaps 0;
XX
XX 4471 TTTT TTTT TTTT TTTT GCTT 4488
XX :|:|:|:|:|:|:|:|:|
XX 1 UUUUUUUUUUUUUUGGUU 18
XX
XX RESULT 2967
XX ADE27597/c
XX ID ADE27597 standard; RNA; 19 BP.
XX
XX AC ADE27597;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:541.
XX
XX short interfering nucleic acid; siNA, downregulation; inhibition; SCD;
XX stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
XX antiatherosclerotic; cytostatic; virucide; obesity; diabetes;
XX atherosclerosis; cancer; viral infection; drug screening;
XX genetic engineering; pharmacogenomic; gene mapping; ss.
XX
XX Synthetic.
XX

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PN W02003070865-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 13-FEB-2003; 2003WO-US004317.  
 XX  
 PR 20-FEB-2002; 2002US-0358560P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 20-SEP-2002; 2002US-0412304P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Thompson J;  
 XX  
 DR WPI; 2003-721687/68.  
 XX  
 PT New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of obesity or diabetes, downregulates expression of the  
 PT stearyl-CoA desaturase gene.  
 XX  
 PS Example 3; SEQ ID NO 541; 139pp; English.  
 XX  
 CC The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of the SCD (stearyl-CoA desaturase) gene  
 CC by RNA interference. Also described: (1) modulating expression of SCD  
 CC genes in cells, tissue explants or organisms by introduction of siNA; (2)  
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
 CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and  
 CC virucide activities. The siNAs can be used to modulate expression of SCD  
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;  
 CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
 CC They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents an SCD siNA, which is  
 CC used in the exemplification of the present invention.  
 XX  
 SQ Sequence 19 BP; 15 A; 3 C; 0 G; 0 T; 1 U; 0 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4471 TTTTCTTTTCTCTT 4488  
 DB 19 TTTTCTTTTCTCTT 2

RESULT 2968  
 AAN81957/c  
 ID AAN81957 standard; DNA; 20 BP.  
 AC  
 XX AAN81957;  
 AC  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-OCT-1990 (first entry)  
 XX  
 DE Probe pool LFI to detect Human Lymphocyte Function Associated Antigen-3.  
 XX  
 KM Lymphocyte function associated antigen-3; adhesion inhibition; probe;  
 KM T-lymphocytes; immune suppression; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W08809820-A.  
 XX  
 PD 15-DEC-1988.

XX  
 PF 03-JUN-1988; 88WO-US001924.  
 XX  
 PR 03-JUN-1987; 87US-00057615.  
 XX  
 PA (BIOJ ) BIOGEN NV.  
 PA (DAND ) DANA FARBER CANCER INST.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Wallner BP, Springer TA, Hession C, Tizard R, Mattaliano R;  
 XX  
 DR WPI; 1988-368634/51.  
 XX  
 PT DNA sequences encoding lymphocyte function associated antigen-3 - which  
 PT inhibits adhesion between T-lymphocytes and target cells.  
 XX  
 PS Disclosure; Page 7; 46pp; English.  
 XX  
 CC Probe pool LFI is a 32-fold degenerate 20-mer. Probe was labelled with  
 CC gamma-32P-ATP and polynucleotide kinase. It was used together with pool  
 CC LFI2 (AAN81958) for screening libraries. See also AAN81956-N81958; esp.  
 CC AAN81958. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 20 BP; 1 A; 3 C; 1 G; 10 T; 0 U; 5 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 2e+03;  
 Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 6344 AACATAAGCCGAGAGAGT 6363  
 DB 20 AATGAAACCAACAAAGT 1

RESULT 2969  
 AAQ03650  
 ID AAQ03650 standard; DNA; 20 BP.  
 AC  
 XX AAQ03650;  
 AC  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-AUG-1990 (first entry)  
 XX  
 DE Probe NN-D for use in Church-Gilbert sequencing of cDNA encoding PI-  
 DE linked LFA-3.  
 XX  
 KM PI-linked lymphocyte function associated antigen 3 polypeptide;  
 KM phage lambda P24; T-cells; autoimmune disease; graft versus host disease;  
 KM allograft rejection; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W09002181-A.  
 PN  
 PD 08-MAR-1990.  
 XX  
 PF 24-AUG-1989; 89WO-US003652.  
 XX  
 PR 26-AUG-1988; 88US-00237309.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA  
 PI Wallner BP, Hession C;  
 XX  
 DR WPI; 1990-099405/13.  
 XX  
 PT New DNA sequences and recombinant DNA - expressing PI-linked lymphocyte  
 PT function associated antigen-3 polypeptide.  
 XX  
 PS Disclosure; Fig 5; 34pp; English.  
 XX



CC Probe NN-D for was used along with 3 other 20-nucleotide long probes, and  
 CC NotI digestion, for sequencing by Church-Gilbert approach, of the ends of  
 CC an inserted sequence in pNN01. This plasmid is a subclone of P24 contg.  
 CC cDNA encoding PI-linked LFA-3. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 CC XX

SQ Sequence 20 BP; 3 A; 1 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

OY 7307 CTTTGAGATTGTGTTG 7324  
 Db 1 CTTTGAGATTGTGTTG 18

RESULT 2970  
 AAQ03648/C  
 ID AAQ03648 standard; DNA; 20 BP.

AC AAQ03648;

DT 25-MAR-2003 (revised)  
 DT 07-AUG-1990 (first entry)

DE Probe NN-B for use in Church-Gilbert sequencing of cDNA encoding PI-  
 DE linked LFA-3.

KW PI-linked lymphocyte function associated antigen 3 polypeptide;  
 KW phage lambda P24; T-cells; autoimmune disease; graft versus host disease;  
 KW allograft rejection; ss.

OS Homo sapiens.

PN WO9002181-A.

PD 08-MAR-1990.

PF 24-AUG-1989; 89WO-US003652.

PR 26-AUG-1988; 88US-00237309.

PA (BIOJ ) BIOGEN INC.

PI Wallner BP, Hession C;

DR WPI; 1990-099405/13.

PT New DNA sequences and recombinant DNA - expressing PI-linked lymphocyte  
 PT function associated antigen-3 polypeptide.

PS Disclosure; Fig 5; 34pp; English.

CC Probe NN-B for was used along with 3 other 20-nucleotide long probes, and  
 CC NotI digestion, for sequencing by Church-Gilbert approach, of the ends of  
 CC an inserted sequence in pNN01. This plasmid is a subclone of P24 contg.  
 CC cDNA encoding PI-linked LFA-3. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 CC XX

SQ Sequence 20 BP; 8 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

OY 7307 CTTTGAGATTGTGTTG 7324  
 Db 20 CTTTGAGATTGTGTTG 3

RESULT 2971  
 AAQ03651/C

ID AAQ03651 standard; DNA; 20 BP.

AC AAQ03651;

DT 25-MAR-2003 (revised)

DT 07-AUG-1990 (first entry)

DE Probe LF-1 for cDNA encoding PI-linked LFA-3 (3'-5').

KW PI-linked lymphocyte function associated antigen 3 polypeptide;  
 KW phage lambda P24; T-cells; autoimmune disease; graft versus host disease;  
 KW allograft rejection; ss.

OS Homo sapiens.

PN WO9002181-A.

PD 08-MAR-1990.

PF 24-AUG-1989; 89WO-US003652.

PR 26-AUG-1988; 88US-00237309.

PA (BIOJ ) BIOGEN INC.

PI Wallner BP, Hession C;

DR WPI; 1990-099405/13.

PT New DNA sequences and recombinant DNA - expressing PI-linked lymphocyte  
 PT function associated antigen-3 polypeptide.

PS Disclosure; Fig 5; 34pp; English.

CC Probe LF-1 is a 32-fold degenerate 20-mer derived from the sequence of  
 CC LFA-3 purified from human erythrocytes. The probe was used to screen  
 CC libraries of PBL cDNA for clones encoding PI-linked LFA-3. (Updated on 25  
 CC -MAR-2003 to correct PA field.)  
 CC XX

SQ Sequence 20 BP; 1 A; 3 C; 1 G; 10 T; 0 U; 5 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 65.0%; Pred. No. 2e+03; Mismatches 5; Indels 0; Gaps 0;

OY 6344 AACATAAGCCGAGAAGT 6363  
 Db 20 AAYAGRAARACRAARAAGT 1

RESULT 2972  
 AAQ14994/C  
 ID AAQ14994 standard; DNA; 20 BP.

AC AAQ14994;

DT 24-FEB-1992 (first entry)

DE Oligonucleotide #9 for modulating HIV-1 gag/pol frameshifting.

KW human immunodeficiency virus; phosphorothioate linkage; retrovirus;  
 KW ribosomal frame shift; gag; pol; fusion protein; ss.

OS Synthetic.

PN WO9117246-A.

PD 14-NOV-1991.

PF 04-MAY-1990; 90US-00518929.

PR 04-MAY-1990; 90US-00518929.

XX

PA (ISIS-) ISIS PHARM INC.  
XX Ecker DJ;  
XX WPI; 1991-353768/48.  
XX  
PT Modulating gene expression for HIV treatment - comprises binding  
PT oligonucleotide(s) to RNA portions which have sec. structure.  
XX  
PS Example 3; Page 26; 40pp; English.  
XX  
CC This oligonucleotide and its analogue, having phosphorothioate bonds,  
CC were designed to specifically bind to the gag-pol frameshift region and  
CC interfere with translation and/or frameshifting. There is potential for  
CC significant RNA secondary structure near the site of frameshifting in HIV  
CC -1. The inhibitory effect of the oligo and its analogue has not yet been  
CC determined  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1178 ATCTGCGCTGCTACAG 1195  
DB 19 ATCTGCGCTGCTACAG 2  
  
RESULT 2973  
AAQ29648/c  
ID AAQ29648 standard; DNA; 20 BP.  
XX  
AC AAQ29648;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-MAR-1993 (first entry)  
XX  
DE PCR primer #55 for identifying Hepatitis C virus.  
XX  
XX Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening; PCR;  
KM primer; polymerase chain reaction; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN EP510952-A1.  
XX  
PD 28-OCT-1992.  
XX  
PF 23-APR-1992; 92EP-00303625.  
XX  
PR 26-APR-1991; 91JP-00191376.  
XX  
PA (IMMO ) IMMUNO JAPAN INC.  
XX  
PI Okamoto H, Nakamura T;  
XX  
DR WPI; 1992-359137/44.  
XX  
PT Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide  
PT primers with nucleotide sequences corresp. to part. of the viral RNA.  
XX  
PS Disclosure; Page 36; 54pp; English.  
XX  
CC This PCR primer was used with AAQ29645 to detect the presence of  
CC Hepatitis C viral RNA in a sample. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2943 AACAGGGCCAGCAAGCA 2960  
DB 20 AGCAGGGCCAGCAAGAA 3  
  
RESULT 2974  
AAQ24460/c  
ID AAQ24460 standard; DNA; 20 BP.  
XX  
AC AAQ24460;  
XX  
DT 09-NOV-1992 (first entry)  
XX  
DE NANB hepatitis virus primer 9.  
XX  
XX non-A, non-B hepatitis virus; NANBH; HC-J5; PCR;  
KM amplification polymerase chain reaction; ss.  
XX  
OS Non-A.  
OS non-B hepatitis virus.  
XX  
PN EP485209-A.  
XX  
PD 13-MAY-1992.  
XX  
PF 07-NOV-1991; 91EP-00310297.  
XX  
PR 08-NOV-1990; 90JP-00304405.  
XX  
PA (IMMO ) IMMUNO JAPAN INC.  
XX  
PI Okamoto H, Nakamura T;  
XX  
DR WPI; 1992-160959/20.  
XX  
PT Recombinant cDNA of NANBH virus strain HC-J5 and corresp. peptides -  
PT useful for diagnosis and in vaccines and immunological pharmaceuticals.  
XX  
PS Disclosure; Page 7; 42pp; English.  
XX  
XX The sequences given in AAQ24460 and AAQ24461 are PCR primers which are  
CC used to amplify the 5' region of non-A, non-B hepatitis virus (NANBH)  
CC strain HC-J5. These probes amplify the region corresponding to  
CC nucleotides 867-1154 of the entire nucleotide sequence and were used to  
CC produced clones C5164, C5303 and C5331. The nucleotide sequences derived  
CC from this amplification can be used to detect NANBH infection which  
CC could not be detected by conventional methods. The detection kits allow  
CC highly specific and sensitive detection at an early phase of infection  
XX  
SQ Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2943 AACAGGGCCAGCAAGCA 2960  
DB 20 AGCAGGGCCAGCAAGAA 3  
  
RESULT 2975  
AAQ31484/c  
ID AAQ31484 standard; DNA; 20 BP.  
XX  
AC AAQ31484;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-APR-1993 (first entry)  
XX  
DE NANB hepatitis virus PCR primer #55.  
XX  
KM Polymerase chain reaction; non-A non-B hepatitis; detection; ss.

```

OS Synthetic.
XX
XX
XX EP516270-A2.
XX
XX
XX 02-DEC-1992.
XX
XX
XX 09-APR-1992; 92EP-00303186.
XX
XX PR 10-APR-1991; 91JP-00196175.
XX
XX PA (IMMO ) IMMUNO JAPAN INC.
XX
XX PI Okamoto H, Nakamura T;
XX
XX DR WPI, 1992-400636/49.
XX
XX
XX Non-A, non-B hepatitis virus related antigens, their polynucleotide(s)
PT and antibodies - are useful for detecting NANBH virus in blood samples
PT intended for transfusion.
XX
XX
XX Example; Page 6; 23pp; English.
XX
XX
XX The sequence is that of PCR primer #55 which was used to determine the 5'
CC terminus sequence from nucleotides 867-1354 of non-A, non-B hepatitis
CC (NANBH) virus strain HC-J5. These nucleotide sequences encode structural
CC proteins of NANBH virus and these proteins can be analysed to locate and
CC provide polypeptides useful as antigens for detection of NANBH virus via
CC antibody-antigen complex detection. Mutants, variants or fragments of the
CC sequence can be used for very sensitive detection. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX
XX Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred.No.26+03; Mismatches 2; Indels 0; Gaps 0;
XX Matches 16; Conservative 0;
XX
XX QY 2943 AACAGGGCCAGCAAGACA 2960
XX | | | | | | | | | | | | | |
XX Db 20 AGCAGGGCCAGCAAGAAA 3
XX
XX
XX RESULT 2976
XX AAQ43865/C
XX ID AAQ43865 standard; DNA; 20 BP.
XX
XX AC AAQ43865;
XX
XX DT 21-OCT-1993 (first entry)
XX
XX DE NANB hepatitis viral gene HC-OM PCR primer #55.
XX
XX Non-A, non-B; virus; polymerase chain reaction; detection; sensitive;
XX specific; ss.
XX
XX OS Synthetic.
XX
XX PN JP05091864-A.
XX
XX PD 16-APR-1993.
XX
XX PF 10-APR-1991; 91JP-00196175.
XX
XX PR 12-JUN-1990; 90JP-00153401.
XX
XX PR 08-NOV-1990; 90JP-00304405.
XX
XX PA (NAKA/) NAKAMURA T.
XX
XX DR WPI, 1993-199637/25.
XX
XX Antigen related to non-A and non-B hepatitis virus - comprises non-
XX translation region comprising 340 - 341 mols. of nucleotides, non-

```

PT	translation region comprising 1885 - 2551 mols. of nucleotides including
PT	region 1,149 and, etc.
XX	
PS	Example; Page 7; 73pp; Japanese.
XX	
CC	The sequence is that of PCR primer #55 which was used in the
CC	amplification by PCR of nucleotides 867-1354 of the non-A, non-B
CC	hepatitis virus gene HC-OM
XX	
SQ	Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;	
OY	2943 AACAGGCGCAGAAGACA 2960           DB 20 AGCAGGGCGCACGACGAAA 3
RESULT 2977	
AAO74282/C	
ID	AAO74282 standard; DNA; 20 BP.
XX	
AC	AAO74282;
XX	
DT	25-MAR-2003 (revised)
DT	12-JUN-1995 (first entry)
XX	
DE	Amyloid precursor protein exon 14 forward PCR primer.
XX	
KW	Amyloid precursor protein; APP; exon 14 PCR primer;
KM	beta-amyloidosis animal model; Down's syndrome; Alzheimers disease;
KV	yeast artificial chromosome; ss.
XX	
OS	Synthetic.
XX	
PN	WO9423049-A2.
XX	
PD	13-OCT-1994.
XX	
PF	01-APR-1994; 94WO-US003619.
XX	
PR	02-APR-1993; 93US-00042390.
XX	
PA	(UYJO ) UNIV JOHNS HOPKINS.
XX	
PI	Gearhart JD, Lamb BT;
DR	WPI, 1994-333207/41.
XX	
PT	Introduction and expression of large genomic sequences in transgenic
PT	animals - which may be used as animal models of Beta-amyloidosis in
PT	Alzheimer's disease and Down's syndrome.
XX	
PS	Example 1; Page 24; 60pp; English.
XX	
CC	AAO74282 and AAO74283 are the forward and reverse PCR primers for human
CC	amyloid precursor protein (APP) exon 14; these were used to screen yeast
CC	artificial chromosome (YAC) libraries for APP. Isolated APP clones were
CC	then injected into blastocysts, from the same species as the embryonic
CC	cells which contained the YAC library. Transgenic animals which could be
CC	used as models of beta-amyloidosis (prevalent in individuals with Down's
CC	syndrome and Alzheimers disease), were then generated from the injected
CC	blastocysts. (Updated on 25-MAR-2003 to correct PW field.)
XX	
SQ	Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;	
OY	704 TGAGGCACCTGGCATCCA 721

Db 19 TGAGGCATGCAATTC A 2

RESULT 2978  
AAQ98015/c  
ID AAQ98015 standard; DNA; 20 BP.  
XX  
AC AAQ98015;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-OCT-1995 (first entry)  
XX  
DE PNA oligomer targeting HIV gag/pol frameshift.  
XX  
KM Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;  
KM antiviral; antisense; triple helix; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..20  
FT /\*tag= a  
FT /note= "at least one (and preferably all) of the backbone  
subunits are composed of N-acetyl N-(2-aminoethyl)glycine  
peptide residues, the nucleobase being attached  
covalently to the acetyl group and the peptide linkage  
being formed by condensation of the glycine carboxy group  
of one residue with the amino group of the 2-aminoethyl  
moiety in the next residue"

XX  
FN W09504068-A1.  
XX  
XX 09-FEB-1995.  
XX  
PD  
XX  
PF 28-JUL-1994; 94WO-US008517.  
XX  
XX 29-JUL-1993; 93US-00099718.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ecker DJ;  
XX  
DR WPI; 1995-082179/11.  
XX  
XX  
PT Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid  
PT sub:unit - binds in complementary manner to DNA and RNA, and useful for  
PT modulating HIV viral activity, e.g. in treating AIDS.  
XX  
XX  
PS Claim 2; Page 177; 186pp; English.  
XX  
CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist  
CC of naturally occurring nucleobases covalently bound to a polyamide  
CC backbone and (b) hybridise to the translation initiation AUG region, 5'  
CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice  
CC junctions or coding sequence of a human immunodeficiency virus gene  
CC chosen from env, gag, pol, rev and tat. The PNAs can be used to target  
CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene  
CC regulation molecules. They have utility as gene-targeted drugs for  
CC modulating HIV processes. Hence they can be used to treat AIDS and other  
CC viral infections. They are also useful in diagnostic applications and as  
CC research tools. PNA oligomers have high affinity for complementary single  
CC stranded DNA. They are also able to form triple helices in which a first  
CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the  
CC resulting double helix or with the first PNA strand. The PNAs possess no  
CC significant charge and are water soluble, which facilitates cellular  
CC uptake. Further, since they contain amides of non-biological amino acids,  
CC they are biostable and resistant to enzymatic degradation by proteases.  
CC The present sequence is a specifically claimed PNA sequence (represented  
CC by the sequence of nucleobases) targeting the HIV gag/pol frameshift.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1178 ATCTGCGCTGCTACAG 1195  
DB 19 ATCTGCGCTTCTTACAG 2

RESULT 2979  
AAT41212  
ID AAT41212 standard; DNA; 20 BP.  
XX  
AC AAT41212;  
XX  
DT 03-DEC-1996 (first entry)  
XX  
DE Human gene signature HUMGS01132-derived anti-sense primer.  
XX  
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KM human; cloning; mapping; non-biased library; diagnosis; detection;  
KM cell typing; abnormal cell function; primer; PCR; amplification;  
KM polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN W09514772-A1.  
XX  
PD 01-JUN-1995.  
XX  
PF 11-NOV-1994; 94WO-JP001916.  
XX  
XX 12-NOV-1993; 93JP-00355504.  
XX  
PA (MATS/) MATSUBARA K.  
PA (OKUB/) OKUBO K.  
XX  
PI Matsubara K, Okubo K;  
XX  
DR WPI; 1995-206931/27.  
XX  
XX  
PT Single-stranded DNA for identifying gene signatures - isolated from 3'-  
PT directed human cDNA library that reflects relative abundance of corresp.  
PT mRNA in specific human tissues.  
XX  
XX  
PS Example 7; Fig 8; 2245pp; Japanese.  
XX  
CC Primers T41001-T41382 are derived from novel human gene signature (GS)  
CC sequences which did not match with sequences deposited in Genbank release  
CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA  
CC libraries prepared from various human tissues; synthesis of cDNA was  
CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.  
CC Each library is constructed so as to reflect accurately the relative  
CC abundance of different mRNAs in the particular tissue from which it was  
CC derived. The appearance frequency of a given GS in a cDNA library can be  
CC determined (esp. using primers and probes derived from the GS sequences)  
CC as a means of diagnosing abnormal cell function or for recognising  
CC different cell types. The primers T41211-2 amplify clone pm0647 which  
CC comprises the GS HUMGS001132 (T20132), located on chromosome 20  
XX  
SQ Sequence 20 BP; 6 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1936 ATCTAGTCCACACCG 1953  
DB 1 ATCTAGTCCACACCG 18

RESULT 2980

AAT28903  
 ID AAT28903 standard; DNA; 20 BP.  
 AC AAT28903;  
 XX  
 DT 10-FEB-1997 (first entry)  
 XX  
 DE Factor XIII subunit "a" gene, exon 1, forward primer.  
 XX  
 KM Primer; amplification; factor XIII "a" gene; deletion;  
 KM splice donor/acceptor site; translational frameshift; substitution;  
 KM nonsense mutation; transition; diagnosis; bleeding; haemorrhage;  
 KM miscarriage; clot formation; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9617953-A2.  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-GB002857.  
 XX  
 PR 08-DEC-1994; 94GB-00024823.  
 XX  
 PA (UTLE-) UNIV LEBDS.  
 XX  
 PI Markham AF;  
 XX  
 DR WPI; 1996-287196/29.  
 XX  
 PT Genetic study of Factor XIII activity - used for diagnosis and treatment  
 PT of Factor XIII disorders, e.g. bleeding, haemorrhage, miscarriage or clot  
 PT formation.  
 XX  
 PS Example; Table 1; 44pp; English.  
 XX  
 CC The sequences given in AAT28903-32 are primers which were used in the  
 CC amplification of the exons of the factor XIII "a" gene. This allows  
 CC analysis of the factor XIII gene and identification of differences in the  
 CC gene sequence which are known to segregate with a reduction or  
 CC enhancement of factor XIII activity. All fifteen exons were amplified  
 CC from five unrelated families showing factor XIII disorders. The PCR  
 CC products obtained for each exon of each individual were found to be of  
 CC the expected size, indicating that there are no gross insertions or  
 CC deletions in the factor XIII "a" gene of these patients. Three mutations  
 CC which may be the cause of "a" subunit deficiency have been described. The  
 CC first is a two base pair deletion at a splice donor acceptor site. This  
 CC deletion does not grossly affect the splicing of the factor XIII pre  
 CC mRNA, but causes a translational frameshift resulting in early  
 CC translation termination. The second mutation is a G to A substitution at  
 CC a splice donor site. The mechanism of how this mutation causes factor  
 CC XIII deficiency is yet to be determined. The third mutation is a nonsense  
 CC mutation in which a C to T transition at position 598, in an Arg codon,  
 CC results in a stop codon TGA. A further eight mutations have been  
 CC identified and include a deletion/insertion event, a nonsense mutation  
 CC and missense/silent mutations. These primers may be used in the diagnosis  
 CC and treatment of disorders involving factor XIII e.g. bleeding,  
 CC haemorrhage, miscarriage or clot formation  
 XX  
 SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;  
 XX

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 5294 TACTCCGACCAAGTT 5311  
1 TACTCCGACCAAGTT 18			

RESULT 2981  
 AAT33418  
 ID AAT33418 standard; cDNA; 20 BP.

XX  
 AC AAT33418;  
 XX  
 DT 16-MAY-1997 (first entry)  
 XX  
 DE Human vascular endothelial growth factor antisense oligonucleotide.  
 XX  
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;  
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;  
 KM degeneration; expression inhibitor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9627006-A2.  
 PD 06-SEP-1996.  
 XX  
 PF 29-FEB-1996; 96WO-US002840.  
 XX  
 PR 02-MAR-1995; 95US-00398945.  
 XX  
 PR 08-DEC-1995; 95US-00569926.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Robinson GS;  
 XX  
 DR WPI; 1996-412773/41.  
 XX  
 PT Human vascular endothelial growth factor anti-sense oligonucleotide -  
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced  
 PT neovascularisation and angiogenesis associated disease states.  
 XX  
 PS Disclosure; Page 14; 92pp; English.  
 XX  
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the  
 CC expression of human vascular endothelial growth factor (VEGF). The  
 CC synthetic oligonucleotides contain phosphorothioate linkages and  
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the  
 CC expression of VEGF is useful in the treatment of hypoxia induced  
 CC neovascularisation and angiogenesis associated disease states,  
 CC retinopathy of prematurity, diabetic retinopathy and age related macular  
 CC degeneration  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;  
 XX

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2402 CTGGGACCACTGAGACA 2419  
Db 2 CTGGGACCACTGAGACA 19			

RESULT 2982  
 AAT33421  
 ID AAT33421 standard; cDNA; 20 BP.  
 XX  
 AC AAT33421;  
 XX  
 DT 16-MAY-1997 (first entry)  
 XX  
 DE Human vascular endothelial growth factor antisense oligonucleotide.  
 XX  
 KM Antisense; VEGF; vascular endothelial growth factor; hypoxia;  
 KM neovascularisation; angiogenesis; metastasis; retinopathy; macular;  
 KM degeneration; expression inhibitor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9627006-A2.  
 PD 06-SEP-1996.

XX 29-FEB-1996; 96WO-US002840.  
 XX 02-MAR-1995; 95US-00398945.  
 PR 08-DEC-1995; 95US-00569926.  
 XX (HYBR-) HYBRIDON INC.  
 PA Robinson GS;  
 PI WPI; 1996-412773/41.  
 DR Human vascular endothelial growth factor antisense oligo:nucleotide -  
 XX inhibits the expression of VEGF, useful in treatment of hypoxia induced  
 PT neovascularisation and angiogenesis associated disease states.  
 PS Disclosure; Page 14; 92pp; English.  
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the  
 CC expression of human vascular endothelial growth factor (VEGF). The  
 CC synthetic oligonucleotides contain phosphorothioate linkages and  
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the  
 CC expression of VEGF is useful in the treatment of hypoxia induced  
 CC neovascularisation and angiogenesis associated disease states.  
 CC retinopathy of prematurity, diabetic retinopathy and age related macular  
 CC degeneration  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 5921 CCCAGAGATGTCACCTG 5938  
 DB 2 CCCAAGATGCCACCTG 19  
 RESULT 2983  
 AAT33412  
 ID AAT33412 standard; CDNA; 20 BP.  
 XX  
 AC AAT33412;  
 XX  
 DT 16-MAY-1997 (first entry)  
 XX  
 DE Human vascular endothelial growth factor antisense oligonucleotide.  
 XX  
 KW Antisense; VEGF; vascular endothelial growth factor; hypoxia;  
 KW neovascularisation; angiogenesis; metastasis; retinopathy; macular;  
 KW degeneration; expression inhibitor; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9627006-A2.  
 XX  
 PD 06-SEP-1996.  
 XX  
 PF 29-FEB-1996; 96WO-US002840.  
 XX  
 PR 02-MAR-1995; 95US-00398945.  
 PR 08-DEC-1995; 95US-00569926.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Robinson GS;  
 XX  
 DR WPI; 1996-412773/41.  
 XX  
 PT Human vascular endothelial growth factor anti:sense oligo:nucleotide -  
 PT inhibits the expression of VEGF, useful in treatment of hypoxia induced  
 PT neovascularisation and angiogenesis associated disease states.  
 XX

PS Disclosure; Page 14; 92pp; English.  
 CC AAT33371-T33431 are antisense oligonucleotides used to inhibit the  
 CC expression of human vascular endothelial growth factor (VEGF). The  
 CC synthetic oligonucleotides contain phosphorothioate linkages and  
 CC essentially consist of 2'-O-alkylated ribonucleotides. Inhibiting the  
 CC expression of VEGF is useful in the treatment of hypoxia induced  
 CC neovascularisation and angiogenesis associated disease states.  
 CC retinopathy of prematurity, diabetic retinopathy and age related macular  
 CC degeneration  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 5921 CCCAGAGATGTCACCTG 5938  
 DB 2 CCCAAGATGCCACCTG 19  
 RESULT 2984  
 AAT48412  
 ID AAT48412 standard; DNA; 20 BP.  
 XX  
 AC AAT48412;  
 XX  
 DT 11-MAR-1997 (first entry)  
 XX  
 DE Oligonucleotide H-14 specific for human VEGF nucleic acid.  
 XX  
 KW Vascular endothelial growth factor; inhibition; decrease; antisense;  
 KW neovascularisation; retinopathy; age-related macular degeneration;  
 KW diabetes; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9623065-A2.  
 XX  
 PD 01-AUG-1996.  
 XX  
 PF 26-JAN-1996; 96WO-US001189.  
 XX  
 PR 26-JAN-1995; 95US-00378860.  
 XX  
 PA (HYBR-) HYBRIDON INC.  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX  
 PI Robinson GS, Smith LEH;  
 XX  
 DR WPI; 1996-362689/36.  
 XX  
 PT Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -  
 PT for treatment of retinopathies and age-related macular degeneration.  
 XX  
 PS Disclosure; Page 12; 66pp; English.  
 CC Neovascularisation can be reduced by blocking vascular endothelial growth  
 CC factor (VEGF) expression using a synthetic oligonucleotide specific for  
 CC VEGF. Inhibiting neovascularisation is useful for treatment of  
 CC retinopathy of prematurity, diabetic retinopathy and age-related macular  
 CC degeneration. The present sequence is an example of a suitable  
 CC oligonucleotide specific for human VEGF  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0;  
 QY 5921 CCCAGAGATGTCACCTG 5938  
 DB 2 CCCAAGATGCCACCTG 19

Db 2 CCCAAGATGCCCACTG 19

RESULT 2985

AA748418  
ID AAT48418 standard; DNA; 20 BP.

XX  
AC AAT48418;

XX  
DT 11-MAR-1997 (first entry)

XX  
DE Oligonucleotide 11/E2 specific for human VEGF nucleic acid.

XX  
KW Vascular endothelial growth factor; inhibition; decrease; antisense;

XX  
KW neovascularisation; retinopathy; age-related macular degeneration;

XX  
KW diabetes; exon-intron boundary; ss.

XX  
OS Synthetic.

XX  
PN WO9623065-A2.

XX  
PD 01-AUG-1996.

XX  
PF 26-JAN-1996; 96WO-US001189.

XX  
PR 26-JAN-1995; 95US-00378860.

XX  
PA (HYBR-) HYBRIDON INC.

XX  
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX  
PI Robinson GS, Smith LEH;

XX  
DR WPI; 1996-362689/36.

XX  
PT Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -

XX  
PS for treatment of retinopathies and age-related macular degeneration.

XX  
PS Disclosure; Page 12; 66pp; English.

CC Neovascularisation can be reduced by blocking vascular endothelial growth

CC factor (VEGF) expression using a synthetic oligonucleotide specific for

CC VEGF. Inhibiting neovascularisation is useful for treatment of

CC retinopathy of prematurity, diabetic retinopathy and age-related macular

CC degeneration. The present sequence is an example of a suitable

CC oligonucleotide specific for human VEGF

CC

XX  
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 2402 CTGGGACCACTGAGACA 2419

Db 2 CTGGGACCACTGAGACA 19

RESULT 2986

AA748421  
ID AAT48421 standard; DNA; 20 BP.

XX  
AC AAT48421;

XX  
DT 11-MAR-1997 (first entry)

XX  
DE Oligonucleotide E3/I3 specific for human VEGF nucleic acid.

XX  
KW Vascular endothelial growth factor; inhibition; decrease; antisense;

XX  
KW neovascularisation; retinopathy; age-related macular degeneration;

XX  
KW diabetes; exon-intron boundary; ss.

XX  
OS Synthetic.

PN WO9623065-A2.

XX  
PD 01-AUG-1996.

XX  
PF 26-JAN-1996; 96WO-US001189.

XX  
PR 26-JAN-1995; 95US-00378860.

XX  
PA (HYBR-) HYBRIDON INC.

XX  
PA (CHIL-) CHILDRENS MEDICAL CENT.

XX  
PI Robinson GS, Smith LEH;

XX  
DR WPI; 1996-362689/36.

XX  
PT Inhibiting neovascularisation using VEGF-specific oligo:nucleotide(s) -

XX  
PS for treatment of retinopathies and age-related macular degeneration.

XX  
PS Disclosure; Page 12; 66pp; English.

CC Neovascularisation can be reduced by blocking vascular endothelial growth

CC factor (VEGF) expression using a synthetic oligonucleotide specific for

CC VEGF. Inhibiting neovascularisation is useful for treatment of

CC retinopathy of prematurity, diabetic retinopathy and age-related macular

CC degeneration. The present sequence is an example of a suitable

CC oligonucleotide specific for human VEGF

CC

XX  
SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 5921 CCCAGAGTGCACCTG 5938

Db 2 CCCAAGATGCCCACTG 19

RESULT 2987

AAV85793  
ID AAV85793 standard; DNA; 20 BP.

XX  
AC AAV85793;

XX  
DT 10-FEB-1999 (first entry)

XX  
DE LRP5 exon primer 58-8 1f.

XX  
KW LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;

XX  
KW insulin dependent diabetes mellitus; autoimmune disease;

XX  
KW glomerulonephritis; inflammation; viral infection; osteoporosis;

XX  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;

XX  
KW PCR primer; ss.

XX  
OS Synthetic.

XX  
OS Homo sapiens.

XX  
PN WO9846743-A1.

XX  
PD 22-OCT-1998.

XX  
PF 15-APR-1998; 98WO-GB001102.

XX  
PR 15-APR-1997; 97US-0043553P.

XX  
PR 05-JUN-1997; 97US-0048740P.

XX  
PA (WELT ) WELLCOME TRUST LTD.

XX  
PA (MERT ) MERCK & CO INC.

XX  
PI Todd JA, Hess JM, Caskey CT, Cox RD, Gerhold D, Hammond H;

XX  
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;

XX  
PI Phillips MS, Twells RCU;

DR	WP1; 1998-594573/50.
XX	
PT	New isolated LDL-receptor related protein - used to develop products for
PT	treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT	disorders, inflammation or Alzheimer's disease.
XX	
PS	Claim 12; Page 106; 200pp; English.
XX	
CC	The present invention describes LRP5 (low density lipoprotein (LDL)
CC	receptor related protein, previously designated LRP-3). AAV8587 to
CC	AAV85882 represent exon primers used for obtaining LRP5 cDNA. Nucleic
CC	acid molecules (NAs) encoding LRP5 can be used for determining if an
CC	individual is susceptible to insulin dependent diabetes mellitus (IDDM).
CC	The NAs or proteins can be used for reducing triglyceride levels in the
CC	serum of an individual. Therapies that affect LRP5 may also be useful in
CC	the treatment of autoimmune diseases such as glomerulonephritis, diseases
CC	and disorders involving disruption of endocytosis and/or antigen
CC	presentation, cytokine clearance and/or inflammation, viral infection,
CC	pathogenic bacterial toxin contamination, elevation of free fatty acids
CC	or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
CC	disease and cardiovascular disease. Products from the present invention
CC	can also be used for detection, diagnosis and drug screening
XX	
SQ	Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
QY	Query Match 0.2%; Score 14.8; DB 1; Length 20;
	Best Local Similarity 88.9%; Pred. No. 2e+03;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB	2075 GCCGATCTGTCCTACTG 2092
	1 GCCAAGACTGTCCTACTG 18
XX	
RESULT 2988	
AAV85871	standard; DNA; 20 BP.
XX	
AC	AAV85871;
XX	
DT	10-FEB-1999 (first entry)
XX	
DB	LRP5 SNP primer 58-8 1f.
XX	
KW	LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW	insulin dependent diabetes mellitus; autoimmune disease;
KW	glomerulonephritis; inflammation; viral infection; osteoporosis;
KW	hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
KW	PCR primer; ss.
XX	
XX	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9846743-A1.
XX	
PD	22-OCT-1998.
XX	
PF	15-APR-1998; 98WO-GB001102.
XX	
PR	15-APR-1997; 97US-0043553P.
XX	
XX	05-JUN-1997; 97US-0048740P.
PA	(WELL ) WELLCOME TRUST LTD.
PA	(MERI ) MERCK & CO INC.
XX	
PI	Todd JA, Hese JM, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX	Hey P, Kawaguchi Y, Merriman TR, Metzger ML, Nakagawa Y;
PI	Phillips MS, Twells RCU;
XX	
DR	WP1; 1998-594573/50.
XX	
PT	New isolated LDL-receptor related protein - used to develop products for
PT	treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT	disorders, inflammation or Alzheimer's disease.

disorders, inflammation or Alzheimer's disease.

Claim 12, Page 111, 200pp; English.

The present invention describes LRP5 (low density lipoprotein (LDL) receptor related protein, previously designated LRP-3). AA85823 to AA85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid molecules (NMs) encoding LRP5 can be used for determining if an individual is susceptible to insulin dependent diabetes mellitus (IDDM). The NM or proteins can be used for reducing triglyceride levels in the serum of an individual. Therapies that affect LRP5 may also be useful in the treatment of autoimmune diseases such as glomerulonephritis, diseases and disorders involving disruption of endocytosis and/or antigen presentation, cytokine clearance and/or inflammation, viral infection, pathogenic bacterial toxin contamination, elevation of free fatty acids or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's disease and cardiovascular disease. Products from the present invention can also be used for detection, diagnosis and drug screening

Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;  
Matches 16; Conservative 0; Indels 2;

2075 GCCGATCTGTGCTACTG 2092  
|||  
1 GCCAAGACTGTGCTACTG 18

RESULT 2989  
AAV52002  
ID AAV52002 standard; DNA; 20 BP.  
AC AAV52002;  
XX AAV52002;  
XX 02-FEB-1999 (first entry)  
DT  
XX  
XX  
XX Zea mays genome reverse PCR primer #298.  
DE  
XX  
XX Polymorphic marker; allele-specific; probe; amplification; PCR primer;  
XX hybridisation; plant; hybrid certification; genetic contribution;  
KW progeny; back-cross; hybrid; ancestry; corn; ss.  
OS Synthetic.  
XX Zea mays.  
XX  
XX  
XX WO9824796-A1.  
PN  
XX  
XX  
PD 11-JUN-1998.  
XX  
XX PF 01-DEC-1997; 97WO-US021782.  
XX  
XX 02-DEC-1996; 96US-0032069P.  
XX 07-MAR-1997; 97US-00813507.  
PR  
XX  
XX (AFVY-) AFFYMETRIX INC.  
PA  
XX  
XX Lemieux B, Landry BS, Sapolsky RJ, Murgineux A;  
XX  
XX WPI; 1998-33352/29.  
DR  
XX  
XX Brassica species allele-specific oligonucleotide probes and primers -  
PT useful for plant breeding.  
XX  
XX Example 1; Page 55; 65pp; English.  
XX  
XX AAV51705-V52008 are reverse PCR primers used to amplify fragments of the  
CC Zea mays genome in order to detect polymorphic markers. Such markers can  
CC be used in the construction of allele-specific primers and probes for  
CC amplification or hybridisation, e.g. to determine common or disparate  
CC ancestry between 2 or more plants, to monitor the genetic contribution of  
CC an ancestral plant, to trace the progeny of proprietary plants, in



CC certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

XX Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1/54 AGCTCATTTATGTCATCC 1771

1 AGCTCATTTATGTCCTCC 18

RESULT 2990

AAV35084/c

ID AAV35084 standard; DNA; 20 BP.

AAV35084;

28-AUG-1998 (first entry)

Antisense MDR1 oligonucleotide #24.

P-glycoprotein; multiple drug resistance; MDR; cellular uptake; cancer; gene expression; chemotherapy; treatment; hyper-proliferative disease; primer; ss.

Synthetic.

MO9814615-A1.

09-APR-1998.

01-OCT-1997; 97WO-US017800.

04-OCT-1996; 96US-00731199.

(ISIS-) ISIS PHARM INC.

Dean NM, Manoharan M;

WPI; 1998-240109/21.

Anti-sense oligo:nucleotide(s) targeted to multiple drug resistance gene - are modified by lipophilic substituent, on sugar and/or with non-natural linkages, used to improve activity of anti-proliferative agents against tumours.

Example 1; Page 21; 64pp; English.

AAV35061-V35101 are primers which have a sequence complementary to the translation initiation or termination region of a nucleic acid encoding a P-glycoprotein associated with multiple drug resistance (MDR) and inhibits expression of the glycoprotein. These primers are composed of 8-30 covalently linked nucleotides and includes at least 1 of the following; a 2'-modification, a lipophilic group (lg) that improves cellular uptake, and at least 1 covalent link that is a phosphorothioate, phospho di- or tri-ester, methylphosphonate, methylene (methylimino), morpholino, polyamide, short chain alkyl or heteroatomic inter-sugar link, or cycloalkyl or heterocyclic inter-sugar link. The primers are used to modulate human MDR gene expression in cells and tissues, i.e. to improve chemotherapeutic treatment of an animal with hyper-proliferative disease, particularly cancer, to prevent development of MDR and to re-sensitise an animal that has developed MDR to a chemotherapeutic agent

Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1103 AGAGTGGACGACGTGTG 1120

19 AGAGTGGACGACGTGTG 2

RESULT 2991

AAV70043/c

ID AAV70043 standard; DNA; 20 BP.

AAV70043;

04-FEB-1999 (first entry)

Rat c-Fos protein antisense oligonucleotide #97.

Rat; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis; antisense oligonucleotide; phosphorothioate; regulation; malignant tumour; cell cycle expression; hyperproliferative disease; ss.

Synthetic.

Rattus sp.

Location/Qualifiers

modified\_base 1..20

/note= "phosphorothioate linkages"

MO9846272-A1.

22-OCT-1998.

14-APR-1998; 98WO-US007386.

14-APR-1997; 97US-00837201.

(ISIS-) ISIS PHARM INC.

Dean NM, McKay R, Miraglia L, Baker B;

WPI; 1998-609906/51.

Antisense oligonucleotides regulating Activating Protein 1 subunits - hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell cycle expression and hyperproliferative disease.

Example 9; Page 57; 120pp; English.

AAV70042 to AAV70052 represent antisense oligonucleotides which are specifically hybridisable with a region of a nucleic acid encoding rat c-Fos protein. The antisense compound regulates the expression of the c-Fos protein. The present invention also describes antisense oligonucleotides which regulate the c-jun protein. The antisense oligonucleotides are used for the diagnosis and treatment of diseases or disorders associated with

Activating Protein 1 expression, of which c-Fos and c-jun are subunits. The antisense oligonucleotides are used in compositions as c-Fos and/or c-jun together with a carrier and a chemotherapeutic agent. They are used to regulate the expression of c-Fos or c-jun in cells or tissues, preferably by inhibiting metastasis. They also regulate cell cycle expression and can be used to treat an animal with, or being prone to, a hyperproliferative disease

Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1284 CCAGACTCGACCATGAT 1301

19 CCAAAACGACGACCATGAT 2

RESULT 2992

AAV22586

```

ID  AAV22586 standard; DNA; 20 BP.
XX
AC  AAV22586;
XX
DT  08-JUL-1998 (first entry)
XX
DE  Antisense oligonucleotide designed to target the R1 message.
XX
KM  R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
XX  antisense; growth; inhibition; sensitivity; hydroxyurea;
XX  chemotherapeutic drug; methotrexate; PMA; treatment; ss.
XX
OS  Synthetic.
XX  Homo sapiens.
XX
PN  WO9805769-A2.
XX
PD  12-FEB-1998.
XX
PF  01-AUG-1997; 97MO-CA000540.
XX
PR  02-AUG-1996; 96US-0023040P.
XX  07-MAR-1997; 97US-0039959P.
XX
PA  (GENE-) GENESENSE TECHNOLOGIES INC.
XX
FI  Wright JA, Young AH;
XX
DR  WPI; 1998-145609/13.
XX
PT  Antisense oligonucleotides to ribonucleotide reductase genes - used to
XX  modulate tumour growth and inhibit tumour cell proliferation.
XX
PS  Claim 8; Page 49; 79pp; English.
XX
CC  AAV22531-89 represent antisense oligonucleotides which are targeted
XX  against the mRNA of the R1 subunit sequence of ribonucleotide reductase.
XX  Aberrant expression of the R2 gene, which encodes the second subunit of
XX  the ribonucleotide reductase gene, can determine the malignant
XX  characteristics of cells. Suppression of R2 and R1 gene expression was
XX  found to reduce transformed properties of tumour cells. The antisense
XX  oligonucleotides can be used for modulating tumour cell growth, or for
XX  inhibiting tumour cell proliferation. They can also be used for
XX  increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
XX  (especially to hydroxyurea, methotrexate (MTX), and PMA). The antisense
XX  oligonucleotides may be used to treat proliferative disorders including
XX  leukaemias, lymphomas, sarcomas, melanomas, various other forms of
XX  cancer, papillomas, atherosclerosis, psoriasis, polychemia, mastocytosis,
XX  autoimmune diseases, angiogenesis, bacterial infections and viral
XX  infections (including HIV hepatitis, or herpes infections)
XX
SQ  Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY  4463 CTTTTTTTTTTTTTTTTT 4480
    |||||
DB  3 CGTTTTTTTTTTCTTTT 20

```

```

XX
OS  Synthetic.
XX  Homo sapiens.
XX
PN  WO9804689-A1.
XX
PD  05-FEB-1998.
XX
PF  31-JUL-1996; 96MO-US012516.
XX
PR  31-JUL-1996; 96MO-US012516.
XX
PA  (UROC-) UROCOR INC.
XX
PI  Veltri R, Ohara SM, An G, Ralph D;
XX
DR  WPI; 1998-130681/12.
XX
PT  Human prostate cancer marker - useful for detection and treatment of
XX  human prostate cancer.
XX
PS  Example 4; Page 121; 229pp; English.
XX
CC  This primer is used in the relative quantitative RT-PCR to examine the
XX  expression of the genes which is used for the identification of markers
XX  of human prostate cancer. Isolated nucleic acid segments shown in
XX  CC AAV16881 to AAV16885, AAV16890 to AAV16903, AAV26351 and AAV26352 which
XX  can act as human prostate cancer markers are provided in the
XX  specification. The specification also provides methods for identifying
XX  markers for human prostate cancer and for detection of prostate cancer
XX  cells. The markers can be identified by amplifying human prostate RNA to
XX  provide nucleic acid amplification products, separating the products and
XX  identifying those RNA that are differentially expressed between human
XX  prostate cancers versus normal or benign human prostate. Prostate cancer
XX  cells in a sample can be detected by detecting a nucleic acid in a
XX  sample, the nucleic acid being a prostate cancer marker. Primers and
XX  CC probes derived from this marker can be used for the detection of prostate
XX  cancer cells in a sample. Antibodies against the protein encoded by the
XX  CC marker nucleic acid fragments, inhibitors of the protein and
XX  oligonucleotides antisense to the markers can be used in the treatment of
XX  prostate cancer. The antibodies can also be used for the diagnosis of
XX  human prostate cancer
XX
SQ  Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY  3414 CTTATTCCTCTGTGCA 3431
    |||||
DB  19 CATATTCCTTTGTGCA 2

```

```

RESULT 2993
AAV26329/c
ID  AAV26329 standard; DNA; 20 BP.
XX
AC  AAV26329;
XX
DT  07-AUG-1998 (first entry)
XX
DE  Human prostate cancer marker UC Band #201 identifying RT-PCR primer 2.
XX  Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.
XX
KW

```

```

RESULT 2994
AAV26076/c
ID  AAV26076 standard; DNA; 20 BP.
XX
AC  AAV26076;
XX
DT  20-MAY-1999 (first entry)
XX
DE  Prostate disease marker gene fragment amplifying RT-PCR primer.
XX  Prostate cancer; benign prostatic hyperplasia; marker gene; tumour;
XX  differentiation; Reverse Transcription Polymerase Chain Reaction;
XX  diagnostic; progression; cancer; metastasis; RT-PCR; primer; ss.
XX
OS  Synthetic.
XX  Homo sapiens.
XX
PN  US582864-A.
XX

```

```

PD 16-MAR-1999.
XX
XX 31-JUL-1996; 96US-00692787.
XX
XX 31-JUL-1995; 95US-0001655P.
XX
XX (UROC-) UROC INC.
XX
XX Veltre R, Ralph D, An G, O'hara SM;
XX
XX WPI; 1999-214055/18.
XX
XX Diagnosing prostate cancer and benign prostatic hyperplasia cells - using
XX oligonucleotide probes specific for marker genes associated with tumor
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction analysis.
XX
XX Example 4; Col 66; 74pp; English.
XX
XX The invention relates to methods for diagnosing prostate cancer or benign
XX prostatic hyperplasia cells in a biological sample. The method uses
XX oligonucleotides specific for marker genes associated with tumour
XX differentiation and progression in Reverse Transcription Polymerase Chain
XX Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful
XX for detecting and monitoring the progression of benign prostatic
XX hyperplasia and human prostate cancer (the most prevalent form of cancer
XX and a major cause of death in males) prior to the tumor undergoing
XX metastasis, therefore allowing the optimal method of treatment to be
XX determined before the condition becomes life threatening
XX
XX Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 3414 CTTATTCCTCTGTGCCA 3431
Db 19 CATATCTCTTTGTCCA 2
XX
XX RESULT 2995
XX ID AAX29179 standard; DNA; 20 BP.
XX
XX AAX29179;
XX
XX 18-JUN-1999 (first entry)
XX
XX Human osteopontin (OPN) specific probe hOPN-PL.
XX
XX Osteopontin; antisense; restenosis; coronary arterial tissue; CASMC;
XX inflammation; coronary artery smooth muscle cell; angioplasty; human;
XX OPN; probe; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9907844-A2.
XX
XX 18-FEB-1999.
XX
XX 07-AUG-1998; 98WO-US016569.
XX
XX 07-AUG-1997; 97US-0054967P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Mukherjee AB, Kundu GC, Panda DK;
XX
XX WPI; 1999-190049/16.
XX
XX New osteopontin antisense sequences - useful to treat restenosis,
XX

```

```

PT particularly following vascular surgery.
XX
XX Example 1; Page 29; 72pp; English.
XX
XX The invention relates to antisense osteopontin oligonucleotide sequences
XX which are complementary to at least a portion of the human osteopontin
XX (OPN) cDNA sequence (AAX29191). The antisense sequences are used to
XX prevent restenosis in tissue, particularly coronary arterial tissue,
XX especially where the patient is undergoing angioplasty, particularly
XX percutaneous trans-luminal coronary angioplasty or directional coronary
XX atherectomy. They prevent secretion of osteopontin by monocytes and
XX macrophages which infiltrate to sites of inflammation following surgery.
XX Osteopontin probably causes restenosis by inducing coronary artery smooth
XX muscle cells (CASMC) to migrate to, and proliferate at, angioplasty
XX injury sites. The present sequence represents a probe specific for human
XX osteopontin cDNA sequence
XX
XX Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Oy 904 TTCATGTGTGAGTGCTG 921
Db 1 TCCATGTGTGAGTGATG 18
XX
XX RESULT 2996
XX ID AAZ04197/c
XX
XX AAZ04197;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX paratrachoma; inclusion conjunctivitis; genital disease; peritropatitis;
XX nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
XX Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX Synthetic.
XX Chlamydia trachomatis.
XX
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffiths R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1669; 1755pp; English.
XX
XX PCR primers AAZ01426-206209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX

```

CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5010 GAATGAGGGCTCTGGGA 5027  
DB 19 GAATGAGGGCTCTGGGA 2  
RESULT 2997  
AAZ05197/c  
ID AAZ05197 standard; DNA; 20 BP.  
XX  
AC AAZ05197;  
XX  
DT 07-OCT-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
XX  
KM Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;  
KM paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;  
KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
XX  
OS Synthetic.  
OS Chlamydia trachomatis.  
XX  
PN WO928475-A2.  
XX  
PD 10-JUN-1999.  
XX  
PF 27-NOV-1998; 98WO-IB001939.  
XX  
PR 28-NOV-1997; 97FR-00015041.  
PR 17-DEC-1997; 97FR-00016034.  
PR 04-NOV-1998; 98US-0107077P.  
XX  
PA (BEST ) GENSET.  
XX  
PI Giffais R;  
XX  
DR WPI; 1999-371125/31.  
XX  
PT Genome sequence of Chlamydia trachomatis.  
PS Disclosure; Page 1751; 1755pp; English.  
XX  
CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
CC be used to control growth of the microorganism. Chlamydia trachomatis is  
CC responsible for a large number of diseases, e.g. eye diseases such as  
CC conventional trachoma, nongonococcal urethritis, and inclusion  
CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases  
XX  
SQ Sequence 20 BP; 2 A; 10 C; 0 G; 8 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3638 AGAGCTAGATGGGAG 3655  
DB 18 AGAGGAGATGGGAG 1  
RESULT 2998  
AAZ04690/c  
ID AAZ04690 standard; DNA; 20 BP.  
XX  
AC AAZ04690;  
XX  
DT 07-OCT-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.  
XX  
KM Vaccine; eye disease; conventional trachoma; nongonococcal urethritis;  
KM paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;  
KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;  
KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.  
XX  
OS Synthetic.  
OS Chlamydia trachomatis.  
XX  
PN WO928475-A2.  
XX  
PD 10-JUN-1999.  
XX  
PF 27-NOV-1998; 98WO-IB001939.  
XX  
PR 28-NOV-1997; 97FR-00015041.  
PR 17-DEC-1997; 97FR-00016034.  
PR 04-NOV-1998; 98US-0107077P.  
XX  
PA (BEST ) GENSET.  
XX  
PI Giffais R;  
XX  
DR WPI; 1999-371125/31.  
XX  
PT Genome sequence of Chlamydia trachomatis.  
PS Disclosure; Page 1709; 1755pp; English.  
XX  
CC PCR primers AAZ01426-206209 were used to amplify open reading frames  
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines  
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
CC be used to control growth of the microorganism. Chlamydia trachomatis is  
CC responsible for a large number of diseases, e.g. eye diseases such as  
CC conventional trachoma, nongonococcal urethritis, and inclusion  
CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;  
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.  
CC The polypeptides of the invention may be of use in treating these  
CC diseases  
XX  
SQ Sequence 20 BP; 0 A; 8 C; 1 G; 11 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4013 AATGAGAAAAAGAG 4030  
DB 20 AGAGGAGAAAAAGAG 3  
RESULT 2999  
AAZ04201/c  
ID AAZ04201 standard; DNA; 20 BP.  
XX  
AC AAZ04201;

```

XX 07-OCT-1999 (first entry)
DT
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
DE
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
XX MO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1669; 1755pp; English.
XX
XX PCR primers AA201426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumonia; in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2851 CCAATCCAGAGGA 2868
Db 20 CCAATCCAGAGGA 3
RESULT 3000
AA201618
ID AA201618 standard; DNA; 20 BP.
XX
XX AA201618;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.

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OS Chlamydia trachomatis.
XX
XX MO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1457; 1755pp; English.
XX
XX PCR primers AA201426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal urethritis,
CC epididymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumonia; in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
XX
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2652 CCACCTGTGACAGGA 2669
Db 1 CCACCTGTGACAGGA 18
RESULT 3001
AA203279
ID AA203279 standard; DNA; 20 BP.
XX
XX AA203279;
XX
XX 07-OCT-1999 (first entry)
XX
XX PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
XX MO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97FR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX

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XX (GEST ) GENSET.  
XX Griffais R;  
XX WPI; 1999-371125/31.  
XX Genome sequence of Chlamydia trachomatis.  
XX  
XX Disclosure; Page 1593; 1755bp; English.  
XX  
XX PCR primers AA201426-206209 were used to amplify open reading frames  
XX (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs  
XX encode polypeptides (see AA136754-Y37949) which can be used as vaccines  
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
XX be used to control growth of the microorganism. Chlamydia trachomatis is  
XX responsible for a large number of diseases, e.g. eye diseases such as  
XX conventional trachoma, nongonococcal urethritis, paratrachoma, and inclusion  
XX conjunctivitis; genital diseases such as nongonococcal urethritis,  
XX epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis,  
XX pneumopathy in breast feeding infants, and venereal lymphogranulomatosis.  
XX The polypeptides of the invention may be of use in treating these  
XX diseases  
XX  
XX Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
XX Best Local Similarity 88.9%; Pred. No. 2e+03;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 5426 AAGGATCAGCTTGGG 5443  
XX 2 AAGGATCAGCTTGGG 19  
XX  
XX  
XX RESULT 3002  
XX AA294878  
XX ID AA294878 standard; DNA; 20 BP.  
XX  
XX AA294878;  
XX  
XX 13-SEP-1999 (first entry)  
XX  
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
XX  
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
XX neutralising epitope; PCR primer; ss.  
XX  
XX Synthetic.  
XX OS Chlamydia pneumoniae.  
XX  
XX WO9927105-A2.  
XX  
XX 03-JUN-1999.  
XX  
XX 20-NOV-1998; 98WO-IB001890.  
XX  
XX 21-NOV-1997; 97FR-00014673.  
XX  
XX 04-NOV-1998; 98US-0107078P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Griffais R;  
XX  
XX WPI; 1999-357842/30.  
XX  
XX Genome sequence of Chlamydia pneumoniae.  
XX  
XX Page 1704; Disclosure; 1912pp; English.  
XX  
XX AA291991-X97517 represent PCR primers used to amplify open reading frames  
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae  
XX

CC (see AA291990). C. pneumoniae causes respiratory disease such as  
CC pneumonia and bronchitis and is thought to be a contributing factor in  
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema  
CC nodosum or pharyngitis. The polypeptides encoded by the open reading  
CC frames of the C. pneumoniae genome (see AA291991- AA291999) can be used  
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae  
CC nucleotide sequences can also be used as immunogenic compositions,  
CC especially where the vector directs the expression of a neutralising  
CC epitope of C. pneumoniae  
XX  
XX Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
XX Best Local Similarity 88.9%; Pred. No. 2e+03;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 1356 GAAATGCCAGCTACAA 1373  
XX 2 GAAATGCCAGCTACAA 19  
XX  
XX  
XX RESULT 3003  
XX AA247569/c  
XX ID AA247569 standard; DNA; 20 BP.  
XX  
XX AA247569;  
XX  
XX 23-MAR-2000 (first entry)  
XX  
XX Antisense oligonucleotide 24 targeted to human MDR1 P-glycoprotein.  
XX  
XX Multidrug resistance gene; MDR1; human; hyperproliferative disease;  
XX cancer; autoradiography; phosphorochiolate; ss.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..20  
XX /tag= a  
XX /note= "Phosphorochiolate internucleoside linkage"  
XX  
XX US6001991-A.  
XX  
XX 14-DEC-1999.  
XX  
XX 30-SEP-1997; 97US-00940250.  
XX  
XX 04-OCT-1996; 96US-00731199.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Manoharan M, Dean NM;  
XX  
XX WPI; 2000-061907/05.  
XX  
XX Antisense oligonucleotide specific for multidrug resistance P-  
XX glycoprotein is useful for treating hyperproliferative diseases and  
XX disorders e.g. cancer.  
XX  
XX Claim 1; Col 13; 24pp; English.  
XX  
XX This sequence is an antisense oligonucleotide that specifically  
XX hybridises to nucleic acids encoding a human multidrug resistance P-  
XX glycoprotein (MDR1). The oligonucleotide inhibits expression of the P-  
XX glycoprotein, which functions as an ATP driven efflux pump. The antisense  
XX oligonucleotides of the invention have a phosphorochiolate modified  
XX backbone, and may contain residues with 2' modifications selected from 2'  
XX -methoxyethoxy, 2'-fluoro, 2'-O-fluoro or 2'-propyl. Some antisense  
XX oligonucleotides have cholesterol bound at the 3' end which ensures  
XX resistance to 3' exonucleases, enhances cellular uptake, and leaves the  
XX 5' termini available for conjugation of additional functional groups. The  
XX oligonucleotides may be used in research, diagnosis or as therapeutic  
XX

CC agents for MDR-associated hyperproliferation of cells. Inhibiting MDR1  
CC gene expression can be used to treat hyperproliferative diseases and  
CC disorders e.g. cancer, in conjunction with chemotherapeutic reagents to  
CC prevent or modulate the development of multidrug resistance during the  
CC treatment. The oligonucleotides can also be used to resensitize  
CC hyperproliferative MDR cells in an animal previously exposed to  
CC chemotherapeutic agents. Radiolabelled oligonucleotides can be used to  
CC perform autoradiography of tissues to determine localization,  
CC distribution and quantitation of MDR P-glycoproteins for research or  
CC diagnostic purposes  
CC  
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1103 AGAGTGACAGACGTGG 1120  
19 AGAGTGACAGACGTGG 2  
Db  
RESULT 3004  
AAC69251/c  
ID AAC69251 standard; DNA; 20 BP.  
XX  
AC AAC69251;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Human ABC1 gene exon 41 5' PCR primer, SEQ ID NO:150.  
XX  
KW Human ABC1 cholesterol transporter; chromosome 9q31;  
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KW Tangier disease; TD; familial HDL deficiency; FHD; polynormolism;  
KW cardiovascular disease; coronary artery disease; coronary restenosis;  
KW cerebrovascular disease; peripheral vascular disease;  
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KW prognosis; prophylaxis; drug screening; transgenic animal; PCR primer;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN W0200055318-A2.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-IB000532.  
XX  
PR 15-MAR-1999; 99US-0124702P.  
PR 08-JUN-1999; 99US-0138048P.  
PR 17-JUN-1999; 99US-0139600P.  
PR 01-SEP-1999; 99US-0151977P.  
XX  
PA (UTBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON BIORESEARCH INC.  
XX  
PI Hayden MR, Wilson AR, Pimstone SN;  
XX  
DR WPI; 2000-587528/55.  
XX  
PT New ABC1 polypeptide is useful for treating diseases associated with ABC1  
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and  
PT cancer.  
XX  
PS Disclosure; Fig 10; 229pp; English.  
XX  
CC The invention relates to the human ABC1 cholesterol transporter protein  
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
CC proteins, and plays a crucial role in cholesterol transport, particularly  
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being

CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
CC located on chromosome 9q31, and mutations in this gene are associated  
CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
CC Tangier disease (TD) and familial HDL deficiency (FHD). These diseases  
CC are distinguishable in that TD is an autosomal recessive disorder, while  
CC FHD is inherited as an autosomal dominant trait. Low levels of HDL ("good  
CC cholesterol") in the blood correlate with a high risk of cardiovascular  
CC disease, particularly coronary artery disease, but also cerebrovascular  
CC disease, coronary restenosis, and peripheral vascular disease.  
CC Conversely, a high level of HDL has protective effects against  
CC cardiovascular disease. The invention provides genetic constructs and  
CC transgenic cells and non-human animals comprising human ABC1 nucleic  
CC acids, and methods of gene therapy for the treatment or prevention of  
CC cardiovascular disease comprising the administration of an expression  
CC vector encoding ABC1 or an active fragment thereof. The invention also  
CC encompasses compounds which mimic ABC1 activity, compounds which  
CC stimulate ABC1 expression and methods of screening for such compounds. It  
CC further relates to methods for determining whether a patient has an  
CC increased risk for cardiovascular disease due to polymorphisms in the  
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or  
CC prevent cardiovascular disease, especially coronary artery disease,  
CC cerebrovascular disease, coronary restenosis or peripheral vascular  
CC disease. They may also be used in the treatment of diseases associated  
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
CC The invention specifically excludes proteins with the exact amino acid  
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
CC present sequence represents a human ABC1 gene PCR primer which may be  
CC used to amplify an exon of the human ABC1 gene  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2810 TGGATGAGAGAAAGCTTT 2827  
20 TGGATGAGAGAAAGCTTT 3  
Db  
RESULT 3005  
AAA13124  
ID AAA13124 standard; DNA; 20 BP.  
XX  
AC AAA13124;  
XX  
DT 17-JUL-2000 (first entry)  
XX  
DE PI3K antisense inhibitor oligonucleotide ISIS# 32136.  
XX  
KW Phosphatidylinositol 3 kinase; PI3K; antisense oligonucleotide; p110;  
KW catalytic subunit; treatment; rheumatoid arthritis; asthma; research;  
KW diagnostic; infection; inflammation; tumour formation; inhibitor; ss.  
XX  
OS Synthetic.  
XX  
FH Key  
FT misc\_feature 1..20 Location/Qualifiers  
FT /\*tag= a  
FT /note= "Phosphorothioate internucleoside linkage"  
FT 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"  
FT 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Optionally 2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN US6046049-A.  
XX

PD 04-APR-2000.  
XX  
XX 19-JUL-1999; 99US-00357070.  
XX  
XX 19-JUL-1999; 99US-00357070.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Coweert LM;  
PI  
XX WPI; 2000-282691/24.  
DR  
XX  
XX  
PT New antisense compounds targeting nucleic acids encoding human PI3 kinase  
PI3 kinase p110 delta expression, e.g. rheumatoid arthritis, asthma.  
PT  
XX  
XX  
PS Claim 16; Col 41; 35pp; English.  
XX  
XX This sequence represents a phosphatidylinositol 3 kinase (PI3K)  
CC targeting antisense oligonucleotide. Phosphatidylinositol 3 kinases act  
CC as downstream effectors of hormone and growth factor receptors, and have  
CC been implicated in growth factor mediated cell transformation.  
CC mtogenesis, protein trafficking, cell survival and proliferation, and  
CC many other cellular activities. PI3K is a heterodimer, consisting of a  
CC 110kD catalytic subunit (p110), and an 85kD regulatory subunit (p85). The  
CC invention relates to antisense oligonucleotides which target the p110  
CC delta mRNA of PI3K. The antisense oligonucleotides specifically hybridise  
CC with various regions of the PI3K mRNA sequence, and inhibit the  
CC expression of PI3K. The antisense oligonucleotides may be used to treat  
CC an animal, particularly human, suspected of having or being prone to a  
CC disease or condition associated with the expression of PI3K, e.g.  
CC rheumatoid arthritis or asthma. The treatment works through the  
CC modulation (preferably inhibition) of the expression of PI3K. The  
CC antisense oligonucleotides may also be used for research and diagnostics,  
CC in pharmaceutical compositions and formulations, in the preparation of  
CC kits for detecting the level of PI3K in a sample, and as prophylaxis,  
CC e.g. to prevent or delay infection, inflammation or tumour formation.  
CC Antisense oligonucleotides, which are able to inhibit gene expression  
CC specifically, are used to elucidate the function of particular genes, and  
CC to distinguish between functions of various members of a biological  
CC pathway  
XX  
XX  
SQ Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3378 GTTGGCTCTCCCGCAGCT 3395  
DB 2 GTTGGCTCTCTCCAGCT 19  
RESULT 3006  
ID AAA96416  
XX AAA96416 standard; DNA; 20 BP.  
AC  
XX  
XX AAA96416;  
DT 08-FEB-2001 (first entry)  
XX  
DE Primer used to amplify a sar47/48 polymorphic microsatellite repeat.  
XX  
XX Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;  
KM ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;  
KM insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;  
KM Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma;  
KM thyroditis; postpartum thyroditis; rheumatoid arthritis;  
KM Hashimoto's disease; coeliac disease; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200056856-A2.

XX  
XX 28-SEP-2000.  
PD  
XX  
XX 24-MAR-2000; 2000WO-US007938.  
PF  
XX  
XX 25-MAR-1999; 99US-0126215P.  
PR  
XX (GEMV ) GENETICS INST INC.  
PA  
XX  
XX Ling V, Wu P, Gray GS;  
PI  
XX  
XX WPI; 2000-628257/60.  
DR  
XX  
XX  
XX  
PT Determining predisposition of humans to develop autoimmune disease  
PT involves detecting polymorphic microsatellite repeat sequence within  
PT human costimulatory receptor gene locus.  
XX  
XX  
XX  
XX Claim 18; Page 155; 160pp; English.  
PS  
XX  
XX PCR primers AAA96415-16 were used to amplify polymorphic microsatellite  
CC repeat (PMR) sequences from the human costimulatory receptor gene locus  
CC (hCGRL). The primers are used in the method of the invention. The  
CC specification describes a method for determining the predisposition of a  
CC human subject to develop autoimmune disease. The method comprises  
CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the  
CC human costimulatory receptor gene locus (hCGRL). PMR sequences vary in  
CC length among individuals and can be amplified to generate products that  
CC differ in size. These products can then be detected by rapid and  
CC convenient high resolution processes. The method is useful for  
CC determining the predisposition of insulin-dependent diabetes mellitus  
CC (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism,  
CC myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis,  
CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.  
CC PMR sequences within hCGRL are useful as markers in a variety of assays  
CC and in the field of forensic medicine, disease diagnosis and human genome  
CC mapping  
XX  
XX  
SQ Sequence 20 BP; 1 A; 10 C; 1 G; 8 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5098 TGCCCTGTCATTGCCTT 5115  
DB 1 TCCTCTCTCATTGCCTT 18  
RESULT 3007  
ID AA287562/c  
XX AA287562 standard; DNA; 20 BP.  
AC  
XX  
XX AA287562;  
DT 19-APR-2000 (first entry)  
XX  
DE Primer specific for cancer biomarker UC Band #201.  
XX  
XX Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer;  
KM benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;  
KM diagnosis; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9964631-A1.  
PN  
XX  
XX 16-DEC-1999.  
PD  
XX  
XX 11-JUN-1999; 99WO-US013151.  
PF  
XX  
XX 12-JUN-1998; 98US-00097199.  
PR  
XX  
XX (UROC-) UROCOR INC.



XX An G, O'hara SM, Ralph D, Veltri RM;  
 XX WPI; 2000-116557/10.  
 DR  
 XX Novel RNA biomarkers for diagnosis, prognosis and management of prostate,  
 PT breast and bladder cancer.  
 XX  
 PS Example 2; Page 110; 191pp; English.  
 XX  
 CC The invention provides nucleic acid markers of prostate, breast and  
 CC bladder cancer. The markers are indicators of malignant transformation of  
 CC prostate, breast and bladder tissues and are diagnostic of the potential  
 CC for metastatic spread of malignant prostate tumours. The nucleic acid can  
 CC also be used as targets for therapeutic intervention in prostate cancer,  
 CC benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The  
 CC markers may be used to design specific probes and primers, for the rapid  
 CC analysis of prostate, bladder or breast biopsy samples. The probes and  
 CC primers may also be used for in situ hybridization or in situ PCR  
 CC detection and diagnosis. They may also be used to identify and isolate  
 CC full length gene sequences from various DNA libraries. Antibodies against  
 CC the polypeptide products of the markers can be used to treat prostate  
 CC cancer, bladder cancer or breast cancer. The encoded proteins may be used  
 CC to detect antibodies. The proteins and antibodies can be used in  
 CC immunodetection methods for detecting or quantifying the cancers, and for  
 CC clinical diagnosis of these cancers. The antibodies may also be used for  
 CC radioimaging to quantify and localize the encoded proteins  
 XX  
 SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3414 CTTATTCCTCTCTGTCCA 3431  
 Db 19 CATAATCCTCTTGTCCA 2  
 RESULT 3008  
 ID AAA11286 standard; DNA; 20 BP.  
 XX AAA11286;  
 AC  
 XX 08-NOV-2000 (first entry)  
 DT  
 XX Human TRPC7 gene intron 1/exon 2 junction.  
 DE  
 XX Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;  
 KW calcium channel function; human; gene therapy; periodic psychosis;  
 KM mutation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT intron 1..10  
 FT /\*tag= a  
 FT /number= 1  
 FT exon 11..20  
 FT /\*tag= b  
 FT /number= 2  
 XX  
 XX WO200029571-A1.  
 XX  
 XX 25-MAY-2000.  
 XX  
 XX 11-NOV-1999; 99WO-JP006289.  
 XX  
 XX 12-NOV-1998; 98JP-00321200.  
 XX  
 XX (EIKE ) EIKEN KAGAKU KK.  
 XX  
 XX

PI Shimizu N, Nagamine K;  
 XX WPI; 2000-387784/33.  
 DR  
 XX Nucleic acids encoding transmembrane protein TRPC7 expressed in brain and  
 PT homologous to transient receptor potential protein useful in the of  
 PT treatment of associated diseases such as periodic psychosis.  
 XX  
 PS Example 7; Page 38; 77pp; Japanese.  
 XX  
 CC The invention relates to the isolation of a nucleic acid (AA11284)  
 CC coding for a transmembrane protein TRPC7 (AA92944) which is expressed in  
 CC brain and is homologous to transient receptor potential (TRP) protein.  
 CC This suggests that the TRPC7 protein may have a calcium channel function.  
 CC The genomic sequence has been shown to contain 31 introns. This sequence  
 CC represents an exon/intron junction from the genomic TRPC7 sequence. The  
 CC DNA and protein can be used in the diagnosis and treatment of disorders  
 CC associated with TRPC7, especially the screening, monitoring and treatment  
 CC (by gene therapy) of periodic psychosis, which appears to be associated  
 CC with mutations in the TRPC7 gene  
 XX  
 SQ Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3676 ACCTTCAGCCAGAAAGCC 3693  
 Db 3 ACCTTCAGCAAGAAAGCC 20  
 RESULT 3009  
 ID AAZ73463/C standard; DNA; 20 BP.  
 XX AAZ73463;  
 AC  
 XX 10-SEP-2001 (first entry)  
 DT  
 XX Human biallelic marker upstream amplification primer SEQ ID NO:7819.  
 DE  
 XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9954500-A2.  
 XX  
 XX 28-OCT-1999.  
 PD  
 XX 21-APR-1999; 99WO-IB000822.  
 XX  
 XX 21-APR-1998; 98US-0082614P.  
 XX  
 XX 23-NOV-1998; 98US-0109732P.  
 XX  
 XX (GEST ) GENSET.  
 XX  
 XX Cohen D, Blumenfeld M, Chumakov I;  
 PI WPI; 2000-013267/01.  
 DR  
 XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX  
 PS Claim 9; Page 1898; 2745pp; English.  
 XX  
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies.  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX  
XX  
SQ Sequence 20 BP; 1 A; 10 C; 1 G; 8 T; 0 U; 0 Other;

Qy Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Dy 2860 GAGGACGACGAGGAGG 2877  
Db 20 GAGGAGGCAAGAGGAGG 3

RESULT 3010  
AAC73675/c  
ID AAC73675 standard; DNA; 20 BP.  
XX  
XX AAC73675;  
AC  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Murine IL-5 antisense oligonucleotide ISIS #17981.  
XX  
XX Mouse; interleukin-5; IL-5; signal transduction;  
KM antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;  
KM IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;  
KM inflammation; cancer; ss.  
XX  
XX Mus musculus.  
OS Synthetic.  
OS  
XX  
XX WO200058512-A1.  
PN  
XX  
PD 05-OCT-2000.  
XX  
PF 17-MAR-2000; 2000WO-US007318.  
XX  
XX  
PR 26-MAR-1999; 99US-00280799.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Dean NM, Karraas JG, McKay R;  
PI  
XX  
DR WPI; 2000-594648/56.  
XX  
XX  
PT Antisense oligonucleotide compound used to treat asthma and eosinophilic  
PT syndrome in humans modulates interleukin-5 signal transduction.  
PT  
XX  
XX Example 14; Page 53; 156pp; English.  
PS  
XX  
CC The present sequence is an oligonucleotide used for antisense modulation  
CC of interleukin-5 (IL-5) signal transduction. Oligonucleotides were  
CC designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha.  
CC The antisense oligonucleotides may be used for the treatment of diseases  
CC associated with IL-5 signal transduction, IL-5 expression or IL-5  
CC receptor-alpha expression. Such diseases include asthma and eosinophilic  
CC syndrome. The oligonucleotides are also useful for research uses and to  
CC prevent or delay infection, inflammation or tumour formation

XX  
XX  
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5272 ATTAGGACGACGTGGCAG 5289  
Db 20 AGACGAGCAGCGTGGCAG 3

RESULT 3011  
AAC60575  
ID AAC60575 standard; DNA; 20 BP.  
XX  
XX AAC60575;  
AC  
XX  
DT 31-JAN-2001 (first entry)  
XX  
XX  
DE Human fra-1 mRNA antisense oligonucleotide ISIS 109066.  
XX  
XX Human; fra-1; antisense oligonucleotide; phosphorothioate; cytostatic;  
KM antinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;  
KM ss.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX  
XX US6124133-A.  
PN  
XX  
PD 26-SEP-2000.  
XX  
PF 15-OCT-1999; 99US-00418641.  
XX  
PR 15-OCT-1999; 99US-00418641.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
XX Taylor JK, Cowsext LM;  
PI  
XX  
DR WPI; 2000-601552/57.  
XX  
XX  
PT Novel antisense compound 8-30 nucleobases in length targeted to human fra  
PT -1 and which specifically hybridizes with and inhibits the expression of  
PT human fra-1, useful for modulating the expression of fra-1 in cells.  
PT  
XX  
XX Example 15; Col 42; 38pp; English.  
PS  
XX  
XX The present sequence is one of a large number of antisense  
CC oligonucleotides which are targeted to nucleic acids encoding fra-1. The  
CC sequences may be oligodeoxynucleotides or chimeric oligonucleotides,  
CC containing a central gap region consisting of ten 2'-deoxynucleotides,  
CC which is flanked on both sides by 2'-methoxyethyl (2'-MOE) wings. The  
CC oligonucleotides have a phosphorothioate backbone and the cytidine  
CC residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense  
CC oligonucleotides are useful for inhibiting the expression of fra-1 in  
CC human cells or tissues. They can be used for diagnostics, therapeutics,  
CC prophylaxis and as research reagents and in kits. Use of the antisense  
CC compounds may also be useful prophylactically, e.g. to prevent or delay  
CC infection, inflammation or tumour formation

XX  
XX  
SQ Sequence 20 BP; 4 A; 1 C; 10 G; 5 T; 0 U; 0 Other;

Qy 4175 TAGGAGGCGGTGCTTAT 4192  
Db 1 TAGGAGGCGGTGCTCAT 18

RESULT 3012  
AAA90815  
ID AAA90815 standard; DNA; 20 BP.  
XX

AC AAA90815;  
 XX  
 DT 20-DEC-2000 (first entry)  
 XX  
 DE Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.  
 XX  
 XX Antisense oligonucleotide; ribonucleotide reductase; R1 protein;  
 KW R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200047733-A1.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000WO-CA000120.  
 XX  
 PR 11-FEB-1999; 99US-00249730.  
 XX  
 PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX  
 PI Wright JA, Young AH;  
 XX  
 DR WPI; 2000-558216/51.  
 XX  
 PT New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting  
 PT tumor cell growth.  
 XX  
 PS Example 3; Page 32; 137pp; English.  
 XX  
 CC The present sequence is an antisense oligonucleotide directed against the  
 CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.  
 CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to  
 CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide  
 CC reductase is altered in cultured malignant cells and increased levels of  
 CC R2 protein and R2 mRNA have been found in pre-malignant and malignant  
 CC tissues as compared to normal control tissue samples. The present  
 CC antisense sequence is therefore useful for inhibiting tumorigenicity of  
 CC neoplastic cells and inhibiting metastasis of tumour cells. It is also  
 CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic  
 CC drugs, thus allowing chemotherapeutic treatments to be used in patients  
 CC who have become resistant or less sensitive to chemotherapy. The sequence  
 CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide  
 CC analogues  
 XX  
 SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4463 CTTTTTTTTTTTTTTT 4480  
 DB 3 CGTTTTTTTTTTCTTTT 20  
 XX  
 RESULT 3013  
 AAA66863  
 ID AAA66863 standard; DNA; 20 BP.  
 XX  
 AC AAA66863;  
 XX  
 DT 09-OCT-2000 (first entry)  
 XX  
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:725.  
 XX  
 KW Dog; genome; genomic marker; radiation hybrid map; identification;  
 KW chromosome location; gene marker; polymorphic microsatellite marker;  
 KW phenotype; behaviour; pedigree; ss.  
 XX  
 OS Canis familiaris.  
 XX

PN WO200029615-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 15-NOV-1999; 99WO-IB001907.  
 XX  
 PR 13-NOV-1998; 98US-0108193P.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Galibert F, Andre C;  
 XX  
 DR WPI; 2000-387821/33.  
 XX  
 FT New radiation hybrid map of the dog, Canine familiaris, genome, useful  
 FT for e.g. identifying genes implicated in phenotypic and behavioral traits  
 FT or in genetic diseases and for studying dog pedigrees.  
 XX  
 PS Claim 1; Page 84; 87pp; English.  
 XX  
 CC The present invention describes a radiation hybrid map of the dog (Canine  
 CC familiaris) genome comprising the genome location of a marker selected  
 CC from AAA66139 to AAA66942. The radiation hybrid map is useful for  
 CC identifying and localising dog genes, since it covers approximately 80 %  
 CC of the dog genome and provides a dense map integrating different types  
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers  
 CC (or complementary sequences) are especially useful to identify genes  
 CC responsible for phenotypic and behavioural traits in dogs, to identify  
 CC morbid genes, to analyse diseases and identify implicated genes in such  
 CC diseases and their alleles, and to study dog pedigrees. They may also be  
 CC useful for isolating corresponding human gene sequences e.g. genes  
 CC involved in genetic diseases  
 XX  
 SQ Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4273 CTGTCCTGCACTTTTCT 4290  
 DB 2 CTGTCCTGCACTTTTCT 19  
 XX  
 RESULT 3014  
 AAA66923/C  
 ID AAA66923 standard; DNA; 20 BP.  
 XX  
 AC AAA66923;  
 XX  
 DT 09-OCT-2000 (first entry)  
 XX  
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:785.  
 XX  
 KW Dog; genome; genomic marker; radiation hybrid map; identification;  
 KW chromosome location; gene marker; polymorphic microsatellite marker;  
 KW phenotype; behaviour; pedigree; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO200029615-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 15-NOV-1999; 99WO-IB001907.  
 XX  
 PR 13-NOV-1998; 98US-0108193P.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Galibert F, Andre C;  
 XX  
 DR WPI; 2000-387821/33.  
 XX

XX New radiation hybrid map of the dog, Canine familiaris, genome, useful  
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits  
 PT or in genetic diseases and for studying dog pedigrees.  
 XX  
 PS Claim 1, Page 87, 87pp; English.  
 CC The present invention describes a radiation hybrid map of the dog (Canine  
 CC familiaris) genome comprising the genome location of a marker selected  
 CC from AAA66139 to AAA66942. The radiation hybrid map is useful for  
 CC identifying and localising dog genes, since it covers approximately 80 %  
 CC of the dog genome and provides a dense map integrating different types  
 CC (i.e. Type I and Type II) of markers. The map and the dog genome markers  
 CC (or complementary sequences) are especially useful to identify genes  
 CC responsible for phenotypic and behavioural traits in dogs, to identify  
 CC morbid genes, to analyse diseases and identify implicated genes in such  
 CC diseases and their alleles, and to study dog pedigrees. They may also be  
 CC useful for isolating corresponding human gene sequences e.g. genes  
 CC involved in genetic diseases  
 CC  
 SQ Sequence 20 BP, 5 A; 8 C; 0 G; 7 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 3187 TTTGATGGGAAAGTGA 3204  
 19 TTGAGATGGGAAAGTGTG 2  
 RESULT 3015  
 ID AAA91212 standard; DNA; 20 BP.  
 AC AAA91212;  
 XX  
 DT 08-MAY-2001 (first entry)  
 XX  
 DE Antisense IGFBP-5 inhibitor #18.  
 XX  
 KM Insulin-like growth factor binding protein-5; IGFBP-5; human;  
 KM antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;  
 KM breast cancer; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200105435-A2.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 19-JUL-2000; 2000WO-CA000853.  
 XX  
 PR 19-JUL-1999; 99US-0144495P.  
 XX  
 PA (UVBR-) UNIV BRITISH COLUMBIA.  
 PA (MIYA/) MIYAKE H.  
 XX  
 PI Gleave M;  
 XX  
 DR WPI; 2001-168448/17.  
 XX  
 PT Composition for treating hormone-regulated cancer, e.g. breast and  
 PT prostatic tumors, comprising an antisense oligonucleotide that inhibits  
 PT expression of insulin like growth factor binding protein-5 by hormone-  
 PT regulated tumor cells.  
 XX  
 PS Disclosure; Page 35; 45pp; English.  
 CC This sequence represents an antisense oligonucleotide targeted against  
 CC human insulin-like growth factor binding protein-5 (IGFBP-5). The  
 CC invention relates to a composition for treatment of hormone-regulated  
 CC cancer, comprising an antisense oligonucleotide (such as this sequence)

CC which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.  
 CC The compositions is useful for delaying progression of hormone-regulated  
 CC tumour cells such as prostatic cancer cells or breast cancer cells, to an  
 CC androgen-independent state, by treating hormone sensitive tumour cells  
 CC with the antisense sequence which inhibits expression of IGFBP-5 by the  
 CC tumour cells. The composition can also be used for treating a hormone-  
 CC responsive cancer in an individual, and administering the composition to  
 CC the individual after initiation of hormone-withdrawal to induce apoptotic  
 CC cell death of hormone-responsive tumour cells, and therefore delaying the  
 CC progression of hormone-responsive cancer cells to a hormone-independent  
 CC state in the individual. It can also be used for inhibiting or delaying  
 CC metastatic bony progression of an IGF-1 sensitive tumour in a mammal, by  
 CC administering the composition to inhibit the expression of IGFBP-5 by the  
 CC hormone-responsive cancer cells, and therefore inhibiting or delaying  
 CC metastatic bony progression of the tumour  
 CC  
 SQ Sequence 20 BP, 1 A; 1 C; 15 G; 3 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 3623 GGCTGGGGGTGGGAGAG 3640  
 1 GGCTGGGGGTGGGAGGCG 18  
 RESULT 3016  
 ID AAD06582/c standard; DNA; 20 BP.  
 AC AAD06582;  
 XX  
 DT 10-AUG-2001 (first entry)  
 XX  
 DE Human alpha1(I) collagen gene coding region amplifying SSCP 2REV primer.  
 XX  
 KM Human; alpha1(I) collagen; gelatin; cytoectatic; viral infection;  
 KM pharmaceutical; food industry; cosmetic; autoimmune disorder; vaccine;  
 KM medical; arterial sealant; bone graft; dermal implant; haemostat; cancer;  
 KM rheumatoid arthritis; beverage; photographic application; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200134647-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 10-NOV-2000; 2000WO-US030792.  
 XX  
 PR 12-NOV-1999; 99US-00439058.  
 XX  
 PA (FIBR-) FIBROGEN INC.  
 PA Bell MP, Neff TB, Polarek JW, Seeley TW;  
 XX  
 DR WPI; 2001-335911/35.  
 XX  
 PT Novel isolated and purified bovine or porcine collagens and gelatins  
 PT useful in medical, pharmaceutical, food and cosmetic industries, as  
 PT vaccine, and for treating autoimmune disorders, infections and cancer.  
 XX  
 PS Example 1; Page 56; 168pp; English.  
 CC The present sequence is a PCR primer used for amplifying the coding  
 CC region of human alpha1(I) collagen gene. The present invention relates to  
 CC recombinant syntheses of collagens and gelatins derived from animals.  
 CC Collagen is useful in medical, pharmaceutical, food and cosmetic  
 CC industries. Collagen is an important component of arterial sealants, bone  
 CC grafts, drug delivery system, dermal implants, haemostats, and  
 CC incontinence implants, and for treating autoimmune disorders such as  
 CC rheumatoid arthritis. Collagen is useful in food products such as sausage

CC casing, and in cosmetics or facial and skin products such as  
CC moisturizers. Recombinant gelatin is useful in vaccine formulations for  
CC treating viral infections, autoimmune diseases and cancer. Gelatin is  
CC useful in the manufacture or as a component of various pharmaceutical and  
CC medical devices and products, in food and beverage industries, in hair  
CC care and skin care products, as a glue or adhesive in various  
CC manufacturing processes, as a light-sensitive coating in various  
CC electronic devices, as photorealist base in photolithographic processes,  
CC in printing and photographic applications, in laboratory application, and  
CC as a component in various gels used for biochemical and electrophoretic  
CC analysis, including enzymographic gels

XX  
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 263 TGCAGCAGGTGTTCCAGG 280  
DB 20 TGCAGCTGTCTTCCAGG 3

RESULT 3017  
AAK95028/C  
ID AAK95028 standard; DNA; 20 BP.

XX AAK95028;

XX 06-NOV-2001 (first entry)

DE Human cDNA clone-specific primer, SEQ ID NO: 4273.

XX Human, full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 98JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.

XX 830 Primers useful for synthesizing full length cDNA clones and their use  
XX in genetic manipulation.

XX Example 18; Page 129; 1380pp + Sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
XX clones. 830 cDNA molecules encoding a human protein have been isolated  
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
XX been determined. Primers for synthesizing the full length cDNA are useful  
XX for clarifying the function of the protein encoded by the cDNA. The full  
XX length clones were obtained by construction of full length enriched cDNA  
XX libraries that were synthesised by the oligo-capping method. The primers  
XX enable the production of the full length cDNA easily without any special  
XX method. The present sequence is a primer used to amplify a human cDNA  
XX clone provided in the invention

XX Sequence 20 BP; 8 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 898 ATTGAGTTCATGTGTGAG 915  
DB 20 AATGAGTTCATGTGTG 3

RESULT 3018

AAF87023  
ID AAF87023 standard; DNA; 20 BP.

XX AAF87023;

XX 18-SEP-2001 (first entry)

DE Sequencing primer for Human CP2/LSF/LBP-1 ARNm sequence.

XX LBP-1; human; intron; Alzheimer's disease; diagnosis; ADN sequence;  
XX CP2/LSF/LBP-1 gene; sequencing primer; ss.

XX Homo sapiens.

XX EP113081-A1.

XX 04-JUL-2001.

XX 28-DEC-1999; 99EP-00403304.

XX 28-DEC-1999; 99EP-00403304.

XX (INSP ) INST PASTEUR LILIE.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX Chartier-Harlin M, Amouyel P, Lambert J;

XX WPI; 2001-427121/46.

XX Predicting increased risk of human developing Alzheimer's disease,  
XX PT comprises identifying polymorphisms located at untranslated regions of  
XX CP2/LSF/LBP-1 gene.

XX Example 1; Page 10; 35pp; English.

XX This sequence is a sequencing primer for the human CP2/LSF/LBP-1 gene  
XX ARNm. The invention relates to a method for predicting an increased risk  
XX of a human subject of developing Alzheimer's disease, comprising assaying  
XX for a mutation within the ADN sequence of the CP2/LSF/LBP-1 gene  
XX including the region controlling the expression of the gene. The method  
XX is useful for predicting an increased risk of a human subject of  
XX developing Alzheimer's disease. Transgenic animals containing sequences  
XX from the CP2/LSF/LBP-1 gene are useful for screening for drugs capable of  
XX reducing or treating symptoms associated with Alzheimer's disease

XX Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3140 ACTCTGTAGCCCTGCAGCA 3157  
DB 1 AATCTGTAGCCCTGCAGCA 18

RESULT 3019

AAAD15632/C  
ID AAAD15632 standard; DNA; 20 BP.

XX AAAD15632;

XX 15-NOV-2001 (first entry)

```
DE Human Bcl-2 protein target DNA #6.
XX
XX Human; Bcl-2 protein; genetic disease; antisense target; therapeutic; ss.
XX
XX Homo sapiens.
XX
XX WO200161030-A2.
XX
XX 23-AUG-2001.
XX
XX 14-FEB-2001; 2001WO-US0004732.
XX
XX 14-FEB-2000; 2000US-00504653.
XX
XX (BOLT/) BOLLON A P.
XX
XX (GRAY/) GRAY D M.
XX
XX (JUSE/) JU-SEOG L.
XX
XX Bollon AP, Gray DM, Ju-Seog L;
XX
XX WPI; 2001-529916/58.
XX
XX Selecting optimal subsequence antisense targets for inhibition of mRNA
XX
XX expression of target mRNA for the therapeutic treatment of genetic
XX
XX disease.
XX
XX Example 9; Page 28; 87pp; English.
XX
XX The invention relates to a method for selecting optimal subsequence
XX
XX antisense targets. The method involves preparing an antisense
XX
XX oligonucleotide capable of inhibiting mRNA expression of target mRNA
XX
XX sequences, as well as antisense oligonucleotides capable of binding DNA.
XX
XX The antisense and antigen libraries are useful for preparing therapeutic
XX
XX agents for the treatment of genetic disease. The present DNA sequence is
XX
XX human Bcl-2 protein target DNA related to the invention. Note: The
XX
XX present sequence is shown as DNA in the specification; however, in vivo,
XX
XX this target sequence would be mRNA
XX
XX Sequence 20 BP; 0 A; 10 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 40 AGGCTCGCGGCGGCGC 57
XX
XX 20 AGGCCCGCGGCGGCGC 3
XX
XX
XX RESULT 3020
XX
XX AAH28626
XX
XX ID AAH28626 standard; DNA; 20 BP.
XX
XX
XX AAH28626;
XX
XX
XX 17-JUL-2001 (first entry)
XX
XX
XX Human interleukin-13 coding sequence fragment PCR primer #1.
XX
XX
XX Human; interleukin-13; IL13; single nucleotide polymorphism; SNP; cancer;
XX
XX inflammation; immune disorder; cytokine; asthma; chromosome 5q31;
XX
XX fibrosis; forensic; disease susceptibility; drug screening; PCR primer;
XX
XX ss.
XX
XX Homo sapiens.
XX
XX
XX WO200123410-A2.
XX
XX
XX 05-APR-2001.
XX
XX
XX 27-SEP-2000; 2000WO-US026556.
XX
XX
XX 28-SEP-1999; 99US-0156489P.
XX
XX
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```
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
XX WPI; 2001-343160/36.
XX
XX
XX Novel polynucleotide comprising single nucleotide polymorphisms in human
XX
XX interleukin-13 gene is useful for studying expression and function of
XX
XX interleukin-13, as well as diagnosing and treating cancer, inflammatory,
XX
XX and immune disorders.
XX
XX Example 1; Page 30; 85pp; English.
XX
XX
XX The present invention provides the protein, cDNA and genomic sequences of
XX
XX human interleukin-13 (IL13), and describes the single nucleotide
XX
XX polymorphisms (SNPs) found within the gene, which is found on chromosome
XX
XX 5q31. IL13 is a pro-inflammatory cytokine thought to be involved in the
XX
XX pathogenesis of asthma and other immune and inflammatory diseases. The
XX
XX IL13 sequences and the SNPs identified can be used in drug screening, to
XX
XX determine an individual's susceptibility to disease, in forensic and
XX
XX paternity testing, and to identify treatments for cancer, immune and
XX
XX inflammatory diseases, including asthma and diseases characterised by
XX
XX fibrosis. The present sequence is an IL13 fragment PCR primer
XX
XX
XX Sequence 20 BP; 6 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 6866 CCTGCGCAGCGAGAGAGC 6883
XX
XX 3 CCTGAGCAGCGCAGAGAGC 20
XX
XX
XX RESULT 3021
XX
XX AAH28642
XX
XX ID AAH28642 standard; DNA; 20 BP.
XX
XX
XX AAH28642;
XX
XX
XX 17-JUL-2001 (first entry)
XX
XX
XX Human interleukin-13 coding sequence fragment PCR primer #17.
XX
XX
XX Human; interleukin-13; IL13; single nucleotide polymorphism; SNP; cancer;
XX
XX inflammation; immune disorder; cytokine; asthma; chromosome 5q31;
XX
XX fibrosis; forensic; disease susceptibility; drug screening; PCR primer;
XX
XX ss.
XX
XX Homo sapiens.
XX
XX
XX WO200123410-A2.
XX
XX
XX 05-APR-2001.
XX
XX
XX 27-SEP-2000; 2000WO-US026556.
XX
XX
XX 28-SEP-1999; 99US-0156489P.
XX
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
XX WPI; 2001-343160/36.
XX
XX
XX Novel polynucleotide comprising single nucleotide polymorphisms in human
XX
XX interleukin-13 gene is useful for studying expression and function of
XX
XX interleukin-13, as well as diagnosing and treating cancer, inflammatory,
XX
XX and immune disorders.
XX
XX Example 1; Page 32; 85pp; English.
XX
XX
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XX The present invention provides the protein, cDNA and genomic sequences of
CC human interleukin-13 (IL13), and describes the single nucleotide
CC polymorphisms (SNPs) found within the gene, which is found on chromosome
CC 5q31. IL13 is a pro-inflammatory cytokine thought to be involved in the
CC pathogenesis of asthma and other immune and inflammatory diseases. The
CC IL13 sequences and the SNPs identified can be used in drug screening, to
CC determine an individual's susceptibility to disease, in forensic and
CC paternity testing, and to identify treatments for cancer, immune and
CC inflammatory diseases, including asthma and diseases characterised by
CC fibrosis. The present sequence is an IL13 fragment PCR primer
XX
SQ Sequence 20 BP; 5 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 6866 CTTGGGAGGAGAGAGG 6883
Db 2 CTTGAGCAGGCGAGAGG 19
RESULT 3022
AAS03979/c
ID AAS03979 standard; DNA; 20 BP.
XX
AC AAS03979;
XX
DT 29-AUG-2001 (first entry)
XX
DE Biomarker UC band 201 primer #2 used in diagnosis/prognosis of cancer.
XX
KW prostate; breast; bladder; cancer; biomarker; probe; diagnostic;
KW benign prostatic hyperplasia; BPH; therapeutic; human; primer; ss.
XX
OS Homo sapiens.
XX
PN US6218529-B1.
XX
PD 17-APR-2001.
XX
PF 12-JUN-1998; 98US-00097199.
XX
PR 31-JUL-1995; 95US-0001655P.
PR 11-JAN-1996; 96US-0013611P.
PR 31-JUL-1996; 96US-00692787.
XX
PA (UROC-) UROCOR INC.
XX
PI An G, O'hara SM, Ralph D, Veltri R;
XX
DR WPI; 2001-289849/30.
XX
PT New nucleic acids as biomarkers and targets useful for detecting,
PT diagnosing, prognosing, and in developing treatments for prostate, breast
PT and bladder cancer.
XX
PS Example 4; Col 71; 78pp; English.
XX
The sequence represents nucleic acid biomarker UC band 201 primer #2,
CC used in detection of prostate, breast and bladder cancer. Biomarker
CC nucleic acid sequences can be used as hybridisation probes and primers
CC that specifically hybridise to prostate cancer, benign prostatic
CC hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins
CC encoded by the nucleic acid markers can be used to produce antibodies for
CC the detection of prostate, breast or bladder cancer. The nucleic acids
CC can be used as targets for therapeutic intervention in these diseases, in
CC the identification and isolation of full-length gene sequences, including
CC regulatory elements for gene expression, from genomic human DNA
CC libraries, as hybridisation probes for screening genomic human DNA
CC libraries. The kits comprising the nucleic acid sequences are useful for
CC detecting bladder, breast or prostate cancer cells in a biological sample

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XX SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 3414 CTTATTCCTCTCTTCCA 3431
Db 19 CATATTCCTCTTGTCCA 2
RESULT 3023
AAF23272
ID AAF23272 standard; DNA; 20 BP.
XX
AC AAF23272;
XX
DT 19-MAR-2001 (first entry)
XX
DE Oligonucleotide for detection of Mycobacterium malmoeense.
XX
KW ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW Mycobacterium dermatitidis; PCR primer; probe; detection; ss.
XX
OS Mycobacterium malmoeense.
XX
PN WO200073436-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000MO-KR000477.
XX
PR 29-MAY-1999; 99KR-00019631.
PR 29-MAY-1999; 99KR-00019632.
PR 29-MAY-1999; 99KR-00019633.
PR 29-MAY-1999; 99KR-00019634.
PR 29-MAY-1999; 99KR-00019635.
PR 07-APR-2000; 2000KR-00018189.
XX
PA (SHT-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
PI Kim CM, Park HK, Jang HJ;
XX
DR WPI; 2001-061527/07.
XX
PT Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
PS Claim 27; Page 65; 89pp; English.
XX
The present sequence is an oligonucleotide developed using a
CC Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC dermatitidis genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridisation probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,

```

CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria  
CC (NTM), and to identify mycobacteria species accurately and effectively  
XX  
SQ Sequence 20 BP; 2 A; 2 C; 3 G; 13 T; 0 U; 0 Other;  
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
4644 TGTGATTTCTCTTTG 4661  
3 TGTGATTTCTCTTTG 20  
Db  
RESULT 3024  
AAF91363/C  
ID AAF91363 standard; DNA; 20 BP.  
XX  
AC AAF91363;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Human E2F transcription factor 1 antisense oligonucleotide #69.  
XX  
KW Antisense; E2F transcription factor 1; human; infection; inflammation;  
KM tumour; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6187587-B1.  
XX  
PD 13-FEB-2001.  
XX  
PF 02-MAR-2000; 2000US-00517584.  
XX  
PR 02-MAR-2000; 2000US-00517584.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Popoff I, Brown-Driver VL, Cowbert LM;  
XX  
DR WPI; 2001-190981/19.  
XX  
PT Antisense compound capable of inhibiting the expression of E2F  
XX transcription factor 1, useful for preventing or delaying infection,  
PT inflammation or tumor formation.  
XX  
PS Example 15; Col 43; 40pp; English.  
XX  
CC The present invention relates to antisense compounds up to 30 nucleobases  
CC in length targeted to a E2F transcription factor 1. The invention is  
CC useful for inhibiting the expression of E2F transcription factor 1 in  
CC cells or tissues. The antisense oligonucleotides may also be used as a  
CC research agent and to prevent infection, inflammation or tumours  
XX  
SQ Sequence 20 BP; 4 A; 14 C; 0 G; 2 T; 0 U; 0 Other;  
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
2870 GGAGAGGGAGTGGGT 2887  
19 GGAGAGGGAGTGGGT 2  
Db  
RESULT 3025  
ABL57890  
ID ABL57890 standard; DNA; 20 BP.  
XX  
AC ABL57890;  
XX  
DT 11-SEP-2003 (revised)

DT 04-JUL-2002 (first entry)  
XX  
DE Hypersensitive reaction and pathogenicity, hrpC2, PCR primer Xcc2.4.  
XX  
KW PCR; primer; hypersensitive reaction and pathogenicity; hrpC2;  
KM exo-polysaccharide; xanthan gum; ss.  
XX  
OS Xanthomonas campestris; pv vesicatoria.  
XX  
PN WO200078967-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-FR001725.  
XX  
PR 22-JUN-1999; 99FR-00007963.  
XX  
PA (RHOD ) RHODIA CHIM.  
XX  
PI Pierrard J, Simon J, Chevallereau P;  
XX  
DR WPI; 2001-102725/11.  
XX  
PT New Xanthomonas campestris bacteria strains for use in production of exo-  
XX polysaccharides are made non-virulent by inactivation of at least one  
XX virulence gene.  
XX  
PS Example 1; Page 25; 33pp; French.  
XX  
CC The present invention relates to new Xanthomonas campestris bacteria  
XX strains made non-virulent by inactivation of at least one virulence gene  
CC but which have retained the capacity to produce exo-polysaccharides  
CC (preferably xanthan gum). One such virulence gene deleted to produce the  
CC bacterial strains was the hrpC2 gene (Hypersensitive Reaction and  
CC Pathogenicity). The hrp genes are essential for pathogenicity in plants.  
CC The present sequence is a PCR primer used to clone the hrpC2 gene in an  
CC example from the invention. (Updated on 11-SEP-2003 to standardise OS  
XX field)  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
2650 TACCACCTGGTGGACAAG 2667  
2 TTCACCTGGTGGACAAG 19  
Db  
RESULT 3026  
AAH46127/C  
ID AAH46127 standard; DNA; 20 BP.  
XX  
AC AAH46127;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE Human CLCA1 sequencing primer PR22, SEQ ID NO:29.  
XX  
KW Human CLCA1; goblet cell; mouse Gob-5 orthologue; drug screening;  
XX expression inhibition; antisense therapy; gene therapy;  
KW chronic obstructive pulmonary disease; bronchial asthma; antiasthmatic;  
KM sequencing primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138530-A1.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-JP008232.  
XX



```

PR 24-NOV-1999; 99JP-00333479.
PR 27-APR-2000; 2000JP-00127589.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Nakanishi A, Morita S;
XX
XX WPI; 2001-355935/37.
XX
XX New antisense nucleotide, useful for treatment and prevention of
XX bronchial asthma and chronic obstructive pulmonary disease.
XX
XX Example 5; Page 95; 104pp; Japanese.
XX
XX The invention relates to an antisense nucleotide targeted to the mouse
XX Gob-5 gene (coding sequence shown in AAH46101) or its human counterpart,
XX the CLCA1 gene (coding sequence shown in AAH46102). The invention also
XX relates to an antibody specific for the Gob-5 protein, medical and
XX diagnostic compositions containing the antisense nucleotide or the
XX antibody, and methods and kits for screening for compounds which inhibit
XX the protein. Gob-5 and CLCA1 are proteins expressed by goblet cells. The
XX antisense oligonucleotides and antibody are therefore useful for the
XX treatment and prevention of bronchial asthma and chronic obstructive
XX pulmonary disease. Sequences AAH46125-AAH46136 represent primers used in
XX an exemplification of the invention to sequence human CLCA1 cDNA
XX (AAH46124)
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;
XX Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
XX
OY 1057 GTTACCCGTCGCCCTGCT 1074
XX ||||| ||||| |||||
XX 20 GTTACCACTGCCCATGCT 3
XX
Db
XX
XX RESULT 3027
XX AAH46128
XX ID AAH46128 standard; DNA; 20 BP.
XX
XX AC AAH46128;
XX
XX DT 11-SEP-2001 (first entry)
XX
XX DE Human CLCA1 sequencing primer PR23, SEQ ID NO:30.
XX
XX KW Human CLCA1; goblet cell; mouse Gob-5 orthologue; drug screening;
XX expression inhibition; antisense therapy; gene therapy;
XX KW chronic obstructive pulmonary disease; bronchial asthma; antiasthmatic;
XX sequencing primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200138530-A1.
XX
XX PD 31-MAY-2001.
XX
XX PF 22-NOV-2000; 2000WO-JP008232.
XX
XX PR 24-NOV-1999; 99JP-00333479.
XX PR 27-APR-2000; 2000JP-00127589.
XX
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX PI Nakanishi A, Morita S;
XX
XX DR WPI; 2001-355935/37.
XX
XX New antisense nucleotide, useful for treatment and prevention of
XX bronchial asthma and chronic obstructive pulmonary disease.
XX

```

```

PS Example 5; Page 95; 104pp; Japanese.
XX
XX The invention relates to an antisense nucleotide targeted to the mouse
XX Gob-5 gene (coding sequence shown in AAH46101) or its human counterpart,
XX the CLCA1 gene (coding sequence shown in AAH46102). The invention also
XX relates to an antibody specific for the Gob-5 protein, medical and
XX diagnostic compositions containing the antisense nucleotide or the
XX antibody, and methods and kits for screening for compounds which inhibit
XX the protein. Gob-5 and CLCA1 are proteins expressed by goblet cells. The
XX antisense oligonucleotides and antibody are therefore useful for the
XX treatment and prevention of bronchial asthma and chronic obstructive
XX pulmonary disease. Sequences AAH46125-AAH46136 represent primers used in
XX an exemplification of the invention to sequence human CLCA1 cDNA
XX (AAH46124)
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 0; Gaps 0;
XX Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
XX
OY 1057 GTTACCCGTCGCCCTGCT 1074
XX ||||| ||||| |||||
XX 1 GTTACCACTGCCCATGCT 18
XX
Db
XX
XX RESULT 3028
XX AAS00329
XX ID AAS00329 standard; DNA; 20 BP.
XX
XX AC AAS00329;
XX
XX DT 17-MAY-2001 (first entry)
XX
XX DE Primer c816F, used to sequence human RAD51 gene.
XX
XX KW Human; RAD51; breast cancer; BRCA1; BRCA2; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200118254-A2.
XX
XX PD 15-MAR-2001.
XX
XX PF 08-SEP-2000; 2000WO-US024786.
XX
XX PR 10-SEP-1999; 99US-0153288P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Wang WW, Struwing JP;
XX
XX DR WPI; 2001-235217/24.
XX
XX New nucleic acids comprising a mutant of the RAD51 gene, useful for
XX diagnosing genetic predisposition or susceptibility to breast cancer.
XX
XX Example; Page 18; 42pp; English.
XX
XX The sequence represents primer c816F, used to sequence the human RAD51
XX gene. The nucleic acid is useful in diagnosing genetic predisposition or
XX susceptibility to breast cancer in an individual using the following
XX steps: (1) detecting a mutation in the RAD51 gene in a human subject,
XX comprising analysing a sample from the subject to detect the mutation;
XX (2) assessing the risk of developing breast cancer, comprising: (a)
XX analysing a sample from the subject for the presence of BRCA1 and/or
XX BRCA2 mutations; and (b) if (a) is positive, analysing the sample for a
XX mutation in the RAD51 gene, where the presence of the RAD51 mutation
XX indicates an increased risk in developing breast cancer in the subject as
XX compared to a subject having at least one of the BRCA mutations and a
XX wild-type RAD51 gene. Primers derived from the sequence can be used in a
XX kit for detecting a mutation in the RAD51 gene of a subject, which is
XX associated with a predisposition to breast cancer, comprising at least 2
XX

```

CC nucleic acid primers derived from the RAD51 gene sequence  
XX Sequence 20 BP; 8 A; 9 C; 2 G; 1 T; 0 U; 0 Other;  
SQ

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2954 CAAGACAGACCCAGCC 2971

DB 2 CAACACAGACCCAGCAG 19

RESULT 3029

AAH80771 standard; cDNA; 20 BP.

AAH80771;

11-SEP-2003 (revised)

19-SEP-2001 (first entry)

Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 735.

Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;

disease diagnosis; ss.

Human immunodeficiency virus 1.

US6251588-B1.

26-JUN-2001.

10-FEB-1998; 98US-00021701.

10-FEB-1998; 98US-00021701.

(AGIL-) AGILENT TECHNOLOGIES INC.

Shannon KM, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

WPI; 2001-424456/45.

Predicting the potential of an oligonucleotide to hybridize to a target  
nucleotide sequence, useful for evaluating oligonucleotide probe  
sequences, by identifying a oligonucleotides based on the evaluation of  
parameters.

Example 2; Col 71; 342pp; English.

The present invention describes a method for predicting the potential of  
an oligonucleotide to hybridize to a (complementary) target nucleotide  
sequence, involving identifying a subset of oligonucleotides within the  
predetermined number of unique oligonucleotides based on the evaluation  
of the parameter. Oligonucleotides in the subset are identified that are  
clustered along a region of the nucleotide sequence that is hybridisable  
to the target nucleotide sequence. This is useful for evaluating  
oligonucleotide probe sequences. The present sequence is an  
oligonucleotide described in the exemplification of the invention.  
(Updated on 11-SEP-2003 to standardise OS field)

Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

QY 5703 CCTTCCTTCTCTCTCT 5720

DB 2 CCTTCCTTCTCTCTCT 19

RESULT 3030

ABA98541  
ID ABA98541 standard; DNA; 20 BP.

ABA98541;

25-APR-2002 (first entry)

Murine G protein-coupled receptor, IGPcr17, PCR primer #2.

G protein-coupled receptor; IGPcr17; analgesic; neuroleptic;  
tranquilliser; antiparkinsonian; neuroprotective; nootropic; murine;  
anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;  
antidiarrhetic; osteopathic; antiaesthetic; antiallergic; antiarthritic;  
immunosuppressive; gene therapy; psychiatric disorder;  
central nervous system disorder; movement dysfunction; schizophrenia;  
multiple sclerosis; Alzheimer's disease; kidney disease; obesity;  
gastrointestinal disorder; osteoporosis; infection;  
gynecological disorder; PCR primer; ss.

Mus musculus.

WO200202599-A2.

10-JAN-2002.

02-JUL-2001; 2001WO-EP007532.

30-JUN-2000; 2000US-0215759P.

(INGE-) INGENIUM PHARM AG.

Wattler F, Wattler S, Trommler P, Nehls MC;

WPI; 2002-140080/18.

New human or mouse G protein-coupled receptor protein, IGPcr17, useful  
for diagnosis, prevention, amelioration or treatment of central nervous  
system disorders such as Tourette's syndrome, Parkinson's disease and  
pain.

Example 7; Page 40; 71pp; English.

The present invention relates to human and murine G protein-coupled  
receptor (GPCR) protein, IGPcr17 (AAM48353 and AAM48354). The coding  
sequence for IGPcr17 is useful in gene therapy for prevention,  
amelioration or treatment of diseases characterised by aberrant  
expression or activity of IGPcr17, where the disease is a psychiatric or  
central nervous system (CNS) disorder associated with signal processing  
in CNS such as learning and memory disorders, movement dysfunctions,  
tics, tremor, Tourette's syndrome, Parkinson's disease, Huntington's  
disease, dyskinesias, dystonia, pain and spasms. In addition, IGPcr17 and  
its coding sequence are useful in diagnosis, prevention, amelioration or  
treatment of diseases associated with signal processing in CNS,  
schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as  
obsessive compulsive disorder (OCD), multiple sclerosis, Alzheimer's  
disease/dementia, anorexia, kidney diseases such as renal failure,  
obesity, gastrointestinal disorders such as irritable bowel syndrome  
(IBS), diarrhoea, motility disorders and conditions of delayed gastric  
emptying, osteoporosis, infections such as bacterial, fungal, protozoal  
and viral infections, asthma, allergy, arthritis, sepsis and  
gynecological disorders. The present sequence is a PCR primer for murine  
IGPcr17 coding sequence. This sequence was used along with the primer of  
ABA98540 for tissue-specific expression analysis of IGPcr17 in an example  
from the invention. The resulting PCR product is given in ABA98542

Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2e+03; Mismatches 2; Indels 0; Gaps 0;

QY 6329 TGGGAAGCTAGGCTTAA 6346

|||||||

Db 3 TGGGAACTTTGGCTGAC 20

RESULT 3031  
ABK9487  
ID ABR9487 standard; DNA; 20 BP.

XX  
AC ABR9487;  
XX  
DT 29-AUG-2002 (first entry)  
XX  
DE Fat regulated gene associated PCR primer #64.

XX  
KM Fatty acid regulated gene; polyunsaturated fatty acid disorder;  
KM dyslipidaemia; cardiovascular disorder; hypertriglyceridaemia;  
KM dyslipidaemia; atherosclerosis; coronary artery disease;  
KM cerebrovascular disease; peripheral vascular disease; inflammation;  
KM sinusitis; asthma; pancreatitis; osteoarthritis; rheumatoid arthritis;  
KM acne; body weight disorder; obesity; cachexia; anorexia;  
KM psychiatric disorder; cancer; cystic fibrosis; pre-menstrual syndrome;  
KM diabetes; diabetic complication; genetic polymorphism; PCR; primer; ss.

XX  
OS Synthetic.  
XX  
PN WO200240666-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 19-NOV-2001; 2001WO-CA001632.  
XX  
PR 17-NOV-2000; 2000US-0248589P.  
XX  
PA (XENON-) XENON GENETICS INC.  
XX  
PI Winther MD, Goldberg YP, Knickle LC, Haardt M, Allen SJ;  
PI Ponton A, De Ardueno RJ, Jenkins DK, Nwaka SO;  
XX  
DR WPI; 2002-508327/54.

XX  
PT Novel isolated polypeptide segment encoded by fat regulated genes, useful  
PT for diagnosing the presence of or a predisposition for a disorder  
PT involving fatty acid regulated genes in a subject.

XX  
PS Example 2; Page 81; 225pp; English.

XX  
CC The invention describes an isolated polypeptide segment (I) whose genes  
CC are fat regulated. (I) or the polynucleotide encoding it (II) are useful  
CC for diagnosing the presence of or a predisposition for a disorder  
CC involving fatty acid regulated genes in a subject. A composition  
CC containing (I) or (II) is useful for treating a disorder involving fatty  
CC acid regulated genes, where the disorder is selected from a  
CC polyunsaturated fatty acid (PUFA) disorder, eczema, cardiovascular  
CC disorders (such as hypertriglyceridaemia, dyslipidaemia, atherosclerosis,  
CC coronary artery disease, cerebrovascular disease or peripheral vascular  
CC disease), inflammation (such as sinusitis, asthma, pancreatitis,  
CC osteoarthritis, rheumatoid arthritis or acne), body weight disorders  
CC (such as obesity, cachexia or anorexia), psychiatric disorders, cancer,  
CC cystic fibrosis, pre-menstrual syndrome, diabetes, and diabetic  
CC complications. (I) or (II) is useful as research agent and materials for  
CC discovery of treatments and diagnostics for a disease, particularly human  
CC disease. (II) is useful for constructing nucleotide probes and primers,  
CC for detecting genetic polymorphism, for detecting changes in the level of  
CC expression of (II), and as a diagnostic tool. This sequence represents a  
CC PCR primer used to isolate DNA encoding fat regulated genes

XX  
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3492 AGGCACCTTGGCACTTAG 3509  
||||| |||||||

Db 2 AGGAGATGAGCACTTTG 19

RESULT 3032  
AAS97790  
ID AAS97790 standard; DNA; 20 BP.

XX  
AC AAS97790;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Murine SACL gene-specific oligonucleotide PCR primer #357.

XX  
KM Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;  
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;  
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;  
XX  
OS Mus sp.  
XX  
PN WO200183749-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 25-APR-2001; 2001WO-US013387.  
XX  
PR 28-APR-2000; 2000US-0200794P.  
XX  
PR 28-JUL-2000; 2000US-0221419P.  
XX  
PR 10-NOV-2000; 2000US-0247443P.

XX  
PA (WARNER) WARNER LAMBERT CO.  
XX  
PA (MONE-) MONEILL CHEM SENSES CENT.  
XX  
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PV, Li S, Li X;  
PI Ohmen JD, Reed DR, Rose D, Tordoff MG;  
XX  
DR WPI; 2002-075162/10.

XX  
PT Novel isolated polypeptide comprising variant form of mouse or human SACL  
PT polypeptide, and is associated with altered preference for carbohydrates  
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.

XX  
PS Claim 14; Page 88; 239pp; English.

XX  
CC The invention relates to an isolated polypeptide, comprising a variant  
CC form of mouse or human SACL polypeptide. The variant form is associated  
CC with altered preference for carbohydrates, other sweeteners or ethanol.  
CC The polypeptide and its associated DNA sequence can be produced by  
CC recombinant techniques and is useful for preventing obesity, diabetes or  
CC alcoholism associated with SACL expression. The sequences are useful in  
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic  
CC embryos may be used in screening for and identifying agents that induce  
CC or repress function of SACL. Predisposition to diabetes, obesity or  
CC alcoholism can be ascertained by testing any fluid or tissue of a human  
CC (such as blood, pancreas or tongue) for sequence variations of the SACL  
CC gene. A sequence variation of the SACL locus may indicate a  
CC predisposition to diabetes, obesity and/or alcoholism and may provide a  
CC diagnostic mark. The polynucleotide can be detected in a biological  
CC sample by contacting the DNA with a probe to form a hybridisation complex  
CC which is then detected. The sequences represent cDNA encoding human and  
CC mouse SACL polypeptides and PCR primers specific for the SACL genes

XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 544 GTCGACTTTGAGGTGACA 561  
||||| |||||||  
Db 3 GTCGACATTTAGGTGACA 20

```

RESULT 3033
AAS97594/c
ID AAS97594 standard; DNA; 20 BP.
XX
AC AAS97594;
XX
DT 12-MAR-2002 (first entry)
XX
DE Murine SACL gene-specific oligonucleotide PCR primer #199.
XX
KM Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KM protein replacement therapy.
XX
OS Mus sp.
XX
PN MO200183749-A2.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013387.
XX
PR 28-APR-2000; 2000US-0200794P.
PR 28-JUL-2000; 2000US-0221419P.
PR 10-NOV-2000; 2000US-0247443P.
XX
PA (WARN ) WARNER LAMBERT CO.
PA (NONE-) MONELL CHEM SENSES CENT.
XX
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohmen JD, Reed DR, Rose D, Tordoff MG;
XX
DR WPI; 2002-075162/10.
XX
PT Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS Claim 14; Page 81; 239pp; English.
XX
CC The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes
XX
SQ Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
QY 6069 TAAATCTGTCCTTTTC 6086
Db 18 TAAATCTGTCCTTTTC 1

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XX
AC AAS97784;
XX
DT 12-MAR-2002 (first entry)
XX
DE Murine SACL gene-specific oligonucleotide PCR primer #351.
XX
KM Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;
KM obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KM blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KM protein replacement therapy.
XX
OS Mus sp.
XX
PN MO200183749-A2.
XX
PD 08-NOV-2001.
XX
PF 25-APR-2001; 2001WO-US013387.
XX
PR 28-APR-2000; 2000US-0200794P.
PR 28-JUL-2000; 2000US-0221419P.
PR 10-NOV-2000; 2000US-0247443P.
XX
PA (WARN ) WARNER LAMBERT CO.
PA (NONE-) MONELL CHEM SENSES CENT.
XX
PI Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI Ohmen JD, Reed DR, Rose D, Tordoff MG;
XX
DR WPI; 2002-075162/10.
XX
PT Novel isolated polypeptide comprising variant form of mouse or human SACL
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS Claim 14; Page 88; 239pp; English.
XX
CC The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SACL polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SACL expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SACL. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SACL
CC gene. A sequence variation of the SACL locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SACL polypeptides and PCR primers specific for the SACL genes
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
QY 544 GTGACATTGAGGTGACA 561
Db 3 GTGACATTGAGGTGACA 20

```

RESULT 3034  
AAS97784  
ID AAS97784 standard; DNA; 20 BP.

RESULT 3035  
AAS97786  
ID AAS97786 standard; DNA; 20 BP.  
XX AAS97786;  
XX

DT 12-MAR-2002 (first entry)  
XX  
XX Murine SACL gene-specific oligonucleotide PCR primer #353.  
DE  
XX  
XX Human; mouse; SACL; carbohydrate; sweetener; ethanol; alcoholism; ss;  
KW obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;  
KW blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;  
KW protein replacement therapy.  
XX  
XX Mus sp.  
OS  
XX WO200183749-A2.  
FN  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 25-APR-2001; 2001WO-US013387.  
PF  
XX  
XX 28-APR-2000; 2000US-0200794P.  
PR 28-JUL-2000; 2000US-0221419P.  
PR 10-NOV-2000; 2000US-0247443P.  
XX  
XX (WARN ) WARNER LAMBERT CO.  
PA (MONE-) MONELL CHEM SENSES CENT.  
XX  
XX Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;  
PI Ohmen JD, Reed DR, Ross D, Tordoff MG,  
XX  
XX WPI; 2002-075162/10.  
DR  
XX  
XX Novel isolated polypeptide comprising variant form of mouse or human SACL  
PT polypeptide, and is associated with altered preference for carbohydrates  
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.  
XX  
XX Claim 14; Page 88; 239pp; English.  
XX  
XX The invention relates to an isolated polypeptide, comprising a variant  
CC form of mouse or human SACL polypeptide. The variant form is associated  
CC with altered preference for carbohydrates, other sweeteners or ethanol.  
CC The polypeptide and its associated DNA sequence can be produced by  
CC recombinant techniques and is useful for preventing obesity, diabetes or  
CC alcoholism associated with SACL expression. The sequences are useful in  
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic  
CC embryos may be used in screening for and identifying agents that induce  
CC or repress function of SACL. Predisposition to diabetes, obesity or  
CC alcoholism can be ascertained by testing any fluid or tissue of a human  
CC (such as blood, pancreas or tongue) for sequence variations of the SACL  
CC gene. A sequence variation of the SACL locus may indicate a  
CC predisposition to diabetes, obesity and/or alcoholism and may provide a  
CC diagnostic mark. The polynucleotide can be detected in a biological  
CC sample by contacting the DNA with a probe to form a hybridisation complex  
CC which is then detected. The sequences represent cDNA encoding human and  
CC mouse SACL polypeptides and PCR primers specific for the SACL genes  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 544 GTGACCTTGTGAGTGACA 561  
DB 3 GTGACATTGTGAGTGACA 20

RESULT 3036  
ABK37182/c  
ID ABK37182 standard; DNA; 20 BP.  
XX  
XX ABK37182;  
AC  
XX  
XX 08-MAY-2002 (first entry)  
DT  
XX  
DE Human lysophospholipase I gene, antisense oligonucleotide #134.

XX  
XX Human; mouse; antiinflammatory; antiarteriosclerotic; vasotropic;  
KW antiinflammatory; cardiant; lysophospholipase I; inflammation; ischaemia;  
KW hyperlipidaemia; cardiovascular disorder; atherosclerosis;  
KW antisense gene therapy; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX WO200210185-A1.  
FN  
XX  
XX 07-FEB-2002.  
PD  
XX  
XX 20-JUL-2001; 2001WO-US022975.  
PF  
XX  
XX 31-JUL-2000; 2000US-00629645.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
XX Bennett CF, Wyatt JR;  
PI  
XX  
XX WPI; 2002-188720/24.  
DR  
XX  
XX Novel antisense compound useful for treating inflammation,  
PT hyperlipidemia, and cardiovascular disorders such as atherosclerosis and  
PT myocardial ischemia, inhibits lysophospholipase I.  
PT  
XX  
XX Claim 3; Page 83; 131pp; English.  
XX  
XX The invention relates to an antisense compound (I) 8-30 nucleobases in  
CC length targeted to a nucleic acid molecule encoding lysophospholipase I  
CC (II), where (I) specifically hybridises with and inhibits the expression  
CC of (II). (I) is useful for inhibiting the expression of (II) in cells or  
CC tissues, and for treating a human having a disease or condition  
CC associated with lysophospholipase I e.g. inflammation, hyperlipidaemia,  
CC and cardiovascular disorders such as atherosclerosis and myocardial  
CC ischaemia. (I) is useful as research reagent and diagnostics. (I) is also  
CC useful for distinguishing functions of various members of a biological  
CC pathway. (I) is useful in antisense gene therapy. ABK37028-ABK37191  
CC represent lysophospholipase I coding sequences, antisense  
CC oligonucleotides and related PCR primers of the invention. Note:  
CC Antisense oligonucleotides are modified such that bases 1-5 and 16-20 are  
CC 2'-methoxyethyl (2'-MOE) nucleotides, all bases have phosphorothioate  
CC linkages, and all cytidines are 5-methyl cytidines  
XX  
SQ Sequence 20 BP; 13 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 6464 CTTTCTTTCTGTTGT 6481  
DB 18 CTGTATTTCTCTTGT 1

RESULT 3037  
ABN83847/c  
ID ABN83847 standard; DNA; 20 BP.  
XX  
XX ABN83847;  
AC  
XX  
XX 10-SEP-2002 (first entry)  
DT  
XX  
XX Insulin gene -2221 MspI polymorphism PCR primer INS56.  
DE  
XX  
XX Non-insulin dependent diabetes; type II diabetes; obesity; human;  
KW diagnosis; prognosis; linkage disequilibrium; polymorphism; marker;  
KW insulin; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200236820-A2.

XX 10-MAY-2002.  
 PD 31-OCT-2001; 2001WO-IB002747.  
 XX 02-NOV-2000; 2000US-0245493P.  
 XX (BOUG/) BOUGNERS P.  
 PA WPI; 2002-519258/55.  
 DR  
 XX  
 PT Determining risk of developing non-insulin dependent diabetes mellitus,  
 PT comprises determining the identity of polymorphic bases of a marker in  
 PT linkage disequilibrium with the insulin HphI locus.  
 XX  
 XX Example 2; Page 57; 74pp; English.  
 CC The present invention provides methods for determining the risk of  
 CC development of non-insulin dependent diabetes mellitus (NIDDM or type II  
 CC diabetes) in a subject. It results from the discovery that homozygotes of  
 CC the HphI locus of the insulin gene along with body fat measurement serve  
 CC as an excellent indicator of NIDDM susceptibility. Thus, obese  
 CC individuals with HphI(+/+) or (-/-) genotypes are significantly more  
 CC likely to develop NIDDM than obese individuals with HphI(+/+) genotypes.  
 CC A method of determining the risk of developing NIDDM in an individual  
 CC involves genotyping at least one marker in linkage disequilibrium with  
 CC the insulin HphI locus. The marker is especially -4217 PstI, -2221 MspI,  
 CC -23 HphI, +1428 FokI, +1100 AluI and +3200 ApaI. In an example, new  
 CC polymorphisms were screened to determine whether they altered a  
 CC restriction site. These sites were then amplified in a panel of random  
 CC diabetes and controls, and a subset of polymorphisms was amplified using  
 CC the primers given in ABN83845-56. The present primer, INSS56, was used  
 CC with primer INSS7 to amplify the -2221 MspI site. PCR products were  
 CC digested with MspI and gel electrophoresed to determine genotype.  
 CC Products of digestion were 108 and 78 bp for +/+, 186, 108 and 78 bp for  
 CC +/-, and 186 bp for -/- genotypes, where (+) indicates the restriction  
 CC enzyme cut the sequence, and (-) indicates a cut was not made. The  
 CC invention provides methods for diagnosing a subtype of NIDDM, for  
 CC estimating the frequency of a haplotype for a set of genetic markers in a  
 CC population suffering from juvenile obesity (claimed), and methods to  
 CC facilitate therapy and maintenance of NIDDM patients  
 CC  
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 4729 CTTGAGGCGCAGCTGAG 4746  
 Db 18 CTTAGAGGCCAGCTGCTG 1  
 RESULT 3038  
 ABS74284/c  
 ID ABS74284 standard; DNA; 20 BP.  
 XX  
 AC ABS74284;  
 XX  
 DT 09-DEC-2002 (first entry)  
 XX  
 DE Human calcium channel alpha2delta SSCP PCR primer #8.  
 XX  
 KM Human; ss; primer; calcium channel alpha2delta; splice isoform; CACNA2D2;  
 KM gene therapy; Lambert-Eaton myasthenic syndrome; LEMS; PCR;  
 KM autoimmune disease; epilepsy; migraine; episodic ataxia; cancer; stroke;  
 KM brain trauma; Alzheimer's disease; multiinfarct dementia; convulsions;  
 KM Korsakoff's disease; amyotrophic lateral sclerosis; seizure;  
 KM Huntington's disease; amnesia; cardiac arrhythmia; angina pectoris;  
 KM hypoxia; ischemia; myocardial infarction; congestive heart failure;  
 KM muscular dystrophy; hypertension; chromosome 3p21.3; lung cancer;  
 KM breast cancer; preneoplastic lesion; hyperplasia; dysplasia; carcinoma;  
 KM SSCP; single strand change polymorphism.

XX Homo sapiens.  
 OS  
 XX US6441156-B1.  
 PN  
 XX 27-AUG-2002.  
 PD  
 XX 22-DEC-1999; 99US-00470443.  
 PF  
 XX 30-DEC-1998; 98US-0114359P.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Lerman MI, Latif F, Wei M, Duh F, Minna JD, Sekido Y, Gao B;  
 PI WPI; 2002-730574/79.  
 DR  
 XX  
 PT Novel purified nucleic acid sequence encoding human calcium channel  
 PT alpha2delta subunit protein, useful for detecting, preventing and  
 PT treating cancer, stroke, brain trauma, Huntington's disease, myocardial  
 PT infarction.  
 XX  
 XX Example 7; Col 46; 77pp; English.  
 PS  
 XX The invention relates to a purified nucleic acid sequence (referred as  
 CC CACNA2D2 gene which encodes human calcium channel alpha2delta-2 subunit  
 CC protein) comprising a fully defined alpha2delta splice isoform 1, 2 or 3  
 CC nucleic acid sequence, or its complement and the encoded proteins. Also  
 CC include are: (1) a method of producing a calcium channel protein which  
 CC involves introducing a recombinant expression vector comprising the  
 CC CACNA2D2 nucleic acid and encoding the calcium channel protein, into a  
 CC cultured host cell under conditions such that the host cell expresses the  
 CC amino acid sequences; and (2) a method for co-expressing calcium channel  
 CC proteins, comprising carrying out the method of (1), but with one or more  
 CC than one expression vector comprising one or more nucleic acid sequences  
 CC encoding the splice variants. CACNA2D2 nucleic acid is useful for  
 CC producing a calcium channel protein. The recombinantly expressed  
 CC polypeptide (LEMS) (an autoimmune disease) and for identifying compounds  
 CC useful for treating other diseases associated with abnormal calcium  
 CC channel protein activity (e.g. epilepsy, migraine, episodic ataxia,  
 CC cancer, stroke, brain trauma, Alzheimer's disease, multiinfarct dementia,  
 CC Korsakoff's disease, amyotrophic lateral sclerosis, convulsions,  
 CC seizures, Huntington's disease, amnesia, cardiac arrhythmia, angina  
 CC pectoris, hypoxic damage to the cardiovascular system, ischemic heart  
 CC to the cardiovascular system, myocardial infarction, congestive heart  
 CC failure, muscular dystrophy and hypertension) CACNA2D2 nucleic acid is  
 CC useful as primers and probes for detecting presence of nucleic acid  
 CC sequence encoding at least a portion of calcium channel protein, in  
 CC detection, identification and isolation of alpha2delta sequences  
 CC diagnosing and typing of preneoplasias and cancers, since genetic  
 CC disruption of 3p21.3 region (in which the alpha2delta gene is located)  
 CC is common in cancer (e.g. lung cancer and breast cancer) and  
 CC preneoplastic lesion (e.g. hyperplasia, dysplasia, carcinoma in situ).  
 CC The present is an SSCP (single strand change polymorphism) PCR primer  
 CC used to detect polymorphisms in sequences encoding a human calcium  
 CC channel alpha2delta splice isoform protein  
 CC  
 SQ Sequence 20 BP; 1 A; 4 C; 10 G; 5 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 5287 CAGCCTTACTCCACAGA 5304  
 Db 20 CAGCCGCGACTCCACAGA 3  
 RESULT 3039  
 ABA90030/c  
 ID ABA90030 standard; DNA; 20 BP.  
 XX



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PN JP2001286300-A.
XX
XX 16-OCT-2001.
XX
XX 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
DR WPI; 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 14 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6682 TTATTTTATATATAT 6699
DB 18 TTTTATATATATATAT 1
RESULT 3042
ABA97650/C
ID ABA97650 standard; DNA; 20 BP.
XX
AC ABA97650;
XX
XX 11-APR-2002 (first entry)
XX
XX probe u.
XX
XX ss; fluorochrome; nucleic acid probe; fluorescence.
XX
XX Unidentified.
XX
XX JP2001286300-A.
XX
XX 16-OCT-2001.
XX
XX 20-APR-2000; 2000JP-00120097.
XX
XX 20-APR-1999; 99JP-00111601.
XX 24-AUG-1999; 99JP-00236666.
XX 30-AUG-1999; 99JP-00242693.
XX 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
XX (KANK-) KANKYO ENG KK.
XX (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
DR WPI; 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
```

```
PS Example 6; Page 18; 34pp; Japanese.
XX
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6682 TTATTTTATATATAT 6699
DB 18 TTTTATATATATATAT 1
RESULT 3043
AAS16663
ID AAS16663 standard; DNA; 20 BP.
XX
AC AAS16663;
XX
XX 14-FEB-2002 (first entry)
XX
XX Human Inhibitor of DNA binding-1, antisense oligonucleotide ISIS #124761.
XX
XX Human; inhibitor of DNA binding-1; Id-1; cytostatic; antiinflammatory;
XX immunosuppressive; antisense therapy; antisense oligonucleotide;
XX hyperproliferative disorder; immune disorder; muscular disorder; ss;
XX vascular disorder; pancreatic disorder; infection; inflammation; tumour.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Location/Qualifiers
FH Key 1..20
FT modified_base
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone. Also, all cytidine
FT residues are 5-methyl cytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT modified_base
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO200183513-A2.
XX
XX 08-NOV-2001.
XX
XX 25-APR-2001; 2001MO-US013209.
XX
XX 28-APR-2000; 2000US-00561497.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Bennett CF, Wyatt JR;
XX
XX WPI; 2002-041477/05.
XX
XX Novel antisense compound, specifically hybridizing to and inhibiting the
PT expression of inhibitor of DNA binding-1, useful for treating
PT hyperproliferative, immune, muscular, vascular or pancreatic disorder.
XX
XX Example 15; Page 82; 105pp; English.
XX
XX The invention relates to novel antisense compounds (I) 8-30 nucleobases
CC
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```
CC in length targeted to a nucleic acid molecule encoding inhibitor of DNA
CC binding-1, where (i) specifically hybridises with and inhibits the
CC expression of inhibitor of DNA binding-1. Antisense inhibition of human
CC inhibitor of DNA binding-1 expression by chimeric phosphorothioate
CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a deoxy gap
CC was tested. A series of oligonucleotides were designed to target
CC different regions of the human inhibitor of DNA binding-1 RNA. The
CC compounds were analysed for their effect on human inhibitor of DNA
CC binding-1 mRNA levels by quantitative real-time polymerase chain reaction
CC (PCR). The result showed that the oligonucleotides showed at least 25%
CC inhibition of human inhibitor of DNA binding-1 expression. (i) is useful
CC for inhibiting the expression of inhibitor of DNA binding-1 in cells or
CC tissues by contacting the cells or tissues with (i). (i) is also useful
CC for treating a human having a disease or condition associated with
CC inhibitor of DNA binding-1 by administering a therapeutically or
CC prophylactically effective amount of (i), where the disease or condition
CC is a hyperproliferative disorder, immune disorder, muscular disorder,
CC vascular disorder or pancreatic disorder. (i) may also be used for
CC diagnostics, therapeutics, prophylaxis (e.g., to prevent or delay
CC infection, inflammation or tumour formation), and as research reagents
CC and kits. (i) may be safely and effectively administered to humans. The
CC present sequence represents a human inhibitor of DNA binding-1, antisense
CC oligonucleotide used in the method of the invention
SQ
SQ Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3270 ATTTGTTAAGAGAGAAA 3287
Db 3 ATTGTTTAATTAACAAA 20
RESULT 3044
ABL94386/c
ID ABL94386 standard; DNA; 20 BP.
AC ABL94386;
XX
XX 29-JUN-2002 (first entry)
XX
XX Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:152.
DE
XX
XX Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;
XX LAP; TCF5; CRP2; NF16; IL6BP; NF-M; AGP/EBP; Apc/EBP;
XX transcription factor; tissue development; cellular function;
XX proliferation; differentiation; hormone responsiveness;
XX oxidative stress response; IL-6 signalling mediator; interleukin-6;
XX carbohydrate metabolism; immunity; Th1 response; female fertility;
XX gluconeogenesis; ovarian; cancer; tumour formation; type II diabetes;
XX infection; inflammation; expression inhibition; phosphorothioate;
XX antisense oligonucleotide; ss.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT cytosines are 5-methylcytosine"
XX
```

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PN US6271030-B1.
XX
XX 07-AUG-2001.
XX
XX 14-JUN-2000; 2000US-00593711.
PF
XX
XX 14-JUN-2000; 2000US-00593711.
PR
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Butler MM, Wyatt J;
XX WPI; 2002-214451/27.
XX
XX Novel antisense compound targeted to nucleic acids encoding human or
XX mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
XX inhibiting expression of human or mouse C/EBP beta in cells/tissues.
XX
XX Example 17; Col 49-50; 69pp; English.
XX
XX Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted
XX to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
XX gene, which inhibit its expression. The antisense oligonucleotides were
XX designed to target different regions of the human and/or mouse C/EBP
XX alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
XX by quantitative real-time PCR. The C/EBP family of proteins are a family
XX of transcription factors which regulate the expression of a wide range of
XX genes that control normal tissue development, cellular function, cellular
XX proliferation and functional differentiation. C/EBP beta (also known as
XX C/EBP2, LAP, TCF5, CRP2, NF16, IL6BP, NF-M, AGP/EBP and Apc/EBP)
XX primarily regulates homeostasis and oxidative stress responses
XX and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
XX thought to be involved in carbohydrate metabolism, immunity, the Th1
XX response, female fertility and gluconeogenic pathways. C/EBP beta is
XX expressed in the liver, lung, spleen, kidney, brain, and testis, with the
XX highest expression found in the lung. It is also expressed at a higher
XX level in malignant ovarian tissue compared with normal ovarian tissue,
XX and its expression in pancreas is upregulated in response to chronically
XX elevated levels of glucose, indicating that it is involved in the
XX impairment of insulin secretion in type II diabetes. The oligonucleotides
XX of the invention are useful for diagnosis, prevention and treatment of
XX conditions associated with C/EBP beta expression, such as cancer
XX (particularly ovarian cancer), tumour formation, diabetes (particularly
XX type II diabetes), infection, or inflammation
XX
XX Sequence 20 BP; 0 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7414 AGCAGCAGCAGCAGCAGC 7431
Db 18 AGCGCAGCAGCAGCGCAGC 1
RESULT 3045
ABI93710
ID ABI93710 standard; DNA; 20 BP.
AC ABI93710;
XX
XX 16-FEB-2002 (first entry)
XX
XX Capture oligonucleotide Zip ID#797 oligo #9.
DE
XX
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX
XX Synthetic.
OS
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XX      WO200179548-A2.
PN      25-OCT-2001.
PD      04-APR-2001; 2001WO-US010958.
PF      14-APR-2000; 2000US-0197271P.
PR      (CORR ) CORNELL RES FOUND INC.
PA      Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
PI      WPI; 2002-034366/04.
DR      Designing capture oligonucleotide probes for use on a support to which
PT      complementary oligonucleotides hybridize with little mismatch.
XX      Example 5; Fig 29; 300pp; English.
XX      The present invention describes a method (M1) for designing capture
CC      oligonucleotide probes (I) for use on a support to which complementary
CC      oligonucleotide probes (II) will hybridise with little mismatch, where
CC      (I) have melting temperatures within a narrow range. The method is useful
CC      for detecting infectious diseases caused by bacterial infectious agents
CC      e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC      infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC      Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC      Epstein-Barr virus and polio virus, and parasitic infectious agents
CC      selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC      medinensis. The method is also useful for detecting genetic diseases such
CC      as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC      Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC      involved in DNA amplification, replication, recombination or repair, the
CC      cancer is specifically associated with a gene selected from BRCA1 gene,
CC      p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC      method is also used for environmental monitoring, forensics and the food
CC      and feed industry, detecting comprises scanning (using e.g. a scanning
CC      electron microscope and infrared microscope) the support at the
CC      particular sites and identifying if ligation of the oligonucleotide probe
CC      sets occurred and correlating (using a computer) identified ligation to a
CC      presence or absence of the target nucleotide sequences. AB182074 to
CC      AB197546 represent oligonucleotide sequences used in the exemplification
CC      of the present invention
XX      Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      6403 CCACCTGCTAGATGCTT 6420
DB      3 CCACCTGCAGATGAGCTT 20
RESULT 3046
AB194356
ID      AB194356 standard; DNA; 20 BP.
XX      AC      AB194356;
XX      DT      16-FEB-2002 (first entry)
XX      DE      Capture oligonucleotide Z1p ID#1443 oligo #9.
XX      Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KM      ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KM      infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KM      oncogene; tumour suppressor; human papillomavirus; forensic;
KM      environmental monitoring; food industry; feed industry; ss.
XX      OS      Synthetic.

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XX      WO200179548-A2.
PN      25-OCT-2001.
PD      04-APR-2001; 2001WO-US010958.
PF      14-APR-2000; 2000US-0197271P.
PR      (CORR ) CORNELL RES FOUND INC.
PA      Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
PI      WPI; 2002-034366/04.
DR      Designing capture oligonucleotide probes for use on a support to which
PT      complementary oligonucleotides hybridize with little mismatch.
XX      Example 5; Fig 29; 300pp; English.
XX      The present invention describes a method (M1) for designing capture
CC      oligonucleotide probes (I) for use on a support to which complementary
CC      oligonucleotide probes (II) will hybridise with little mismatch, where
CC      (I) have melting temperatures within a narrow range. The method is useful
CC      for detecting infectious diseases caused by bacterial infectious agents
CC      e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
CC      infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC      Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC      Epstein-Barr virus and polio virus, and parasitic infectious agents
CC      selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC      medinensis. The method is also useful for detecting genetic diseases such
CC      as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC      Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC      involved in DNA amplification, replication, recombination or repair, the
CC      cancer is specifically associated with a gene selected from BRCA1 gene,
CC      p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC      method is also used for environmental monitoring, forensics and the food
CC      and feed industry, detecting comprises scanning (using e.g. a scanning
CC      electron microscope and infrared microscope) the support at the
CC      particular sites and identifying if ligation of the oligonucleotide probe
CC      sets occurred and correlating (using a computer) identified ligation to a
CC      presence or absence of the target nucleotide sequences. AB182074 to
CC      AB197546 represent oligonucleotide sequences used in the exemplification
CC      of the present invention
XX      Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      3117 TGCTTGACAGCTTGCTTA 3134
DB      3 TGCTTGACGCTTGCGCA 20
RESULT 3047
ABK8754
ID      ABK8754 standard; DNA; 20 BP.
XX      AC      ABK8754;
XX      DT      09-APR-2002 (first entry)
XX      DE      Human CDC14 gene donor splice site #14.
XX      Human; ds; cell-cycle control; CDC14A; cancer; splice site;
KM      prostate cancer; breast cancer; lymph node metastasis;
KM      malignant mesothelioma; chromosome 1p21; dual specificity phosphatase;
KM      gene therapy; protein replacement therapy.
XX      OS      Homo sapiens.

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PN US6331614-B1.
XX
XX 18-DEC-2001.
XX
XX 22-DEC-1999; 99US-00468872.
XX
XX 23-DEC-1998; 98US-0113833P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Wong AKC, Teng DHF, Tavtigian SV;
XX
XX WPI; 2002-129551/17.
XX
XX Nucleic acid encoding mutated form of human dual-specificity phosphatase
XX CDCl4A polypeptide, useful to diagnose and treat cancers.
XX
XX Example 2; Col 43-44; 41pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a CDCl4A
XX polypeptide (cell-cycle control protein 14A, a dual specificity
XX phosphatase), its complement or RNA molecule corresponding to it. Also
XX included are an expression vector comprising the nucleic acid and a host
XX cell transformed with the vector. The gene for CDCl4A is located on human
XX chromosome 1p21. The nucleic acid and protein are useful to diagnose and
XX treat human cancers (e.g. breast cancer, prostate cancer) and tumours
XX (e.g. lymph node metastasis, malignant mesothelioma) which have a
XX mutation in the CDCl4A gene. By gene therapy, protein replacement therapy
XX or protein mimetics. They can also be used to screen for drugs to treat
XX cancer. The present sequence is a splice donor or splice acceptor
XX sequence from the CDCl4A gene
XX
XX Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5479 TGTAAAGATTAATTTT 5496
DB 2 TGTAAAGAGTAAATTTT 19
RESULT 3048
ABLS6505/C
ID ABL56505 standard; DNA; 20 BP.
XX
XX ABL56505;
XX
XX 22-JUL-2002 (first entry)
XX
XX PCR primer Cx30-S3 used to amplify a fragment of the human GJB6 gene.
XX
XX GJB6 gene; connexin-30; Cx-30; Clouston syndrome; alopecia; hair loss;
XX hydrotic ectodermal dysplasia; hair growth; hair disorder; PCR; primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200226976-A1.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-FR002997.
XX
XX 29-SEP-2000; 2000FR-00012473.
XX
XX (GENE-) GENETHON III.
XX (UYDE-) UNIV DEVRV VAL DESSONNE.
XX
XX Waksman G, Lamartine J;
XX
XX WPI; 2002-340014/37.
XX
XX
```

```
XX New mutant forms of connexin-30 nucleic acid, useful for the diagnosis
XX and treatment of Clouston syndrome and other forms of alopecia.
XX
XX Example 1; Page 19; 44pp; French.
XX
XX PCR primers ABL56504-07 were used to amplify fragments of the human GJB6
XX gene. The GJB6 gene encodes connexin-30 (Cx-30). A G to A mutation at
XX position 31 and/or a C to T mutation at position 263 causes Clouston
XX syndrome (hydrotic ectodermal dysplasia). Nucleic acids encoding Cx-30,
XX antisense oligonucleotides and vectors containing them, are used to treat
XX Clouston syndrome and other forms of alopecia with a genetic component.
XX They are also used to reduce growth of hair and/or promote hair loss.
XX They may also be used for (cosmetic) treatment and/or prevention of
XX disorders of the hair. Transgenic animals/cells that contain Cx-30 are
XX used to screen for agents that are potentially useful for treating some
XX forms of alopecia. Primers derived from GJB6 gene are useful in
XX amplification assays for diagnosis of Clouston syndrome
XX
XX Sequence 20 BP; 7 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5714 CTCTTCCTCTTGCCTG 5731
DB 20 CTCTTCCTCTCTGCGCTG 3
RESULT 3049
ABQ87739/C
ID ABQ87739 standard; DNA; 20 BP.
XX
XX ABQ87739;
XX
XX 18-SEP-2002 (first entry)
XX
XX Human ESR1 exon 8.18 sequencing PCR primer BR1x8.18er3_54048.
XX
XX Human; oestrogen; receptor; oestrogen receptor alpha; cytostatic;
XX osteopathic; cardiac; cancer; osteoporosis; cardiovascular disorder;
XX ESR-alpha; ESR1; sequencing; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200234945-A2.
XX
XX 02-MAY-2002.
XX
XX 21-AUG-2001; 2001WO-US025990.
XX
XX 20-OCT-2000; 2000US-00692414.
XX 24-JAN-2001; 2001US-00768184.
XX 13-MAR-2001; 2001US-00804076.
XX 05-APR-2001; 2001US-00826314.
XX
XX (APPL-) APPLERA CORP.
XX
XX Kalush F, Casseel MJ, Hwang SS, Winn_deen ES;
XX
XX WPI; 2002-479722/51.
XX
XX Peptide of estrogen receptor alpha genes variant or its fragment for use
XX in identifying modulators for treating disorders e.g. a susceptibility to
XX cancer, osteoporosis, cardiovascular disorder.
XX
XX Example 1; Fig 2E; 352pp; English.
XX
XX The invention relates to novel human oestrogen receptor variant peptides,
XX and the polynucleotides encoding them. The peptides of the invention have
XX cytosolic, osteopathic and cardiac activity. The peptides of the
XX invention are useful to mediate or modulate a variety of disorders such
XX
```

CC as a susceptibility to cancer, osteoporosis, cardiovascular disorder, etc., and hence are useful in the treatment of the disorders. The CC sequences shown in AB087720-AB087746 represent PCR primers used in the CC invention to sequence individual exons of the human oestrogen receptor alpha (ESR-alpha or ESR1) gene

XX

SO Sequence 20 BP; 10 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4842 TATCCAGTTCGTCT 4859  
Db 19 TATGCCAGTTTCTTCT 2

RESULT 3050  
AAL47461  
ID AAL47461 standard; DNA; 20 BP.  
XX  
AC AAL47461;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human MTHFR gene probe.  
XX  
KM Human; MTHFR; sequencing; single nucleotide polymorphism; SNP; probe; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "modified by FITC"  
XX  
PN DEL0058915-A1.  
XX  
PD 06-JUN-2002..  
XX  
PF 20-NOV-2000; 2000DE-01058915.  
XX  
PR 20-NOV-2000; 2000DE-01058915.  
XX  
PA (ATTO-) ATTOMOL GMBH MOLEKULARE DIAGNOSTIKA.  
XX  
DR WPI; 2002-520952/56.  
XX  
PT Determining nucleic acid sequence, useful for characterizing single-  
PT nucleotide polymorphisms, by incubating with probe in presence of  
PT phosphorothioate nucleotide and exonuclease.  
XX  
PS Example 1; Page 6; 12pp; German.  
XX  
CC The present invention relates to a method of determining a nucleic acid  
CC sequence, involving incubating with a probe, adding at least one  
CC phosphorothioate nucleotide in presence of an enzyme that synthesises a  
CC complementary sequence on the 3'-end of the probe, and adding a second  
CC enzyme that degrades the phosphorothioate-free complement. The method can  
CC be used to determine very short (up to 10 base pair) sequences,  
CC especially for characterisation of single-nucleotide polymorphisms. The  
CC present sequence is a probe for the human MTHFR gene which was used to  
CC demonstrate the method of the invention  
XX  
SO Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5816 CTATGATGATGAATC 5833  
|| |||||

Db 2 CTGCGTATGATGAATC 19

RESULT 3051  
AAL49188/c  
ID AAL49188 standard; DNA; 20 BP.  
XX  
AC AAL49188;  
XX  
DT 30-OCT-2002 (first entry)  
XX  
DE Porcine CD 151 coding sequence PCR primer #12.  
XX  
KM CD 151; porcine reproductive and respiratory syndrome virus; PRRSV; pig;  
KM selective breeding; xenotransplant; anti-RNA entry protein; anti-REP;  
KM anti-viral; vaccine; PCR; primer; ss.  
XX  
OS Sus scrofa.  
XX  
PN WO200260924-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 29-JAN-2002; 2002WO-US002868.  
XX  
PR 29-JAN-2001; 2001US-00772044.  
PR 28-JAN-2002; 2002US-00772044.  
XX  
PA (UNITV ) UNITV KANSAS STATE RES FOUND.  
XX  
PI Kapil S, Shanmukhappa K;  
XX  
DR WPI; 2002-619225/66.  
XX  
PT Determining susceptibility and resistance to porcine reproductive and  
PT respiratory syndrome virus (PRRSV), useful for improving swine breeding,  
PT by assaying for CD 151 in a sample of cellular material of known origin  
PT from the animal.  
XX  
PS Example 17; Page 35; 77pp + Sequence Listing; English.  
XX  
CC The present invention relates to a method of determining the  
CC susceptibility or resistance of an animal to porcine reproductive and  
CC respiratory syndrome virus (PRRSV). This involves assaying for CD 151 in  
CC a sample of cellular material of known origin from the animal. In  
CC addition, coding sequences of CD 151 are described, and anti-viral  
CC compounds designated anti-RNA entry proteins (anti-REPs). The method is  
CC useful for determining susceptibility and resistance to PRRSV in an  
CC animal. This is particularly useful for improving swine breeding or for  
CC screening different pig breeding lines. The method is also useful for  
CC developing non-simian recombinant cell lines for propagating the virus,  
CC for producing anti-viral compounds or vaccines for inducing immunity  
CC against PRRSV, and for diagnosing PRRSV infection in a swine. The present  
CC sequence is a PCR primer used to isolate the porcine CD 151 coding  
CC sequence. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SO Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CAAGGCTTGAAGTGA 1010  
Db 19 CAAGAGCTGAAGTGA 2

RESULT 3052  
AB292414  
ID AB292414 standard; DNA; 20 BP.  
XX

AC AB292414;  
XX  
XX 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002MO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyge JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX  
PS Disclosure; SEQ ID NO 7656; 872bp; English.  
XX  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cyclostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3226 AGGAGGAGGAGTTT 3243  
|||  
Db 1 AGCAGGAGGAGGTTT 18

RESULT 3053  
AB292635/C  
ID AB292635 standard; DNA; 20 BP.  
XX

AC AB292635;  
XX  
XX 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002MO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyge JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX  
PS Disclosure; SEQ ID NO 7877; 872bp; English.  
XX  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cyclostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 6 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6795 TTCTAAGCAGATGGGA 6812  
|||  
Db 19 TTCTAAGCAATGGGA 2

RESULT 3054  
AB288435  
ID AB288435 standard; DNA; 20 BP.  
XX

AC AB288435;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 3677; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 1 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2167 TACAAGTCACCCGTTTC 2184  
Dy |||||||  
Db 1 TTCAAGTCACCCGTTTC 18  
XX  
RESULT 3055  
AB290375/C  
ID AB290375 standard; DNA; 20 BP.  
XX

AC AB290375;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 5617; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4464 TTTTGTGTTTTTTTTTTT 4481  
Dy |||||||  
Db 18 TTTTGTGTTTTTTGTTT 1  
XX  
RESULT 3056  
AB287286  
ID AB287286 standard; DNA; 20 BP.  
XX

AC AB287286;  
XX 17-OCT-2003 (first entry)  
DT  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PE 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 2528; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 2 A; 10 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3385 CTCCCGCAGTCGCCACC 3402  
DB 3 CTTCCCGCAGTCGCCACTC 20

RESULT 3057  
AB287732/C  
ID AB287732 standard; DNA; 20 BP.  
XX

AC AB287732;  
XX 17-OCT-2003 (first entry)  
DT  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PE 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 2974; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 15 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2999 CCCCACCCCTCACCCTCAT 3016  
DB 19 CCCCACCCCTCACCCTCT 2

RESULT 3058  
AB293605/C  
ID AB293605 standard; DNA; 20 BP.  
XX

AC AB293605;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antisthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahbuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 8847; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
 CC immunosuppressive, and cyclostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 DB Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 564 CCTGGGAGGAGGAGA 581  
 19 CCTGGGAGGAGGAGA 2  
 RESULT 3059  
 AB297793  
 ID AB297793 standard; DNA; 20 BP.  
 XX

AC AB297793;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human CCR3 oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antisthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahbuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 13035; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
 CC immunosuppressive, and cyclostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 6 A; 7 C; 6 G; 1 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 DB Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 2405 GACCCACAGTGACACCA 2422  
 1 GACCCACAGTGACACCA 18  
 RESULT 3060  
 AB293220/c  
 ID AB293220 standard; DNA; 20 BP.  
 XX



AC	AB293220;	
XX	17-OCT-2003 (first entry)	
XX	Human oligonucleotide sequence.	
DE		
XX	Human; antisense; lung dysfunction; nasal airway dysfunction;	
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;	
KW	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;	
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;	
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	
KW	lung inflammation; respiratory disease; de.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200285308-A2.	
XX		
PD	31-OCT-2002.	
XX		
XX	23-APR-2002; 2002WO-US013135.	
PF		
XX	24-APR-2001; 2001US-0286137P.	
PR		
XX	(EPIC-) EPIGENESIS PHARM INC.	
PA		
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PI	Miller S, Tang L, Shahabuddin S;	
XX	WPI, 2003-229219/22.	
DR		
XX	Pharmaceutical composition for treating ailments associated with impaired	
PT	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT	ubiquinone.	
XX		
XX	Disclosure; SEQ ID NO 8462; 879pp; English.	
XX		
XX	The invention relates to a novel pharmaceutical composition, which has a	
CC	first active agent comprising an oligonucleotide antisense to the	
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	junctions of genes encoding a polypeptide associated with lung and/or	
CC	nasal airway dysfunction and a second active agent comprising an	
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC	immunosuppressive, and cytostatic activity. The composition may have a	
CC	use in antisense gene therapy. The composition is useful for treating or	
CC	preventing a respiratory, lung or malignant disease or condition, also	
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	Note: The sequence data for this patent is not represented in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences	
XX		
XX		
XX	Sequence 20 BP; 11 A; 0 C; 8 G; 1 T; 0 U; 0 Other;	
XX		
XX	Query Match 0.2%; Score 14.8; DB 1; Length 20;	
XX	Best Local Similarity 88.9%; Pred. No. 2e+03;	
XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	5709 TTTTCCTCTCTCTCTTT 5726	
DB	19 TTTTCCTCTCTCTCTTT 2	
XX		
XX	RESULT 3061	
XX	AB286063/C	
XX	ID AB286063 standard; DNA; 20 BP.	

AC	ABZ86063;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
KV	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	antiaschematic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KX	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KH	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
PN	MO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIC-) EPIGENESIS PHARM INC.
XX	
P1	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S,
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	ubiquinone.
PS	
PS	Claim 15; SEQ ID NO 1305; 872bp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiaschematic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX	
Query Match	0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 2e+03;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0
OY	7415 GCAGCAGCAGCAGCA 7432       
Db	18 GCAGCAGCAGCATCACCA 1
RESULT 3062	
ID	ABZ90434 standard; DNA; 20 BP.
XX	

AC AB290434;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahbuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 5676; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1341 GATCAGTCGCTGATGAA 1358  
Db 1 GATCGTCCCTGATGAA 18  
|||||  
|||||

RESULT 3063  
AB290042  
ID AB290042 standard; DNA; 20 BP.  
XX

AC AB290042;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahbuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 5284; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 2 C; 2 G; 12 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3955 TCTTATGTTTCATTAATT 3972  
Db 1 TCTTATGTTTCATTAATT 18  
|||||  
|||||

RESULT 3064  
AB285315/c  
ID AB285315 standard; DNA; 20 BP.  
XX

```

AC  ABZ85315;
XX
DT  17-OCT-2003 (first entry)
DE
DE  Human oligonucleotide sequence.
XX
XX  Human; antisense; lung dysfunction; nasal airway dysfunction;
KM  antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM  antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KM  antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM  adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX  lung inflammation; respiratory disease; ds.
XX
OS  Homo sapiens.
XX
PN  WO200285308-A2.
XX
PD  31-OCT-2002.
XX
PE  23-APR-2002; 2002WO-US013135.
XX
PR  24-APR-2001; 2001US-0286137P.
XX
PA  (EPIG-) EPIGENESIS PHARM INC.
XX
PI  Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI  Miller S, Tang L, Shahabuddin S;
XX  WPI; 2003-229219/22.
XX
DR  Pharmaceutical composition for treating ailments associated with impaired
PT  respiration, has oligo(s) antisense to specific gene(s) or its
PT  corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT  ubiquinone.
XX
XX  Claim 15; SEQ ID NO 557; 872pp; English.
XX
XX  The invention relates to a novel pharmaceutical composition, which has a
CC  first active agent comprising an oligonucleotide antisense to the
CC  initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC  5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC  junctions of genes encoding a polypeptide associated with lung and/or
CC  nasal airway dysfunction and a second active agent comprising an
CC  antiinflammatory steroid and ubiquinone. A composition of the invention
CC  has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC  immunosuppressive, and cyclostatic activity. The composition may have a
CC  use in antisense gene therapy. The composition is useful for treating or
CC  preventing a respiratory, lung or malignant disease or condition, also
CC  for enhancing the prophylactic or therapeutic respiratory effect of an
CC  antiinflammatory steroid in a subject, for reducing or depleting levels
CC  of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC  receptor, producing bronchodilation, increasing levels of ubiquinone or
CC  lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC  lung inflammation, lung allergies, or a respiratory disease or condition.
CC  Note: The sequence data for this patent is not represented in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 20 BP; 12 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
SQ

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Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY  6461 ATACTTTTTCGT 6478
    |||||
DB  19 AACTTTTTCGTGT 2

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RESULT 3065  
 ABZ93982/C  
 ID ABZ93982 standard; DNA; 20 BP.  
 XX

```

AC  ABZ93982;
XX
DT  17-OCT-2003 (first entry)
DE
DE  Human oligonucleotide sequence.
XX
XX  Human; antisense; lung dysfunction; nasal airway dysfunction;
KM  antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM  antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KM  antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM  adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX  lung inflammation; respiratory disease; ds.
XX
OS  Homo sapiens.
XX
PN  WO200285308-A2.
XX
PD  31-OCT-2002.
XX
PE  23-APR-2002; 2002WO-US013135.
XX
PR  24-APR-2001; 2001US-0286137P.
XX
PA  (EPIG-) EPIGENESIS PHARM INC.
XX
PI  Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI  Miller S, Tang L, Shahabuddin S;
XX  WPI; 2003-229219/22.
XX
DR  Pharmaceutical composition for treating ailments associated with impaired
PT  respiration, has oligo(s) antisense to specific gene(s) or its
PT  corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT  ubiquinone.
XX
XX  Disclosure; SEQ ID NO 9224; 872pp; English.
XX
XX  The invention relates to a novel pharmaceutical composition, which has a
CC  first active agent comprising an oligonucleotide antisense to the
CC  initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC  5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC  junctions of genes encoding a polypeptide associated with lung and/or
CC  nasal airway dysfunction and a second active agent comprising an
CC  antiinflammatory steroid and ubiquinone. A composition of the invention
CC  has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC  immunosuppressive, and cyclostatic activity. The composition may have a
CC  use in antisense gene therapy. The composition is useful for treating or
CC  preventing a respiratory, lung or malignant disease or condition, also
CC  for enhancing the prophylactic or therapeutic respiratory effect of an
CC  antiinflammatory steroid in a subject, for reducing or depleting levels
CC  of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC  receptor, producing bronchodilation, increasing levels of ubiquinone or
CC  lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC  lung inflammation, lung allergies, or a respiratory disease or condition.
CC  Note: The sequence data for this patent is not represented in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 20 BP; 7 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
SQ

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Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY  3302 AGATCATATTTAGAT 3319
    |||||
DB  20 AGATTAAGATTTAGAT 3

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RESULT 3066  
 ABZ98928/C  
 ID ABZ98928 standard; DNA; 20 BP.  
 XX

AC ABZ98928;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human PDE4A oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiallathmic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 14170; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiallathmic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Db Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6406 CCTGCTAGTAGCTTCTC 6423  
 |||||  
 Db 19 CCTGCTAGTAGTACTACTC 2  
 |||||  
 RESULT 3067  
 ABZ88693/C  
 ID ABZ88693 standard; DNA; 20 BP.  
 XX

AC ABZ88693;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiallathmic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 3935; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiallathmic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 12 A; 0 C; 0 G; 8 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Db Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5473 TTTTGTGTAAGATTA 5490  
 |||||  
 Db 18 TTTTGTGTAAGATTA 1  
 |||||  
 RESULT 3068  
 ABZ91491/C  
 ID ABZ91491 standard; DNA; 20 BP.  
 XX

AC ABZ91491;  
 XX  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.  
 DE  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 6733; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cyclostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 3385 CTCCCCAGCTGCCACCC 3402  
 DB 19 CTCTGCGAGCTGCCACCC 2

AC ABZ93213;  
 XX  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.  
 DE  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 8455; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cyclostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 11 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 6463 ACCTTTTTCGTTG 6480  
 DB 18 ACCTTTTTCGTTG 1

RESULT 3069  
 ABZ93213/C  
 ID ABZ93213 standard; DNA; 20 BP.  
 XX

RESULT 3070  
 ABZ92117  
 ID ABZ92117 standard; DNA; 20 BP.  
 XX

AC AB292117;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;  
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KM lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-028617P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nlyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
DR WPI; 2003-229219/22.  
XX  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 7359; 872bp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytoskeletal activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4301 TCTTTTCCTTCCCTGG 4318  
|||  
Db 2 TCTTTTCCTTCCCTGG 19

RESULT 3071  
AC62225/c  
ID ACC62225 standard; DNA; 20 BP.  
XX

AC ACC62225;  
XX  
DT 20-JUN-2003 (first entry)  
XX  
DE Mouse alpha protein B antisense oligonucleotide SEQ ID NO: 114.  
XX  
KW alpha protein B; Apob; antilipemic; antiarteriosclerotic; antidiabetic;  
KM anorectic; cardiovascular; gene therapy; lipid metabolism;  
KM cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;  
KM type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;  
KM glucose; antisense oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
PN W02003011887-A2.  
XX  
PD 13-FEB-2003.  
XX  
PF 30-JUL-2002; 2002WO-US024247.  
XX  
PR 01-AUG-2001; 2001US-0092003.  
PR 30-APR-2002; 2002US-00135985.  
PR 15-MAY-2002; 2002US-00147196.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Crooke RM, Graham MJ;  
PI Miller S, Tang L, Shahabuddin S;  
DR WPI; 2003-268105/26.  
XX  
XX  
PT New antisense oligonucleotides for modulating apolipoprotein B,  
PT especially for preventing or treating atherosclerosis, hyperlipidaemia or  
PT diabetes, or for modulating glucose, cholesterol, lipoprotein or  
PT triglyceride levels.  
XX  
PS Example 17, Page 100; 160bp; English.  
XX  
XX The invention relates to a novel compound that is 8-50 nucleotides in  
CC length that is targeted to a nucleic acid molecule encoding  
CC apolipoprotein B (Apob), and specifically hybridises with and inhibits  
CC the expression of a nucleic acid molecule encoding Apob; or which  
CC specifically hybridises with at least an 8-nucleotide portion of an  
CC active site on a nucleic acid molecule encoding Apob. A compound of the  
CC invention has antilipemic, antiarteriosclerotic, antidiabetic,  
CC anorectic, and cardiovascular activity. The compound may have a use in  
CC gene therapy. The antisense oligonucleotide is useful for treating an  
CC animal having a disease or conditions associated with Apob, e.g. a  
CC condition involving abnormal lipid metabolism, a condition involving  
CC abnormal cholesterol metabolism, atherosclerosis, or a condition  
CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes  
CC (specifically Type 2 diabetes), obesity, atherosclerosis or  
CC cardiovascular disease). The new compound or the antisense  
CC oligonucleotide is also useful for modulating glucose levels  
CC (particularly plasma or serum glucose levels) in a human or diabetic  
CC animal, or for modulating serum cholesterol levels, lipoprotein levels  
CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,  
CC particularly in a human. The antisense compound is also useful for  
CC preventing or delaying the onset of a disease or condition associated  
CC with Apob, or the onset of an increase in glucose levels in the animal or  
CC human. The present sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6291 ACACTGGCTTCAGGAT 6308  
|||  
Db 19 ACACTGGCTTCAGGAT 2

RESULT 3072  
 ID AB277000 standard; DNA; 20 BP.  
 AC AB277000;  
 DT 07-MAY-2003 (first entry)  
 DE Bovine DGAT PCR primer #36.  
 KW Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;  
 KW milk; meat marbling; low fat; polymorphic; SNP;  
 KW single nucleotide polymorphism; PCR primer; ss.  
 OS Bos taurus.  
 OS Synthetic.  
 PN WO2003004630-A2.  
 PD 16-JAN-2003.  
 PF 05-JUL-2002; 2002WO-EP007520.  
 PR 06-JUL-2001; 2001EP-00116412.  
 PR 13-MAY-2002; 2002US-0379412P.  
 PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.  
 PI Fries H, Winter A;  
 PS WPI; 2003-239205/23.  
 DR WPI; 2003-239205/23.  
 PT New nucleic acid molecule comprising a sequence of an allele of a  
 PT polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for  
 PT testing a mammal for its predisposition for fat content of milk and for  
 PT meat marbling.  
 PS Example 1; Page 36; 91pp; English.  
 CC The present invention describes a nucleic acid molecule (NA) (I) encoding  
 CC a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or  
 CC indicative for low fat content of milk and to low meat marbling  
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and  
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a  
 CC mammal for its predisposition for fat content of milk and/or its  
 CC predisposition for meat marbling. The method comprises analysing the gene  
 CC encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide  
 CC polymorphisms (SNPs)) which are connected with the predisposition. The  
 CC nucleotide polymorphisms are located in the coding region of the DGAT  
 CC gene and result in substitution, deletion and/or addition of an amino  
 CC acid sequence of the polypeptide which is encoded by the gene. The  
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT  
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or  
 CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a  
 CC thymine, which correlate with a predisposition for low fat content of  
 CC milk and low meat marbling. The nucleic acid molecule has at the position  
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine  
 CC residues which correlate with a predisposition for high content of milk  
 CC and high meat marbling. The nucleotide polymorphisms are located in a  
 CC region which is responsible for the regulation of the expression of the  
 CC product of the gene encoding DGAT. AB276924 to AB277045 and AB276035 to  
 CC AB276046 represent sequences used in the exemplification of the present  
 CC invention  
 CC XX  
 SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1095 ACAGCTGAGAGTGAGACA 1112  
 1 ACAGCTGAGAGTGAGAGACA 18

RESULT 3073  
 ID AB276933 standard; DNA; 20 BP.  
 AC AB276933;  
 DT 07-MAY-2003 (first entry)  
 DE Bovine DGAT BAC-DNA sequencing primer #6.  
 KW Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;  
 KW milk; meat marbling; low fat; polymorphic; SNP;  
 KW single nucleotide polymorphism; PCR primer; ss.  
 OS Bos taurus.  
 OS Synthetic.  
 PN WO2003004630-A2.  
 PD 16-JAN-2003.  
 PF 05-JUL-2002; 2002WO-EP007520.  
 PR 06-JUL-2001; 2001EP-00116412.  
 PR 13-MAY-2002; 2002US-0379412P.  
 PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.  
 PI Fries H, Winter A;  
 PS WPI; 2003-239205/23.  
 DR WPI; 2003-239205/23.  
 PT New nucleic acid molecule comprising a sequence of an allele of a  
 PT polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for  
 PT testing a mammal for its predisposition for fat content of milk and for  
 PT meat marbling.  
 PS Example 1; Page 35; 91pp; English.  
 CC The present invention describes a nucleic acid molecule (NA) (I) encoding  
 CC a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or  
 CC indicative for low fat content of milk and to low meat marbling  
 CC (intramuscular fat content). Human DGAT is located to chromosome 8, and  
 CC bovine DGAT is located to chromosome 14. (I) is useful for testing a  
 CC mammal for its predisposition for fat content of milk and/or its  
 CC predisposition for meat marbling. The method comprises analysing the gene  
 CC encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide  
 CC polymorphisms (SNPs)) which are connected with the predisposition. The  
 CC nucleotide polymorphisms are located in the coding region of the DGAT  
 CC gene and result in substitution, deletion and/or addition of an amino  
 CC acid sequence of the polypeptide which is encoded by the gene. The  
 CC nucleic acid molecule has at the position 10433 and 10434 of the DGAT  
 CC gene a guanine and a cytosine residue, at position 3343 a cytosine or  
 CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a  
 CC thymine, which correlate with a predisposition for low fat content of  
 CC milk and low meat marbling. The nucleic acid molecule has at the position  
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine  
 CC residues which correlate with a predisposition for high content of milk  
 CC and high meat marbling. The nucleotide polymorphisms are located in a  
 CC region which is responsible for the regulation of the expression of the  
 CC product of the gene encoding DGAT. AB276924 to AB277045 and AB276035 to  
 CC AB276046 represent sequences used in the exemplification of the present  
 CC invention  
 CC XX  
 SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1095 ACAGCTGAGAGTGAGACA 1112

Db 1 ACAGCTGAGTGAGGACA 18

RESULT 3074  
ABT34193/c  
ID ABT34193 standard; DNA; 20 BP.

XX ABT34193;

XX 12-JUN-2003 (first entry)

XX Mouse short heterodimer partner-1 expression oligo SEQ ID No 68.

XX Antiartherosclerotic; cardiact; vasotropic; antiinfective; cytostatic;  
XX antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;  
XX short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;  
XX cardiovascular disease; infection; inflammation; tumour formation; mouse;  
XX antisense; ds.

XX OS Unidentified.

XX WO2003012033-A2.

XX 13-FEB-2003.

XX 17-JUL-2002; 2002WO-US023245.

XX 31-JUL-2001; 2001US-00919197.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

XX WPI; 2003-248161/24.

XX New antisense oligonucleotide targeted to a nucleic acid encoding short  
PT heterodimer partner-1, useful for treating diseases involving abnormal  
PT lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular  
PT diseases.

XX Example 16; Page 95; 121pp; English.

XX The invention relates to a novel compound of 8 - 50 nucleobases in length  
CC targeted to a nucleic acid molecule encoding a short heterodimer partner-  
CC 1. The novel compound specifically hybridizes with a nucleic acid  
CC molecule encoding the short heterodimer partner-1, and inhibits the  
CC expression of the nucleic acid molecule. The compound, and a composition  
CC comprising it are useful for treating a disease or condition associated  
CC with the short heterodimer partner-1, particularly a condition involving  
CC abnormal lipid or cholesterol metabolism such as atherosclerosis or a  
CC cardiovascular disease. They are also useful in research and diagnostics  
CC for modulating the expression of short heterodimer partner-1. They can  
CC also be useful prophylactically in preventing or delaying infection,  
CC inflammation or tumour formation. This polynucleotide sequence represents  
CC a mouse antisense oligo relating to the heterodimer partner-1 of the  
CC invention

XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 860 ATGTCAGCCAGCTGCT 877  
DB 18 ATCTCAGCCAGCTGCT 1

RESULT 3075  
AB270582/c  
ID AB270582 standard; DNA; 20 BP.

AC AB270582;  
XX 23-MAY-2003 (first entry)

XX Insulin gene VNTR allele genotyping primer INS56.

XX Insulin; genotyping; obesity; variable number of tandem repeats; VNTR;  
XX human; PCR; primer; ss.

XX Homo sapiens.

XX WO2003012139-A2.

XX 13-FEB-2003.

XX 31-JUL-2002; 2002WO-IB003347.

XX 31-JUL-2001; 2001US-0309235P.

XX 21-AUG-2001; 2001US-0316830P.

XX (BOUG/) BOUGNERES P.

XX Bougnere P;

XX WPI; 2003-248167/24.

XX Determining the risk of developing obesity for treating or reducing the  
PT risk of developing obesity by determining a paternal insulin variable  
PT number of tandem repeats allele in the individual.  
XX Disclosure; Page 16; 62pp; English.

XX The invention provides methods for determining the risk of development of  
CC obesity in a subject by examining the paternal insulin variable number of  
CC tandem repeats (VNTR) class. The presence of a paternal insulin VNTR  
CC class I allele indicates that the subject has an approximately 2-fold  
CC increase in risk of developing obesity compared with a subject carrying a  
CC paternal insulin VNTR class II allele. Methods are provided to facilitate  
CC rational therapy and maintenance of individuals predisposed to obesity.  
CC The insulin VNTR allele may be genotyped by determining the identity of a  
CC nucleotide at an insulin-related genetic marker that is in linkage  
CC disequilibrium with the insulin HphI locus. This includes any marker that  
CC is a surrogate for the VNTR in the insulin gene. The -2221 MspI marker is  
CC an example of a genetic marker associated with the insulin gene, and can  
CC be detected by PCR using primers INS56 (present sequence) and INS57 (see  
CC AB270583)

XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
XX Best Local Similarity 88.9%; Pred. No. 2e+03; 2; Indels 0; Gaps 0;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4729 CTTGAGGCCAGCTGGAG 4746  
DB 18 CTTGAGGCCAGCTGGAG 1

RESULT 3076  
ACC47290/c  
ID ACC47290 standard; DNA; 20 BP.

XX ACC47290;

XX 11-AUG-2003 (first entry)

XX Human apolipoprotein(a) mRNA inhibiting antisense oligo ISIS 144373.

XX Apolipoprotein(a); antiarteriosclerotic; cardiact; gene therapy; human;  
XX antisense; ss.

XX Synthetic.  
XX Homo sapiens.



XX WO2003014307-A2.  
 XX 20-FEB-2003.  
 XX 05-AUG-2002; 2002WO-US024920.  
 XX 07-AUG-2001; 2001US-00923515.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Crooke RM, Graham MJ;  
 XX WPI; 2003-255656/25.  
 XX New antisense compound, useful for preparing a composition for treating  
 XX abnormal lipid or cholesterol metabolism, atherosclerosis or  
 XX cardiovascular disease.  
 XX Claim 3; Page 87; 120pp; English.  
 XX The invention relates to a new compound, 8-50 nucleobases in length  
 XX targeted to a nucleic acid molecule encoding human apolipoprotein(a),  
 XX specifically hybridizes with and inhibits the expression of human  
 XX apolipoprotein(a). The antisense compounds are useful for preparing a  
 XX composition for treating abnormal lipid or cholesterol metabolism,  
 XX atherosclerosis or cardiovascular disease. Sequences ACC47284-318  
 XX represent specific examples of chimeric antisense phosphorothioate  
 XX oligonucleotides having 2'-MOE wings and a deoxy gap targeting human  
 XX apolipoprotein(a) mRNA  
 XX Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 XX Best Local Similarity 88.9%; Pred. No. 2e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 1752 GCAGCTCATTTATTCAT 1769  
 XX 18 GCAGCTCCTTATTTAT 1  
 XX  
 XX RESULT 3077  
 XX ABX04329/C  
 XX ID ABX04329 standard; DNA; 20 BP.  
 XX  
 XX ABX04329;  
 XX  
 XX 13-JAN-2003 (first entry)  
 XX  
 XX Mouse Interleukin 5 antisense oligonucleotide ISIS 17981.  
 XX  
 XX Mouse; ss; antisense; interleukin 5; IL-5; IL-5 receptor; antiasthmatic;  
 XX immunosuppressant; eosinophilic syndrome; asthma.  
 XX Mus musculus.  
 XX Synthetic.  
 XX US2002128216-A1.  
 XX 12-SEP-2002.  
 XX  
 XX 07-MAR-2001; 2001US-00800629.  
 XX  
 XX 26-MAR-1999; 99US-00280799.  
 XX 17-MAR-2000; 2000WO-US007318.  
 XX  
 XX (DEAN/) DEAN N M.  
 XX (KARR/) KARRAS J G.  
 XX (MCKA/) MCKAY R.  
 XX (MANO/) MANOHARAN M.  
 XX  
 XX Dean NM, Karras JG, McKay R, Manoharan M;

XX WPI; 2003-039602/03.  
 XX Novel antisense compound for treating disease/condition e.g. eosinophilic  
 XX syndrome or asthma associated with interleukin-5 or IL-5 receptor  
 XX expression or IL-5 signal transduction, modulates IL-5 signal  
 XX transduction.  
 XX Example 14; Page 16; 77pp; English.  
 XX The invention relates to an antisense compound of 8-30 nucleobases in  
 XX length, which modulates interleukin (IL)-5 signal transduction. Also  
 XX include are a pharmaceutical composition comprising the antisense  
 XX oligonucleotide and a pharmaceutically acceptable carrier or diluent, and  
 XX a diagnostic kit for detecting the expression level of the membrane form  
 XX versus soluble form of IL-5 receptor a. The antisense compound is useful  
 XX for modulating IL-5 signal transduction, modulating expression of  
 XX mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,  
 XX in cells or tissues, for altering the ratio of the isoforms of mammalian  
 XX IL-5 receptor a in mammalian cells or tissues, treating a mammalian  
 XX having a disease or condition associated with IL-5 signal transduction,  
 XX IL-5 expression or IL-5 receptor a, expression, where the disease or  
 XX condition include eosinophilic syndrome or asthma. An antisense compound  
 XX which alters splicing of an RNA encoding IL-5 receptor a is also useful  
 XX for treating a mammal having a disease or condition. The present sequence  
 XX is an antisense oligonucleotide targeting mouse IL5  
 XX  
 XX Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 XX Best Local Similarity 88.9%; Pred. No. 2e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 5272 ATACGAGCAGGTGCAG 5289  
 XX 20 AGACGAGCAGGTGCAG 3  
 XX  
 XX RESULT 3078  
 XX ABX17722  
 XX ID ABX17722 standard; DNA; 20 BP.  
 XX  
 XX ABX17722;  
 XX  
 XX 05-FEB-2003 (first entry)  
 XX  
 XX Human urokinase plasminogen activator antisense oligonucleotide #27.  
 XX  
 XX Urokinase plasminogen activator; gene therapy; cancer;  
 XX hyperproliferative disorder; cancer; breast cancer; colon cancer;  
 XX bone cancer; brain cancer; ovary cancer; cervix cancer;  
 XX endometrium cancer; stomach cancer; kidney cancer; tumor metastasis;  
 XX antisense oligonucleotide; ss.  
 XX Synthetic.  
 XX WO200279515-A1.  
 XX 10-OCT-2002.  
 XX  
 XX 18-MAR-2002; 2002WO-US008112.  
 XX  
 XX 30-MAR-2001; 2001US-00821972.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Baker BF, Freiler SM, Watt AT;  
 XX WPI; 2003-058441/05.  
 XX  
 XX New antisense compound, useful for preparing a composition for treating  
 XX hyperproliferative disorders, cancer e.g., breast, colon, bone, brain,  
 XX ovary, cervix, endometrium, stomach or kidney cancer, or tumor

```

PT metastasis.
XX
PS Example 15; Page 91; 153bp; English.
XX
CC A new compound, which is 8-50 nucleobases in length targeted to a nucleic
CC acid molecule encoding uridine plasminogen activator, specifically
CC hybridizes with and inhibits the expression of urokinase plasminogen
CC activator. The compound is useful for preparing a composition for
CC treating (e.g. by gene therapy) hyperproliferative disorder, cancer e.g.,
CC breast, colon, bone, brain, ovary, cervix, endometrium, stomach or kidney
CC cancer, or tumour metastasis. This sequence represents an antisense
CC oligonucleotide used to modulate expression of urokinase plasminogen
CC activator
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1965 TTTTCAACAGCCAGTGAT 1982
DB 2 TTTTCCAAAGCCAGTGAT 19
RESULT 3079
AAD53839/c
ID AAD53839 standard; DNA; 20 BP.
XX
AC AAD53839;
XX
DT 28-MAY-2003 (first entry)
XX
DE BMPRIA exon 8 specific PCR primer, ALK3-8b.
XX
KM Juvenile polyposis; JP; colorectal carcinoma; BMPRIA; gene therapy;
KM diagnosis; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200294084-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US016053.
XX
PR 21-MAY-2001; 2001US-0292691P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Howe JR;
XX
DR WPI; 2003-120737/11.
XX
PT Diagnosing or treating juvenile polyposis or colorectal carcinoma,
PT comprises obtaining a tissue or fluid sample from a subject and
PT determining the loss or alteration of a functional BMPRIA gene in cells
PT of the sample.
XX
PS Example 1; Page 74; 108bp; English.
XX
CC The invention relates to a method of diagnosing juvenile polyposis (JP)
CC or colorectal carcinoma. The method involves obtaining a sample from a
CC subject and determining the loss or alteration of a functional BMPRIA
CC gene in cells of the sample. The method is useful in diagnosing or
CC treating JP or colorectal carcinoma. The invention is also useful in gene
CC therapy. The present sequence is BMPRIA exon specific PCR primer, used to
CC illustrate the method of the invention
XX
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5685 CTTTGACCACTGTTTG 5702
DB 20 CTTTGCCCACTGTTTG 3
RESULT 3080
AAD53846
ID AAD53846 standard; DNA; 20 BP.
XX
AC AAD53846;
XX
DT 28-MAY-2003 (first entry)
XX
DE PCR primer #3 used in BMPRIA exon mutation analysis.
XX
KM Juvenile polyposis; JP; colorectal carcinoma; BMPRIA; gene therapy;
KM diagnosis; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200294084-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US016053.
XX
PR 21-MAY-2001; 2001US-0292691P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Howe JR;
XX
DR WPI; 2003-120737/11.
XX
PT Diagnosing or treating juvenile polyposis or colorectal carcinoma,
PT comprises obtaining a tissue or fluid sample from a subject and
PT determining the loss or alteration of a functional BMPRIA gene in cells
PT of the sample.
XX
PS Example 1; Page 74; 108bp; English.
XX
CC The invention relates to a method of diagnosing juvenile polyposis (JP)
CC or colorectal carcinoma. The method involves obtaining a sample from a
CC subject and determining the loss or alteration of a functional BMPRIA
CC gene in cells of the sample. The method is useful in diagnosing or
CC treating JP or colorectal carcinoma. The invention is also useful in gene
CC therapy. The present sequence is a PCR primer used in BMPRIA exon
CC mutation analysis. This primer is used to illustrate the method of the
CC invention
XX
SQ Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7246 AGCATGATGGGGAATG 7263
DB 2 AGTATGATGGGCAATG 19
RESULT 3081
ACC86760/c
ID ACC86760 standard; DNA; 20 BP.
XX
AC ACC86760;
XX
DT 04-AUG-2003 (first entry)
XX
DE Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:55.
XX

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AC AAL61734;
XX
XX 22-SEP-2003 (first entry)
XX
DE Human PCTAIRE protein kinase 1 antisense oligo, ISIS 204171.
XX
KM Human, PCTAIRE protein kinase 1; PCTAIRE-1; sideroblastic anaemia;
KM hyperproliferative disease; neurological disease; thrombocytopenia;
KM retinitis pigmentosa; X-linked Charcot-Marie-Tooth disease; therapy;
KM mental retardation; Wiskott-Aldrich syndrome; dysontia; Parkinsonism;
KM PTK1, crk5; incontinentia pigmenti; phosphorothioate backbone;
KM antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key
XX Location/Qualifiers
XX
XX modified_base
XX 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; All cytidines are 5-
XX methylcytidines"
XX
XX modified_base
XX 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "2' methoxyethyl nucleotides"
XX
XX modified_base
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2' methoxyethyl nucleotides"
XX
XX
XX MO2003049691-A2.
XX
XX 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US039138.
XX
XX 07-DEC-2001; 2001US-00017621.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Freier SM, Roach MP;
XX
XX WPI; 2003-577271/54.
XX
XX
XX New antisense oligonucleotides for modulating PCTAIRE protein kinase 1
XX gene expression, particularly useful for treating hyperproliferative or
XX neurological disorders for example, mental retardation, or
XX thrombocytopenia.
XX
XX Claim 3; Page 74; 104pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of PCTAIRE protein kinase 1 (also known as
XX PCTAIRE-1, PTK1 and crk5). The antisense oligonucleotide is useful for
XX treating an animal having a disease or condition associated with PCTAIRE
XX protein kinase 1, particularly a hyperproliferative disease or a
XX neurological disease. These diseases include thrombocytopenia, mental
XX retardation, Wiskott-Aldrich syndrome, retinitis pigmentosa, dysontia
XX with Parkinsonism, sideroblastic anaemia, X-linked Charcot-Marie-Tooth
XX disease, or incontinentia pigmenti. The antisense oligonucleotide is
XX particularly useful for inhibiting the expression of PCTAIRE protein
XX kinase 1 in cells or tissues. It is useful for diagnostics, prophylaxis,
XX or as research reagents or kits. The present sequence is an antisense
XX oligonucleotide targeted to human PCTAIRE protein kinase 1 DNA. This
XX sequence is used to illustrate the method of the invention
XX
XX Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1412 AGGATGACATGACGGAG 1429
Db 2 AGGCTGACACGACGGAG 19
XX
XX
XX RESULT 3084
XX ACD25682/c
XX ID ACD25682 standard; DNA; 20 BP.
XX
XX ACD25682;
XX
XX 26-AUG-2003 (first entry)
XX
XX
XX Human calcium channel alpha2delta SSCP primer c1636R.
XX
XX DE
XX
XX Human; ss; PCR; calcium channel alpha2delta; chromosome 3p21.3; primer;
XX transgenic; cancer; lung cancer; small cell carcinoma; epilepsy; stroke;
XX non-small cell carcinoma; breast cancer; nasopharyngeal cancer;
XX cervical cancer; head and neck cancer; neurological disease;
XX brain trauma; Alzheimer's disease; multifarct dementia; seizure;
XX amyotrophic lateral sclerosis; convulsions; Huntington's disease;
XX amnesia; cardiovascular disease; cardiac arrhythmia; angina pectoris;
XX hypoxic damage; ischaemia; myocardial infarction; SSCP;
XX congestive heart failure; Lambert-Baton myasthenic syndrome;
XX single strand conformation polymorphism.
XX
XX OS Homo sapiens.
XX
XX
XX US2003044911-A1.
XX
XX 06-MAR-2003.
XX
XX 05-APR-2002; 2002US-00116949.
XX
XX 30-DEC-1998; 98US-0114359P.
XX
XX 22-DEC-1999; 99US-00470443.
XX
XX
XX (LERM/) LERMAN M I.
XX (LATT/) LATT F.
XX (WEIM/) WEI M.
XX (DUHE/) DUH F.
XX (MINN/) MINNA J D.
XX (SEKI/) SEKIDO Y.
XX (GAOB/) GAO B.
XX
XX Lerman M, Latt F, Wei M, Duh F, Minna J, Sekido Y, Gao B;
XX
XX WPI; 2003-492262/46.
XX
XX
XX New substantially pure human calcium channel alpha2delta subunit splice
XX isoform 1, 2 and 3 sequence useful in preventing, treating and diagnosing
XX cancer, neurological disorders and cardiovascular disease.
XX
XX Example 7; Page 25; 79pp; English.
XX
XX The invention relates to a substantially purified amino acid sequence
XX comprising at least a portion of human calcium channel alpha2delta
XX subunit splice isoform 1, splice isoform 2 sequence or splice isoform 3,
XX or their variants, and their encoding nucleic acids (or their
XX complements, variants, or homologues). Also included are screening a test
XX compound for modulating calcium channel activity, an antibody which binds
XX to the calcium channel or its variants and producing a transgenic non-
XX human animal (where the animal expresses a reduced level of calcium
XX channel alpha2delta subunit relative to a corresponding wild-type
XX animal. The calcium channel proteins are useful for generating an
XX antibody (which is useful for detecting the proteins or their portions).
XX The transgenic animal (preferably a rodent e.g. mouse) is useful for
XX identifying a therapeutic compound for treating a transgenic animal
XX having cancer, especially lung cancer (small cell carcinoma or non-small
XX cell carcinoma), breast cancer, nasopharyngeal cancer, cervical cancer,
XX head and neck cancer, a neurological disease, especially epilepsy,
XX stroke, brain trauma, Alzheimer's disease, multifarct dementia,
XX amyotrophic lateral sclerosis, convulsions, seizures, Huntington's

```

CC disease, and amnesia, a cardiovascular disease, especially cardiac  
CC arrhythmia, angina pectoris, hypoxic damage to the cardiovascular system,  
CC ischemic damage to the cardiovascular system, myocardial infarction, and  
CC congestive heart failure; or Lambert-Baton myasthenic syndrome. The  
CC proteins and nucleic acids are useful in the diagnosis, prevention and  
CC treatment of the above mentioned diseases. The human gene for the calcium  
CC channel is located on chromosome 3p21.3. The present sequence is an SSCP  
CC (single strand conformation polymorphism) primer used to detect  
CC polymorphisms in the calcium channel alpha2delta subunit gene  
XX

Seq Sequence 20 BP; 1 A; 4 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5287 CAGCCTTACTCTCCAGCA 5304  
DB 20 CAGCCGCGACTCCAGCA 3

RESULT 3085  
ABT44169/C  
ID ABT44169 standard; DNA; 20 BP.  
AC ABT44169;  
XX  
XX 06-NOV-2003 (first entry)  
DT  
DE Chimeric antisense oligonucleotide ISIS 199165 to inhibit human NOD1.  
XX  
XX Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;  
XX caspase associated recruitment domain 4; programmed cell death; cancer;  
XX apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;  
XX amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;  
XX viral infection; human; chimeric.  
XX  
XX OS Chimeric - Homo sapiens.  
XX  
XX WO2003050246-A2.  
XX  
XX 19-JUN-2003.  
XX  
XX 04-DEC-2002; 2002WO-US038606.  
XX  
XX 05-DEC-2001; 2001US-00006883.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX PA  
XX  
XX PI Dobie KW, Roach MP;  
XX  
XX WPI; 2003-577293/54.  
XX  
XX  
XX New compound, comprising a sequence targeted to a nucleic acid encoding  
XX nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing  
XX a composition for treating hyperproliferative disease, e.g., cancer.  
XX  
XX Example 15; Page 75; 138pp; English.  
XX  
XX This invention relates to novel chimeric antisense oligonucleotides that  
XX specifically hybridize to and inhibit the expression of the nucleotide  
XX binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4  
XX (caspase associated recruitment domain 4) is a domain that is involved in  
XX the elimination of cells via programmed cell death and in the host  
XX defence against pathogens, i.e., it works to regulate apoptosis. Apoptosis  
XX is a naturally occurring process, however, if it becomes overstimulated  
XX it can lead to cell loss and neurodegenerative conditions including  
XX Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis  
XX pigmentosa and blood cell disorders. Conversely, insufficient apoptosis  
XX can contribute to the development of cancer, autoimmune disorders and  
XX viral infections. The present invention describes antisense  
XX oligonucleotides that can modulate NOD1 expression (and variants  
XX thereof), such that these compounds, via gene therapy, can be used to

CC treat various human diseases caused by aberrant apoptosis. This  
CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit  
CC expression of human NOD1, the aim of the invention. Note that it has two  
CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a  
CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate  
CC throughout  
XX

Seq Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2093 TGGCGGTACAGCCGACAC 2110  
DB 18 TGGCGGCGACGACGACAC 1

RESULT 3086  
AAD56488/C  
ID AAD56488 standard; DNA; 20 BP.  
AC AAD56488;  
XX  
XX 27-AUG-2003 (first entry)  
DT  
DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 11.  
XX  
XX EPHA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;  
XX epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;  
XX Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;  
XX memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;  
XX amyotrophic lateral sclerosis; attention deficit disorder; depression;  
XX injury; human; RT; reverse transcription; PCR; primer; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX WO2003040304-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 11-NOV-2002; 2002WO-IB004930.  
XX  
XX 09-NOV-2001; 2001US-0345206P.  
XX  
XX 02-JUN-2002; 2002US-0393272P.  
XX  
XX (NEUR-) NEURONOVA AB.  
XX  
XX PA  
XX  
XX PI Holmberg J, Friesen J;  
XX  
XX WPI; 2003-441543/41.  
XX  
XX  
XX Alleviating a symptom of a disease or disorder of the nervous system by  
XX administering a modulator of neural stem or neural progenitor cell  
XX activity in vivo to a patient.  
XX  
XX Example 6; Page 54; 93pp; English.  
XX  
XX The invention relates to a method for alleviating a symptom of a disease  
XX or disorder of nervous system which involves administering a modulator to  
XX modulate an activity of a neural stem cell or a neural progenitor cell in  
XX vivo to a patient suffering from the disease or disorder of the nervous  
XX system (the modulator disrupts an interaction between Epha7 and ephrin-A5  
XX or an interaction between Epha7 and ephrin-A2). The method is useful for  
XX alleviating a symptom of a disease or disorder of the nervous system,  
XX e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,  
XX neural stem cell, neural progenitor, ischaemic, affective,  
XX neuropsychiatric or learning and memory disorders, such as Parkinson's  
XX disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,  
XX amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or  
XX cancer-related brain/spinal cord injury, schizophrenia, psychoses,  
XX depression, bipolar depression/disorder, anxiety syndromes/disorders,  
XX phobias, stress and related syndromes, cognitive function disorders,

CC aggression, obsessive compulsive behaviour syndromes, multi-infarct  
CC dementia, seasonal mood disorder, Lewy body dementia, borderline  
CC personality disorder, cerebral palsy, age related/geriatric dementia,  
CC epilepsy and injury related to epilepsy, spinal cord injury, brain  
CC injury, trauma related brain/spinal cord injury, anticancer treatment  
CC related brain/spinal cord tissue injury, infection and inflammation  
CC related brain/spinal cord injury, environmental toxin related brain/  
CC spinal cord injury, multiple sclerosis, autism, attention deficit  
CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma  
CC to the retina or sleep disorders. The invention is also used in gene  
CC therapy. The present sequence is a RT (reverse transcription)-PCR primer  
CC used for amplifying human ephrin-A2 cDNA. This sequence is used to  
CC illustrate the method of the invention

XX  
SQ Sequence 20 BP, 1 A, 7 C, 5 G, 7 T, 0 U, 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7408 AACATCAGCAGCAGCAGC 7425  
Db 19 AACGACGAGCAGCAGCAGC 2

RESULT 3087  
AAD56486/c  
ID AAD56486 standard; DNA, 20 BP.  
XX  
AC AAD56486;  
XX  
DT 27-AUG-2003 (first entry)

DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 9.

XX  
XX EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;  
KM epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;  
KM Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;  
KM memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;  
KM amyotrophic lateral sclerosis; attention deficit disorder; depression;  
KM injury; human; RT; reverse transcription; PCR; primer; ss.

XX  
OS Homo sapiens.

XX  
PN WO2003040304-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 11-NOV-2002; 2002WO-1B004930.  
XX  
PR 09-NOV-2001; 2001US-0345206P.  
PR 02-JUL-2002; 2002US-0393272P.

XX  
PA (NEUR-) NEURONOVA AB.  
XX  
PI Holmberg J, Friesen J;  
XX  
DR WPI; 2003-441543/41.  
XX  
PT Alleviating a symptom of a disease or disorder of the nervous system by  
PT administering a modulator of neural stem or neural progenitor cell  
PT activity in vivo to a patient.

XX  
PS Example 6; Page 54; 93pp; English.

XX  
CC The invention relates to a method for alleviating a symptom of a disease  
CC or disorder of nervous system which involves administering a modulator to  
CC modulate an activity of a neural stem cell or a neural progenitor cell in  
CC vivo to a patient suffering from the disease or disorder of the nervous  
CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5  
CC or an interaction between EphA7 and ephrin-A2). The method is useful for  
CC alleviating a symptom of a disease or disorder of the nervous system,  
CC e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,

CC neural stem cell, neural progenitor, ischaemic, affective,  
CC neuropsychiatric or learning and memory disorders, such as Parkinson's  
CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,  
CC amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or  
CC cancer-related brain/spinal cord injury, schizophrenia, psychosis,  
CC depression, bipolar depression/disorder, anxiety syndromes/disorders,  
CC phobias, stress and related syndromes, cognitive function disorders,  
CC aggression, obsessive compulsive behaviour syndromes, multi-infarct  
CC dementia, seasonal mood disorder, Lewy body dementia, borderline  
CC personality disorder, cerebral palsy, age related/geriatric dementia,  
CC epilepsy and injury related to epilepsy, spinal cord injury, brain  
CC injury, trauma related brain/spinal cord injury, anticancer treatment  
CC related brain/spinal cord tissue injury, infection and inflammation  
CC related brain/spinal cord injury, environmental toxin related brain/  
CC spinal cord injury, multiple sclerosis, autism, attention deficit  
CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma  
CC to the retina or sleep disorders. The invention is also used in gene  
CC therapy. The present sequence is a RT (reverse transcription)-PCR primer  
CC used for amplifying human ephrin-A2 cDNA. This sequence is used to  
CC illustrate the method of the invention

XX  
SQ Sequence 20 BP, 1 A, 7 C, 5 G, 7 T, 0 U, 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7408 AACATCAGCAGCAGCAGC 7425  
Db 19 AACGACGAGCAGCAGCAGC 2

RESULT 3088  
ACF36185  
ID ACF36185 standard; DNA, 20 BP.  
XX  
AC ACF36185;  
XX  
DT 04-DEC-2003 (first entry)

DE Delta constant region specific forward primer Delta1F.

XX  
XX Embryonic stem cell; transgene; chimeric chicken; avian; transgenic; PCR;  
KM primer; ss.

XX  
OS Synthetic.

XX  
PN WO2003064627-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 03-FEB-2003; 2003WO-US003235.  
XX  
PR 01-FEB-2002; 2002US-00067148.

XX  
PA (ORIG-) ORIGIN THERAPEUTICS.  
XX  
PI Etches RJ, Van De Lavoie M, Heyer B, Diamond J, Macher C;  
PI Beemer K, Myers H;  
XX  
DR WPI; 2003-646148/61.  
XX  
PT New compositions comprising sustained chicken embryonic stem (ES) cell  
PT culture having a transgene integrated into genome of ES cell progenies,  
PT useful in producing engineered chickens for avian transgenics, e.g.  
PT protein production.

XX  
PS Example 4; Page 18; 46pp; English.

XX  
CC The invention relates to a composition comprising a sustained culture of  
CC chicken embryonic stem cells with a transgene stably integrated into the  
CC genome of substantially all of the progeny of the embryonic stem cells.  
CC The embryonic stem cell progeny contribute to a somatic tissue of a

CC chimeric chicken produced by the injection of the chicken embryonic cells  
CC into a chicken embryo. Compositions comprising cultures of embryonic  
CC chicken embryonic stem cells are useful in producing engineered chickens  
CC for avian transgenics, including protein production for pharmaceutical  
CC industry, production of chickens that deposit human antibodies in their  
CC eggs, and site-specific modification of the avian genome for other  
CC applications. The cultures may be used in the selection of desirable  
CC phenotypes in chimeric animals and modifications to the genome of chicken  
CC embryonic cells to introduce exogenous DNA into a chimeric offspring.  
CC Sequences AC936177-186 represent primers used in a PCR analysis of  
CC transgenes for the presence of an unrearranged human heavy chain locus  
XX  
SQ Sequence 20 BP; 6 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6223 GGGAGAGGAGCACTGT 6240  
Db |||||  
3 GGGAGAGGAGCACAGT 20  
  
RESULT 3089  
ADC37131  
ID ADC37131 standard; DNA; 20 BP.  
XX  
AC ADC37131;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE CK19 forward primer #2.  
XX  
KM directly amplifying nucleic acid; inhibit; breakdown; cancer metastasis;  
KM PCR; primer; ss; CK19.  
XX  
OS unidentified.  
XX  
PN WO2003060116-A1.  
XX  
PD 24-JUL-2003.  
XX  
PF 08-JAN-2003; 2003WO-JP000060.  
XX  
PR 09-JAN-2002; 2002JP-00002046.  
PR 13-NOV-2002; 2002JP-00329958.  
XX  
PA (SYSM-) SYSMEX CORP.  
XX  
PI Tada S, Yoshida T, Shohmi K, Nishida M, Nakabayashi K;  
PI Yamagata K;  
XX  
DR WPI; 2003-587284/55.  
XX  
PT Directly amplifying nucleic acids in a sample by inhibiting nucleic acid  
PT breakdown.  
XX  
PS Example 7; SEQ ID NO 20; 56pp; Japanese.  
XX  
CC The invention relates to a novel method for directly amplifying nucleic  
CC acids in a sample without having to isolate it. The method comprises a  
CC step to inhibit the breakdown of nucleic acids. The invention further  
CC comprises: a solution for treating the nucleic acid sample; a method for  
CC treating the sample; a reagent for detecting nucleic acids; a nucleic  
CC acid detection system; and a method for detecting cancer metastasis. This  
CC polynucleotide represents a PCR primer used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 AGATCAAGGCGCTGAAG 1006  
Db |||||  
2 AGATCAAGGCGCTGAAG 19  
  
RESULT 3090  
ADD20586  
ID ADD20586 standard; DNA; 20 BP.  
XX  
AC ADD20586;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Oreochromis niloticus microsatellite primer SEQ ID NO:1221.  
XX  
KM single nucleotide polymorphism; SNP; fish; Salmo salar;  
KM Oreochromis niloticus; Atlantic halibut; microsatellite; cod;  
KM polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;  
KM detection; primer; ss.  
XX  
OS Synthetic.  
OS Oreochromis niloticus.  
XX  
PN WO2003060160-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 17-JAN-2003; 2003WO-IB000112.  
XX  
PR 18-JAN-2002; 2002US-0349950P.  
PR 16-AUG-2002; 2002US-0404200P.  
XX  
PA (GENO-) GENOMAR ASA.  
XX  
PI Lie O, Slettan A, Hoyum M, Lingaas F;  
XX  
DR WPI; 2003-627388/59.  
XX  
PT Novel isolated nucleic acid molecule comprising single nucleotide  
PT polymorphism associated with fish, useful for forming PCR primers which  
PT are used for detecting single nucleotide polymorphisms in fish nucleic  
PT acids.  
XX  
PS Claim 18; SEQ ID NO 1221; 233pp; English.  
XX  
CC The present invention describes an isolated nucleic acid (I) comprising a  
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of  
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;  
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to  
CC (i), or its complement under highly stringent hybridisation conditions.  
CC Also described: (1) an isolated oligonucleotide (II) comprising at least  
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.  
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod  
CC polymorphic sites and seabass polymorphic sites, or their complement; (2)  
CC a primer pair (III) suitable for use in PCR, comprising two (II) capable  
CC of amplifying a nucleotide sequence chosen from S. salar SNPs and O.  
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod  
CC polymorphic sites and seabass polymorphic sites; and determining (MI) the  
CC origin of fish sample comprising providing a parentage genotype database  
CC comprising a collection of candidate parent genotypes, where each of the  
CC candidate parent genotype represents a distinct origin, and comparing a  
CC sample genotype to the parentage genotype database, where a match between  
CC the sample genotype and one of the candidate parent genotype identifies  
CC to the origin of the sample. (MI) is useful for determining the origin of  
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,  
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for  
CC detecting nucleic acid molecule comprising SNP in a sample, which  
CC involves contacting the sample containing nucleic acids with one or more  
CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus  
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is  
CC useful for detecting nucleic acid molecule comprising a polymorphic  
CC sequence in a sample, comprising contacting the sample containing nucleic

CC acids with one or more (II) which is derived from O. niloticus  
 CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic  
 CC sites or seabase polymorphic sites, and identifying a nucleic acid that  
 CC hybridizes to (II). (III) is useful for detecting nucleic acid molecule  
 CC comprising a microsatellite sequence in sample. The present sequence is  
 CC used in the exemplification of the present invention.

XX  
 SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7021 ACAGAGGAATATGAGAA 7038  
 DB 2 ACAGCGGACATATGAGAA 19

RESULT 3091  
 AAD62234/C  
 ID AAD62234 standard; DNA; 20 BP.

XX  
 AC AAD62234;  
 XX  
 DT 15-JAN-2004 (first entry)

XX Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150789.  
 XX  
 KW Haematopoietic cell; tyrosine kinase; hyperproliferative disorder;  
 KW cancer; therapy; inflammation; diabetes; viral infection; inflammation;  
 KW tumour; cytostatic; virucide; antisense therapy; antisense; human;  
 KW phosphorothioate backbone; ss.

XX  
 OS Homo sapiens.  
 OS Synthetic.

XX  
 FH Key location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone; All cytidines are 5-  
 FT methy1 cytidines"  
 FT 1..5  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"

XX  
 FT US2003125275-A1.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 04-DEC-2001; 2001US-00007010.  
 XX  
 XX 04-DEC-2001; 2001US-00007010.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Borchers AH, Dobie KW;  
 XX  
 XX WPI; 2003-811000/76.  
 XX  
 XX  
 XX New antisense oligonucleotides targeted to nucleic acids encoding  
 XX haematopoietic cell protein tyrosine kinase, useful for diagnosing or  
 XX treating cancer (e.g. leukemia), inflammation, diabetes or viral  
 XX infections.  
 XX  
 XX Example 15; Page 27; 59pp; English.  
 XX  
 XX The invention relates to a compound targeted to a nucleic acid molecule

CC encoding haematopoietic cell protein tyrosine kinase. The compound  
 CC inhibits the expression of haematopoietic cell protein tyrosine kinase  
 CC and it specifically hybridizes with the nucleic acid molecule encoding  
 CC the tyrosine kinase or with at least an 8-nucleotide portion of an active  
 CC site on the nucleic acid molecule encoding the tyrosine kinase. The  
 CC antisense compounds are useful for modulating the expression of  
 CC haematopoietic cell protein tyrosine kinase and treating diseases or  
 CC conditions associated with the expression of the tyrosine kinase, such as  
 CC hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a  
 CC viral infection. The antisense compounds are also useful for diagnostics,  
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,  
 CC inflammation or tumour formation, as research reagents and kits and in  
 CC distinguishing between functions of various members of a biological  
 CC pathway. The present sequence is human haematopoietic cell tyrosine  
 CC kinase antisense oligonucleotide

XX  
 SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7140 CCAGCCTAATGCTATGT 7157  
 DB 19 CCAGCCTAATGCTATGT 2

RESULT 3092  
 ADD42189  
 ID ADD42189 standard; DNA; 20 BP.

XX  
 AC ADD42189;  
 XX  
 DT 15-JAN-2004 (first entry)

XX Human infertility associated primer SEQ ID 50.  
 XX  
 KW primer; male infertility; infertility-associated mutation;  
 KW azoospermia factor; y-chromosome;  
 KW cystic fibrosis transmembrane conductance regulator; CFR;  
 KW Kallmann syndrome; KAL1; androgen resistance; steroid 21-hydroxylase;  
 KW CYP21; microarray; quantitative trait locus; in vitro fertilization;  
 KW oligospermia; ss.

XX  
 OS Homo sapiens.  
 OS  
 XX WO2003050299-A2.  
 XX  
 XX 19-JUN-2003.  
 XX  
 XX 10-DEC-2002; 2002WO-EP013995.  
 XX  
 XX 10-DEC-2001; 2001DE-01060563.  
 XX  
 XX (OGHA-) OGHAM GMBH.  
 XX  
 XX Cullen P, Seedorf U;  
 XX  
 XX WPI; 2003-505402/47.  
 XX  
 XX  
 XX Investigating male genetic infertility, useful for diagnosis e.g. for  
 XX assessing suitability for in vitro fertilization, based on multifactorial  
 XX analysis of infertility-related mutations.  
 XX  
 XX Claim 13; SEQ ID NO 50; 110pp; German.  
 XX  
 XX This invention describes a novel method for investigating genetic  
 XX infertility or predisposition in males. The method involves selecting at  
 XX least two infertility-associated mutations which are recessive or  
 XX intermediate that are associated with infertility in the heterozygous  
 XX state and/or only in the homozygous state. Preferably at least one  
 XX azoospermia factor is detected which may be lost by microdeletions in  
 XX intervals 5 or 6 of the Y-chromosome. Also any of several hundred



CC mutations, listed, present in the cystic fibrosis transmembrane  
 CC conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen  
 CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.  
 CC Probes for the mutated genes and/or native nucleic acid, or their  
 CC complementary strands, are fixed to a carrier, particularly as a  
 CC microarray, then tested for hybridization with oligonucleotides from or  
 CC synthesized from, a patient sample and hybridization detected.  
 CC Multifactorial analysis is by standard statistical methods, particularly  
 CC the quantitative trait locus method. The method is used to diagnose  
 CC inherited male infertility or predisposition to its, especially in  
 CC conjunction with in vitro fertilization programs, e.g. for assessing  
 CC subjects with oligospermia for possible application of the  
 CC intracytoplasmic sperm injection method. Analysis of many mutations  
 CC improves diagnosis of the genetic basis of male infertility, including  
 CC polygenic origins (complex interactions between different heterozygotic  
 CC mutations). A chip for analyzing genetic infertility in males comprises  
 CC oligonucleotides that represent known mutations (nonsense or missense,  
 CC insertions, allelic variants deletions or rearrangements) in the cystic  
 CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen  
 CC resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent  
 CC oligonucleotides used in the microarray described in the method of the  
 CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the  
 CC SEQ ID list of the specification.

XX  
 SO Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2275 GCGTCATCAACTGGAA 2292  
 DB 1 GCGTCATCAACTGGAA 18  
 |||||

RESULT 3093  
 ADD81662  
 ID ADD81662 standard; DNA; 20 BP.  
 XX  
 AC ADD81662;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE HIV PRT antisense derived probe #591.  
 XX  
 KM ss; oligonucleotide hybridisation potential; efficient hybridisation;  
 KM large array; minimum oligonucleotide synthesis; probe.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN US2003054346-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 15-FEB-2001; 2001US-00784674.  
 XX  
 PR 10-FEB-1998; 98US-00021701.  
 XX  
 PA (SHAN/) SHANNON K W.  
 PA (WOLB/) WOLBER P K.  
 PA (DELE/) DELENSTARR G C.  
 PA (WEBB/) WEBB P G.  
 PA (KINC/) KINCAID R H.  
 PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;  
 DR WPI; 2003-743746/70.  
 XX  
 PT Predicting potential of oligonucleotides to hybridize to target  
 PT nucleotide sequence comprises determining and evaluating for each  
 PT oligonucleotide a parameter predictive of the oligonucleotides ability to  
 PT hybridize with target.  
 XX

PS Example 2; SEQ ID NO 735; 423bp; English.  
 XX  
 CC The invention relates to a method of predicting the potential of  
 CC oligonucleotides to hybridize to target nucleotide sequences. The method  
 CC is useful for predicting the potential of an oligonucleotide to hybridize  
 CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that  
 CC contains chemically modified nucleotides. The method is also useful for  
 CC predicting the potential of the oligonucleotides to hybridize to a  
 CC complementary target nucleotide sequence. The method is useful to predict  
 CC efficient hybridisation oligonucleotides for each of multiple target  
 CC sequences therefore very large arrays may be constructed and tested with  
 CC minimum synthesis of oligonucleotides. The present sequence represents a  
 CC HIV PRT antisense derived probe.

XX  
 SO Sequence 20 BP; 1 A; 8 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5703 CCTTCCTTTCTCTCTCT 5720  
 DB 2 CCTTCCTTTCTCTCTCT 19  
 |||||

RESULT 3094  
 ADE39777/c  
 ID ADE39777 standard; DNA; 20 BP.  
 XX  
 AC ADE39777;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Porcine CD 151 related PCR primer seq id 13.  
 XX  
 KM porcine reproductive and respiratory syndrome virus; PRRSV;  
 KM susceptibility; CD 151; susceptibility standard; PRRSV infection;  
 KM vaccine; vaccine virus stock; non-simian vaccine; xenotransplantation;  
 KM non-simian cell line; drug testing; transformed cell line; porcine; pig;  
 KM PCR; primer; ss.  
 XX  
 OS Sus sp.  
 XX  
 PN US2003186236-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 28-JAN-2002; 2002US-00058597.  
 XX  
 PR 29-JAN-2001; 2001US-00772044.  
 XX  
 PA (KAP1/) KAPIL S.  
 PA (SHAN/) SHANMUKHAPPA K.  
 PI Kapil S, Shanmukhappa K;  
 DR WPI; 2003-811729/76.  
 XX  
 PT Determination of susceptibility to porcine reproductive and respiratory  
 PT syndrome virus non-invasively useful e.g. to breed pigs with low  
 PT susceptibility or classify infection resistance in an animal, by assaying  
 PT for CD 151.  
 XX  
 PS Example 17; SEQ ID NO 13; 45bp; English.  
 XX  
 CC The invention describes a method to identify susceptibility to porcine  
 CC reproductive and respiratory syndrome virus (PRRSV) in an animal by  
 CC assaying a cellular material sample from known origin in the animal for  
 CC CD 151. The method is useful to determine the susceptibility of animals  
 CC (especially pigs) to PRRSV and to compare susceptibility to a known  
 CC susceptibility standard, especially for material of the same cellular  
 CC origin. It can be used to determine if an animal is resistant to PRRSV  
 CC infection, by determining presence/absence of CD 151, and to classify

resistance levels. It is especially useful to select animals for breeding by selecting animals with CD 151 levels lower (especially a least 50 % lower) than a known standard (especially for material of same cellular origin). Polynucleotides encoding CD 151 are useful to produce vaccines and to modify PRSV production in cells susceptible to PRSV infection, especially to increase PRSV production e.g. in vaccine virus stock. They are especially useful to produce non-simian vaccines, avoiding possible introduction of primate viruses into organs xenotransplanted from pigs to humans. They may be used to determine the effect of single nucleotide polymorphisms on PRSV susceptibility, and to compare PRSV susceptibility factors between individual swine. They can also be used to modulate viral RNA (especially PRSV RNA) entry into cells by altering CD 151 amounts in cells. Polynucleotides may be included in plasmids useful to render a cell line susceptible to PRSV infection, useful to produce non-simian lines for drug testing. They may be included in vectors and used to integrate CD 151 into a chromosome. They can also be used to produce transformed cell lines, useful e.g. to diagnose PRSV infection in swine herds or produce vaccines for inducing immunity against PRSV. This sequence represents a primer used to determine sequence of a porcine CD 151 intron in order to determine the entire sequence of porcine CD 151.

XX Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 CAAGGCGCTGAAGGTGA 1010

Db 19 CAAGAGCTGAGAGCTGA 2

RESULT 3095

AD840361

ID ADE40361 standard; DNA; 20 BP.

XX ADE40361;

DT 29-JAN-2004 (first entry)

XX Reverse Ag4809 RT-PCR primer used to amplify human NOV RNA.

XX NOX; cardiact; antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;

XX antiparkinsonian; antidiabetic; gynaecological; cardiomyopathy;

XX atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;

XX multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;

XX asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;

XX tissue typing; human; NOV; ss; primer; PCR; RT-PCR.

OS Homo sapiens.

XX WO2003064589-A2.

XX 07-AUG-2003.

PF 02-AUG-2002; 2002WO-US024483.

XX 02-AUG-2001; 2001US-0309501P.

PR 03-AUG-2001; 2001US-0310291P.

PR 07-AUG-2001; 2001US-0310544P.

PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.

PR 13-AUG-2001; 2001US-0311979P.

PR 16-AUG-2001; 2001US-0312892P.

PR 17-AUG-2001; 2001US-0313201P.

PR 17-AUG-2001; 2001US-0313415P.

PR 20-AUG-2001; 2001US-0313643P.

PR 20-AUG-2001; 2001US-0313703P.

PR 21-AUG-2001; 2001US-0314031P.

PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.

PR 29-AUG-2001; 2001US-0315853P.  
PR 17-SEP-2001; 2001US-0322716P.  
PR 21-SEP-2001; 2001US-0323949P.  
PR 14-DEC-2001; 2001US-0340233P.  
PR 05-FEB-2002; 2002US-0354591P.  
PR 19-MAR-2002; 2002US-0365478P.  
PR 19-APR-2002; 2002US-0373814P.  
PR 19-APR-2002; 2002US-0373825P.  
PR 19-APR-2002; 2002US-0373899P.  
PR 23-APR-2002; 2002US-0374632P.  
PR 07-JUN-2002; 2002US-0386571P.  
PR 01-AUG-2002; 2002US-00210172.

(CURA-) CURAGEN CORP.

PI Kekuda R, Miller CE, Raturajan M, Pena CE, Rieger DK;  
PI Shimeke RA, Zernusen BD, Li L, Ji W, Padigaru M, Carman SJ;  
PI Voss EZ, Boldog FL, Gotman L, Leite MW, Vernet CAM, Anderson DW,  
PI Guo X, Zhong M, Gerlach VL, Hjalte T, Raestelli L, Spytek KA;  
PI Edinger SR, Ellerman K, Malyanar UM, MacDougall JR, Stone DJ;  
PI Alsobrook JP, Lepley DM, Burgess CE, Majumder K, Wolenc AR;  
PI Smithson G;

DR WPI; 2003-663472/62.

XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

XX Example C; SEQ ID NO 267; 560bp; English.

XX The invention relates to a novel NOVX polypeptide. The polypeptide of the  
CC invention demonstrates cardiact, antidiabetic, immunosuppressive, anti-HIV,  
CC cytoactive, anorectic, antidiabetic, immunosuppressive, anti-HIV,  
CC neuroprotective, nootropic, antiparkinsonian, antidiabetic and  
CC gynaecological activities and may be useful in diagnosing, treating or  
CC preventing NOVX-associated disorders including cardiomyopathy,  
CC atherosclerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple  
CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's  
CC disease, asthma or fertility disorders. Furthermore, the polypeptides may  
CC be utilised as vaccines whilst the nucleic acids may be used as  
CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,  
CC preventive medicine and pharmacogenomics. The current sequence is that of  
CC the RT-PCR primer of the invention which was used to amplify human NOV  
CC RNA.

XX Sequence 20 BP; 6 A; 8 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CCATCACACCCGCTTTT 2354

Db 1 CCATCACACACGCACTTT 18

RESULT 3096

AAQ50784

ID AAQ50784 standard; RNA; 21 BP.

XX AAQ50784;

DT 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX HBV target sequence 10.

XX RNA; enzyme; enzymatic RNA molecule; BRM; cleave; RNA; mRNA; hnRNA;  
KM picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
KM papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;  
KM T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus;



```

XX 20-JAN-1994.
PD
XX 30-JUN-1993; 93WO-AU000320.
XX
XX 03-JUL-1992; 92AU-00003330.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Scott NS, Thomas MR;
XX
XX WPI; 1994-035083/04.
XX
XX Novel ribosome DNA probe sequences - for the accurate identification of
PT grape cultivars.
XX
XX Claim 14; Page 22; 55pp; English.
XX
XX The sequences given in AA055251-56 are primers which were used in a
CC method for the analysis of nucleic acid derived from ribosomes of the
CC grapevine genus Vitis. The amplified sequences represent the 5S region of
CC the ribosomal (r)DNA repeat and contain polymorphisms. These
CC polymorphisms may be used in a method for the identification of different
CC grape cultivars. The amplified clones contain simple repeat sequences and
CC may be identified in a genomic library of grapevine DNA using simple di-
CC tri- or tetra- nucleotide repeats such as (AT)8, (GT)10, (GGT)10 and such
CC like as probes. See also AA055231-50. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5197 TGGATACATTTTGGGGCT 5214
DB 19 TGGATACATTTTACGGGCT 2
RESULT 3099
AA16749/c
ID AA16749 standard; RNA; 21 BP.
XX
XX AA16749;
AC
XX 09-OCT-1996 (first entry)
DT
XX
XX E. coli tRNA(Pro) anticodon stem-loop used for generating analogues.
DE
XX
XX Analogue; ligand binding; 16S rRNA; parental molecule; conformation;
KM stem-loop structure; stable; helix; nucleotide clamp; decoding region;
KM tRNA; tRNA; A site; ribosome; protein synthesis; assay; antibiotics;
KM tRNA; aminoglycoside protection assay; ss.
XX
XX Synthetic.
OS
XX
XX WO9606106-A1.
XX
XX 29-FEB-1996.
PD
XX
XX 23-AUG-1995; 95WO-US010721.
PF
XX 23-AUG-1994; 94US-00294450.
PR
XX 05-JUL-1995; 95US-00498402.
XX
XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
PA
XX Stern S, Purohit P;
PT
XX WPI; 1996-151324/15.
XX
XX Oligo:ribonucleotide analogue for identifying new antibiotics - have same
PT

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```

PT binding pattern as parental RNA derivative, and assays for detecting
therapeutic activity of cpd.
XX
XX Disclosure; Page 18; 57pp; English.
XX
XX Novel analogues able to assume the same conformation as the parent mol.
CC are generated from two sections, the first section corresp. to sequences
CC in the parental RNA mol., whilst the second section consists of an
CC artificial nucleotide structure (i.e. not found in the parental RNA) that
CC can combine with the first section to stabilise the analogue. The second
CC structure also contains a stem-loop structure and a second nucleic
CC nucleotide clamp. The analogues pref. contain the complete sequence of
CC the 16S rRNA decoding region (the decoding region being the region which
CC correctly aligns the mRNA with the tRNA in the "A site" of the ribosome
CC during protein synthesis). The sequences AA16748-52 were used to
CC generate analogues of the invention esp. for aminoglycoside protection
CC assays. The analogues can be used in assays to detect potential ligands
CC e.g. new antibiotics or anti-viral agents, that could bind to the parent
CC molecule
XX
XX Sequence 21 BP; 3 A; 4 C; 8 G; 0 T; 6 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4187 GGTATCGCCCAAGATG 4204
DB 21 GGTATCACCACCAAGATG 4
RESULT 3100
AA11723
ID AA11723 standard; DNA; 21 BP.
XX
XX AA11723;
AC
XX 25-MAR-2003 (revised)
DT
XX 18-JUL-1996 (first entry)
DT
XX
XX Polycystic kidney disease 1 gene antisense primer, KG8-R27.
DE
XX
XX Polycystic kidney disease; PKD; autosomal dominant; ADPKD; mutation;
KM exon; short arm; chromosome 16; repeated region; alternative splicing;
KM extracellular matrix proteins; antibody; detection; diagnosis;
KM mini gene therapy; single strand conformational polymorphism analysis;
KM SSCP; primer; amplify; ss.
XX
XX Synthetic.
OS
XX
XX WO9534573-A1.
XX
XX 21-DEC-1995.
PD
XX
XX 02-JUN-1995; 95WO-US007079.
PF
XX 03-JUN-1994; 94US-00253524.
PR
XX 30-MAR-1995; 95US-00413580.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (MILL-) MILLENITUM PHARM INC.
XX
XX Reeders S, Schneider M, Glucksmann S;
PT
XX WPI; 1996-049618/05.
XX
XX DNA encoding poly-cystic kidney disease gene product - for use in gene
PT therapy of ADPKD, and in the evaluation of treatment for PKD.
XX
XX Example; Page 68; 126pp; English.
XX
XX The sequences given in AA11709-29 are primers which were used in single-
CC

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```

XX AAV20817;
XX
XX 16-JUL-1998 (first entry)
XX
XX DE Primer for Human haematopoietic stem cell growth factor.
XX
XX KW Haematopoietic stem cell growth factor; SCGF, burst-promoting activity;
XX BPA; granulocyte macrophage colony stimulating activity; gene therapy;
XX GPA; haematopoietic cell disorder; bone marrow inhibition; human;
XX PCR primer; ss.
XX
XX OS Synthetic.
XX Homo sapiens.
XX
XX PN MO9808869-A1.
XX
XX PD 05-MAR-1998.
XX
XX PF 27-AUG-1997; 97MO-JP002985.
XX
XX PR 27-AUG-1996; 96JP-00262252.
XX 24-MAR-1997; 97JP-00087242.
XX 07-JUL-1997; 97MO-JP002349.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PI Hiraoka A, Sugimura A, Mio H;
XX
XX DR WPI; 1998-179383/16.
XX
XX PT Hematopoietic stem cell growth factor - useful for, e.g. treatment and
XX diagnosis of haematopoietic cell abnormalities and bone marrow
XX inhibition.
XX
XX PS Example 21; Page 49; 85pp; Japanese.
XX
XX CC This sequence is a primer for DNA encoding the human haematopoietic stem
XX cell growth factor (SCGF) of the invention. The polypeptide of the
XX invention is of mammalian origin and has haematopoietic stem cell growth
XX factor SCGF activity, including burst-promoting activity (BPA) and
XX granulocyte macrophage colony stimulating activity (GPA). The products
XX can be used for treatment, diagnosis and analysis of haematopoietic cell
XX disorders and bone marrow inhibition, e.g. by cytotoxic anticancer agents
XX such as 5-fluorouracil. The products can also be used for amplification
XX of haematopoietic cells in vitro, e.g. for use in marrow grafting and
XX gene therapy by insertion of SCGF gene using a suitable therapeutic
XX vector.
XX
XX SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2274 TGCCTGCATCAACTGGA 2291
DB 21 TGCCTGCATTAAGCTGGA 4

RESULT 3104
AAZ26119
ID AAZ26119 standard; DNA; 21 BP.
XX
XX AC AAZ26119;
XX
XX DT 30-NOV-1999 (first entry)
XX
XX DE Human polymorphic region 308.
XX
XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX allele specific inhibitor; somatic cell; diagnosis; prevention; ss.

```

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KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX OS Homo sapiens.
XX
XX PN MO9841648-A2.
XX
XX PD 24-SEP-1998.
XX
XX PF 19-MAR-1998; 98MO-US005419.
XX
XX PR 20-MAR-1997; 97US-0041057P.
XX
XX PA (VAR-) VARIAGENICS INC.
XX
XX PI Housman D, Ledley FD, Stanton VP;
XX
XX DR WPI; 1998-521232/44.
XX
XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancer, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX PS Disclosure; Fig 7; 605pp; English.
XX
XX CC This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
XX human polymorphic sites described in the method of the invention

SQ Sequence 21 BP; 6 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4198 CAAGATGGGTCGAGGCT 4215
DB 1 CAAGAAAGGAGCACGAGCT 18

RESULT 3105
AAZ26693
ID AAZ26693 standard; DNA; 21 BP.
XX
XX AC AAZ26693;
XX
XX DT 30-NOV-1999 (first entry)
XX
XX DE Human polymorphic region 882.
XX
XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX cell viability; loss of heterozygosity; precancerous condition; ASI;
XX allele specific inhibitor; somatic cell; diagnosis; prevention;
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX graft versus host disease; malignant cell removal; bone marrow; ss.

```

OS Homo sapiens.  
 XX  
 PN WO9841648-A2.  
 XX  
 PD 24-SEP-1998.  
 XX  
 PF 19-MAR-1998; 98WO-US005419.  
 XX  
 PR 20-MAR-1997; 97US-0041057P.  
 XX  
 PA (VARI-) VARIAGENICS INC.  
 XX  
 PI Housman D, Ledley PD, Stanton VP;  
 XX  
 DR WPI; 1998-521232/44.  
 XX  
 PT Identifying target genes for allele-specific drugs - used for diagnosis,  
 PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
 PT dysplastic lesions, endometriosis or graft versus host disease.  
 XX  
 PS Disclosure; Fig 7; 605pp; English.  
 XX  
 CC This invention describes a novel method for identifying an inhibitor  
 CC potentially useful for treatment of cancer, where the inhibitor is active  
 CC on a gene vital for cell growth or viability, and where the gene is  
 CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
 CC used for preventing the development of cancer in a patient having a  
 CC precancerous condition, by administering to the patient a first allele  
 CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
 CC present in cells of the precancerous condition, where the normal somatic  
 CC cells of the patient are heterozygous for the first gene, the inhibitor  
 CC is active on at least one but less than all allelic forms of the gene  
 CC present in a population and targets only one allelic form present in the  
 CC normal somatic cells, and the first gene. The products and methods can be  
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
 CC lesions, benign tumors, endometriosis, polycystic kidney disease, and  
 CC graft versus host disease. The method can also be used to remove  
 CC malignant cells from bone marrow transplants. AA225812-226825 represent  
 CC human polymorphic sites described in the method of the invention  
 XX  
 SQ Sequence 21 BP; 10 A; 4 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5420 AAAGCAAGAGATCAGC 5437  
 Db 3 AAAAGGAGATGATCAGC 20  
 RESULT 3106  
 AAX35653  
 ID AAX35653 standard; DNA; 21 BP.  
 XX  
 AC AAX35653;  
 XX  
 DT 09-JUL-1999 (first entry)  
 XX  
 DE PCR primer used to amplify human heparanase cDNA.  
 XX  
 KW Heparanase; hpa; modulator; heparin-binding growth factor;  
 KW cellular response; cytokine; cell interaction; plasma lipoprotein;  
 KW cellular susceptibility; infection; disintegration;  
 KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;  
 KW atherosclerosis; inflammation; neurodegenerative disease; neuritis;  
 KW plasma heparin; micrometastasis; autoimmune lesion; renal failure;  
 KM PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9911798-A1.

XX  
 PD 11-MAR-1999.  
 XX  
 PF 31-AUG-1998; 98WO-US017954.  
 XX  
 PR 02-SEP-1997; 97US-00922170.  
 XX  
 PR 02-JUL-1998; 98US-00109386.  
 XX  
 PA (INST-) INSIGHT STRATEGY & MARKETING LTD.  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX  
 PI (FRIE/) FRIEDMAN M M.  
 XX  
 PI Pecker I, Vlodevsky I, Feinstein E;  
 XX  
 DR WPI; 1999-302255/25.  
 XX  
 PT New human polynucleotide useful for treating angiogenesis, restenosis,  
 PT and inflammation.  
 XX  
 PS Example 7; Page 30; 63pp; English.  
 XX  
 CC The specification describes a polypeptide having heparanase (hpa)  
 CC activity. The recombinant protein is used as a modulator of heparin-  
 CC binding growth factors, cellular responses to heparin-binding growth  
 CC factors and cytokines, cell interaction with plasma lipoproteins,  
 CC cellular susceptibility to viral, protozoal and bacterial infections or  
 CC disintegration of neurodegenerative plaques. Heparanase may be useful for  
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral  
 CC infections. Mammalian heparanase can be used to neutralize plasma  
 CC heparin, and anti-heparanase antibodies may be applied for  
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and  
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The  
 CC present PCR primer was used to amplify hpa cDNA, in the course of the  
 XX  
 SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 7413 CAGGAGCAGCAGCAGCAG 7430  
 Db 4 CAGGAGCAGCAGCAGCAG 21  
 RESULT 3107  
 AAX18314  
 ID AAX18314 standard; DNA; 21 BP.  
 XX  
 AC AAX18314;  
 XX  
 DT 26-JUL-1999 (first entry)  
 XX  
 DE PCR primer for telomerase coding sequence.  
 XX  
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukemia;  
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;  
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms tumor;  
 KW stem cell differentiation; organ regeneration; organ differentiation;  
 KM PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9901560-A1.  
 XX  
 PD 14-JAN-1999.  
 XX  
 PF 01-JUL-1998; 98WO-US013835.  
 XX  
 PR 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.  
 PR 21-JUL-1997; 97US-0053329P.  
 PR 04-AUG-1997; 97US-0054642P.  
 PR 09-SEP-1997; 97US-0058287P.  
 XX  
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.  
 XX  
 PI Killian A, Bowtell D;  
 DR WPI; 1999-106060/09.  
 XX  
 PT New isolated vertebrate telomerase genes - used to develop products for  
 PT treating cancers or for organ regeneration, nerve cell or brain cell  
 PT growth following injury or bone marrow transplantation.  
 XX  
 PS Example 1; Page 42; 134pp; English.  
 XX  
 CC This sequence is a PCR primer for DNA encoding a truncated human  
 CC telomerase of the invention. Primers that amplify the telomerase coding  
 CC sequence can be used in a method for diagnosing cancer in a patient. The  
 CC telomerase can be used for detection, diagnosis and drug screening.  
 CC Inhibitors of telomerase activity can be used to treat cancers such as  
 CC melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon  
 CC carcinomas, leukemias, lymphomas, osteosarcomas or smooth muscle cell  
 CC hyperplasias or skin growths. Enhancers of telomerase may be used to  
 CC stimulate stem cell proliferation and differentiation (expansion of  
 CC hematopoietic stem cells could be administered in the bone marrow  
 CC transplant context). As well, many tissues have stem cells. Proliferation  
 CC of these cells may be useful in wound healing, hair growth, treatment of  
 CC disease such as Wilm's tumour, organ regeneration or differentiation  
 CC after injury or diseases, nerve cell or brain cell growth following  
 CC injury  
 XX  
 SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
 QY  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 7335 TGAAGCTGTACTTGTCTCA 7352  
 4 TGAAGCTGTACTTGTCTCA 21  
 RESULT 3108  
 AAX79141/C  
 ID AAX79141 standard; DNA; 21 BP.  
 XX  
 AC AAX79141;  
 XX  
 DT 17-AUG-1999 (first entry)  
 XX  
 DE Primer NGAL107-L for A.thaliana SLP marker.  
 XX  
 KM MSH6; Muts homologue; plant; DNA mismatch repair; genetic variation;  
 KM characteristic; microsatellite; primer; PCR; amplification; SLP; ss;  
 KM sample sequence length polymorphism.  
 XX  
 OS Synthetic.  
 OS Arabidopsis thaliana.  
 XX  
 PN WO9919492-A2.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 09-OCT-1998; 98WO-EP006977.  
 XX  
 PR 10-OCT-1997; 97AU-00009745.  
 XX  
 PA (RHON) RHON-POULENC AGROCHIMIE.  
 XX  
 PI Doutriaux M, Betzner AS, Freysinet G, Perez P;  
 XX

DR WPI; 1999-277644/23.  
 XX  
 PT DNA encoding protein functionally involved in the DNA mismatch repair  
 PT system of a plant.  
 XX  
 PS Example 3; Page 28; 117pp; English.  
 XX  
 CC The invention relates to the isolation of the Arabidopsis thaliana MSH3  
 CC (AAX79066) and MSH6 (AAX79067) genes. These genes are Muts homologues  
 CC (MSH) from plants and are involved in DNA mismatch repair. The DNA  
 CC sequence can be used in processes for at least partially inactivating a  
 CC DNA mismatch repair system of a plant, for increasing genetic variation  
 CC in a plant, and for obtaining a plant with a desired characteristic.  
 CC Primers AAX79105-X79160 represent 28 primer pairs used to amplify short  
 CC allelic repeat fragments designated Simple Sequence Length Polymorphisms  
 CC (SSLP). These fragments can be used as markers in the analysis of  
 CC homologous recombination between genomes of A.thaliana subspecies  
 XX  
 SQ Sequence 21 BP; 14 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 QY  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 4459 TGAAGCTTTTGTCTTTT 4476  
 21 TGAAGCTTTTGTCTTTT 4  
 RESULT 3109  
 AAZ28937/C  
 ID AAZ28937 standard; DNA; 21 BP.  
 XX  
 AC AAZ28937;  
 XX  
 DT 07-FEB-2000 (first entry)  
 XX  
 DE Reverse primer cmr8 for amplification of paraplegin gene exon.  
 XX  
 KM Reverse primer cmr8; paraplegin; human; hereditary spastic paraplegia;  
 KM HSP; mutation; diagnosis; treatment; neurodegenerative condition;  
 KM Amyotrophic Lateral Sclerosis; ALS; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9958556-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 06-MAY-1999; 99WO-EP003112.  
 XX  
 PR 08-MAY-1998; 98IT-MI001003.  
 XX  
 PA (TELE-) FOND TELETHON.  
 XX  
 PI Ballabio A, Casari G;  
 XX  
 DR WPI; 2000-039065/03.  
 XX  
 PT A novel protein associated to hereditary spastic paraplegia used for the  
 PT diagnosis of neurodegenerative conditions.  
 XX  
 PS Claim 4; Fig 3; 53pp; English.  
 XX  
 CC The present sequence is a reverse primer cmr8 used for amplification and  
 CC detection of mutations in paraplegin gene exon from hereditary spastic  
 CC paraplegia (HSP) patients. Detection of mutations in paraplegin gene  
 CC helps in the diagnosis and treatment of various forms of HSP or other  
 CC neurodegenerative conditions, such as Amyotrophic Lateral Sclerosis  
 XX  
 SQ Sequence 21 BP; 8 A; 6 C; 4 G; 3 T; 0 U; 0 Other;





```

DT 04-DEC-2000 (first entry)
XX PCR primer used to amplify cDNA encoding full length human DAGKbeta.
DE
XX Human: diacylglycerol kinase beta; DAGKbeta; diacylglycerol; DAG;
XX phosphatidic acid; DAG-dependent protein kinase C activation;
KM mood disorder; epilepsy; neurodegenerative disorder; anxiety;
KM schizophrenia; migraine; drug dependence; stroke; Alzheimer's dementia;
KM Parkinson's disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200047723-A2.
XX
XX 17-AUG-2000.
XX
XX 23-DEC-1999; 99WO-GB004421.
XX
XX 15-FEB-1999; 99GB-00003430.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Carisazole A, Caldara F, Sala CF;
XX
XX WPI; 2000-506093/45.
XX
XX New human diacylglycerol kinase beta (hDAGKbeta) protein and its
XX modulating compounds, useful for treatment of neurodegenerative and mood
XX disorders.
XX
XX Disclosure; Page 15; 57pp; English.
XX
XX PCR primers AAA63845-46 were used to amplify cDNA encoding full length
XX human diacylglycerol kinase beta (DAGKbeta). DAGK converts diacylglycerol
XX (DAG) to phosphatidic acid and attenuates DAG-dependent protein kinase C
XX activation. Compounds that modulate the activity of DAGKbeta may be
XX administered to a human patient for the treatment or prophylaxis of a
XX disorder that is responsive to modulation of DAGK activity. The disorder
XX may be a mood disorder, epilepsy, a neurodegenerative disorder, anxiety,
XX schizophrenia, migraine, drug dependence, stroke, Alzheimer's dementia or
XX Parkinson's disease
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4418 ATTTTCCTGCTGCCA 4435
Db 19 ATTTTCCTGCTGTCGA 2
RESULT 3113
AAA63843/c
ID AAA63843 standard; DNA; 21 BP.
XX
XX AAA63843;
XX
XX 04-DEC-2000 (first entry)
XX
XX PCR primer used to amplify cDNA encoding full length human DAGKbeta.
DE
XX Human: diacylglycerol kinase beta; DAGKbeta; diacylglycerol; DAG;
XX phosphatidic acid; DAG-dependent protein kinase C activation;
KM mood disorder; epilepsy; neurodegenerative disorder; anxiety;
KM schizophrenia; migraine; drug dependence; stroke; Alzheimer's dementia;
KM Parkinson's disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200047723-A2.
XX

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PD 17-AUG-2000.
XX
XX 23-DEC-1999; 99WO-GB004421.
XX
XX 15-FEB-1999; 99GB-00003430.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Carisazole A, Caldara F, Sala CF;
XX
XX WPI; 2000-506093/45.
XX
XX New human diacylglycerol kinase beta (hDAGKbeta) protein and its
XX modulating compounds, useful for treatment of neurodegenerative and mood
XX disorders.
XX
XX Disclosure; Page 15; 57pp; English.
XX
XX PCR primers AAA63843-44 were used to amplify cDNA encoding full length
XX human diacylglycerol kinase beta (DAGKbeta). DAGK converts diacylglycerol
XX (DAG) to phosphatidic acid and attenuates DAG-dependent protein kinase C
XX activation. Compounds that modulate the activity of DAGKbeta may be
XX administered to a human patient for the treatment or prophylaxis of a
XX disorder that is responsive to modulation of DAGK activity. The disorder
XX may be a mood disorder, epilepsy, a neurodegenerative disorder, anxiety,
XX schizophrenia, migraine, drug dependence, stroke, Alzheimer's dementia or
XX Parkinson's disease
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4418 ATTTTCCTGCTGCCA 4435
Db 19 ATTTTCCTGCTGTCGA 2
RESULT 3114
AAF95448
ID AAF95448 standard; DNA; 21 BP.
XX
XX AAF95448;
XX
XX 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #209.
DE
XX Human: variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KM pulmonary embolism; paternity test; db.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Variation replace(11,G)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-015357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHEH ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX

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XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX
XX WPI; 2001-226749/23.
DR
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 63; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 5 A; 6 C; 3 G; 7 T; 0 U; 0 Other;
XX
OY Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
DB 7194 GACTACTCTGCTTTTCAC 7211
3 GACTACTCAGCTTTTCAC 20
XX
RESULT 3115
AAF96689
ID AAF96689 standard; DNA; 21 BP.
XX
AC AAF96689;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1450.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,T)
FT /*tag=a
FT /standard_name="single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
```

```
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 146; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
XX
OY Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
DB 5069 CCTAAGAGAGTGATGCT 5086
2 CCTGAAGAGCGTGATGCT 19
XX
RESULT 3116
AAF96584
ID AAF96584 standard; DNA; 21 BP.
XX
AC AAF96584;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1345.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,T)
FT /*tag=a
FT /standard_name="single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
```

PT atherosclerosis.  
 XX  
 PS Example, Page 141; 242pp; English.  
 XX  
 CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and  
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification  
 XX  
 SQ Sequence 21 BP; 6 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4509 CTTGACGAGCTGAGAG 4526  
 DB 2 CTGACGAGCTGAGAG 19  
 RESULT 3117  
 AAF96360  
 ID AAF96360 standard; DNA; 21 BP.  
 XX  
 AC AAF96360;  
 XX  
 DT 06-JUN-2001 (first entry)  
 XX  
 DE Human gene single nucleotide polymorphism #1121.  
 XX  
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Variation /tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN W0200118250-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PP 07-SEP-2000; 2000MO-US024503.  
 XX  
 PR 10-SEP-1999; 99US-0153357P.  
 PR 26-JUL-2000; 2000US-0220947P.  
 PR 16-AUG-2000; 2000US-0225724P.  
 XX  
 PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JT;  
 XX WPI; 2001-226749/23.  
 DR  
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis.  
 XX  
 PS Example; Page 129; 242pp; English.  
 XX

CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and  
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification  
 XX  
 SQ Sequence 21 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 1 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 896 TGATTGATTCATGTCGAG 915  
 DB 2 TGCTTGATTCATGTCGAG 21  
 RESULT 3118  
 AAF95480  
 ID AAF95480 standard; DNA; 21 BP.  
 XX  
 AC AAF95480;  
 XX  
 DT 06-JUN-2001 (first entry)  
 XX  
 DE Human gene single nucleotide polymorphism #241.  
 XX  
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Variation /tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN W0200118250-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PP 07-SEP-2000; 2000MO-US024503.  
 XX  
 PR 10-SEP-1999; 99US-0153357P.  
 PR 26-JUL-2000; 2000US-0220947P.  
 PR 16-AUG-2000; 2000US-0225724P.  
 XX  
 PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JT;  
 XX WPI; 2001-226749/23.  
 DR  
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis.  
 XX  
 PS Example; Page 66; 242pp; English.  
 XX  
 CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided

CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and  
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification

XX Sequence 21 BP; 11 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032  
DB 4 ATGAGAAAGTAGAGAGAA 21

## RESULT 3119

AAH28472  
ID AAH28472 standard; DNA; 21 BP.

XX AAH28472;  
XX 17-SEP-2001 (first entry)

DE PCR primer for cDNA encoding human slit polypeptide Zslit3.

XX Slit protein; Zslit3; neurite growth; cellular proliferation;  
KW immune response; stroke; brain damage; paralysis; Huntington's disease;  
KW neurodegenerative disease; amyotrophic lateral sclerosis;  
KW Alzheimer's disease; Parkinson's disease; peripheral neuropathy;  
KW demyelinating disease; multiple sclerosis; lung organogenesis;  
KW pulmonary disease; respiration; circulation; cystic fibrosis; asthma;  
KW immunosuppression; autoimmune disease; insulin dependent diabetes;  
KW rheumatoid arthritis; PCR primer; ss.

XX Homo sapiens.

XX WO200146418-A1.

XX 28-JUN-2001.

XX 14-DEC-2000; 2000WO-US034230.

XX 21-DEC-1999; 99US-00469847.

XX (ZYMO) ZYMOGENETICS INC.

XX Holloway JL, Chandrasekhar VA;

XX WPI; 2001-441677/47.

XX Novel human slit polypeptide, ZSLIT3, useful for treating and diagnosing  
PT cystic fibrosis, insulin dependent diabetes and multiple sclerosis.

XX Example 2; Page 123; 125pp; English.

CC PCR primers AAH28472-73 were used to amplify DNA encoding a human slit  
CC protein polypeptide, designated Zslit3. Zslit is a neurite growth and  
CC development modulator, and an cellular proliferation and differentiation  
CC and immune response modulator. Zslit3 polypeptides and polynucleotides  
CC are useful for regenerating and directing neurite outgrowth following  
CC strokes, brain damage caused by head injuries, paralysis caused by spinal  
CC injuries, and for treating neurodegenerative diseases such as amyotrophic  
CC lateral sclerosis, Alzheimer's disease, Huntington's disease, Parkinson's  
CC disease and peripheral neuropathies, or demyelinating diseases e.g.

CC multiple sclerosis. They are useful for lung organogenesis and repair,  
CC and thus useful for diagnosing and treating pulmonary diseases such as  
CC respiration and circulation, cystic fibrosis and asthma. They also act as  
CC a mediator of immunosuppression, and thus are useful for diagnosing and  
CC treating autoimmune diseases such as insulin dependent diabetes and

CC rheumatoid arthritis

XX Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2530 ACACGACATGAGCTCCAG 2547  
DB 4 ACAGAGATGTGTCCAG 21

## RESULT 3120

AAH78643  
ID AAH78643 standard; DNA; 21 BP.

XX AAH78643;

XX 10-DEC-2001 (first entry)

DE PCR primer for mechanically sensitive potassium channel gene fragment.

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;  
KW polysaturated fatty acid; arachidonic acid; hTRPAK; chromosome 11q13;  
KW neuronal excitation; muscle excitation; cardiac rhythm; anoxia;  
KW hormone secretion; cardiac disease; vascular disease; ischemia;  
KW nervous system disorder; endocrinal disease; muscle disease;  
KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration;  
KW PCR primer; ss.

XX Homo sapiens.

XX WO200168670-A2.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-FR000758.

XX 14-MAR-2000; 2000FR-00003264.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Maingret F;

XX WPI; 2001-590037/66.

XX New mechanically sensitive potassium channel, useful for treating  
PT cardiovascular diseases and in drug screening, is activated by  
PT polysaturated fatty acids.

XX Disclosure; Page 15; 37pp; French.

CC PCR primers AAH78642-43 were used to amplify a gene fragment of the human  
CC mechanically sensitive potassium channel gene. The channel is activated  
CC by polysaturated fatty acids (particularly arachidonic acid (AA)) and  
CC by riluzole. The polypeptide is designated human TWICK-related AA-  
CC activated potassium channel (hTRPAK). The hTRPAK gene is located on  
CC chromosome 11q13. hTRPAK is involved in regulation of neuronal and muscle  
CC excitation, cardiac rhythm and secretion of hormones. Cells that express  
CC hTRPAK, designated to screen for modulators of hTRPAK activity. Such  
CC modulators are potentially useful for prevention or treatment, in humans  
CC and animals, of cardiac and/or vascular disease; nervous system  
CC disorders associated with ischemia and anoxia; endocrinal diseases  
CC associated with anomalous hormone secretion or muscle diseases; and  
CC retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and  
CC neurodegeneration

XX Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 GCGCGCGCGGATCCCG 129  
 DB 4 GCGCGCGCGGATCTTG 21

## RESULT 3121

AAH78640  
 ID AAH78640 standard; DNA; 21 BP.

AC AAH78640;

DT 10-DEC-2001 (first entry)

XX PCR primer for mechanically sensitive potassium channel gene fragment.

XX Human; mechanically sensitive potassium channel; riluzole; TWICK;  
 KW polyunsaturated fatty acid; arachidonic acid; hTRPAK; chromosome 11q13;  
 KW neuronal excitation; cardiac excitation; cardiac rhythm; anoxia;  
 KW hormone secretion; cardiac disease; vascular disease; ischemia;  
 KW nervous system disorder; endocrinal disease; muscle disease;  
 KW retinal disease; epilepsy; cardiac arrhythmia; neurodegeneration;  
 KW PCR primer; ss.

XX Homo sapiens.

OS WO200168670-A2.

PN 20-SEP-2001.

PD 14-MAR-2001; 2001WO-FR000758.

PF 14-MAR-2000; 2000FR-00003264.

PR 14-MAR-2000; 2000FR-00003264.

PA (CNRS ) CNRS CENT NAT RECH SCT.

PI Lazdunski M, Lesage F, Maingret F;

PS WPI; 2001-590037/66.

PT New mechanically sensitive potassium channel, useful for treating

PT cardiovascular diseases and in drug screening, is activated by

PT polyunsaturated fatty acids.

PS Disclosure; Page 15; 37pp; French.

XX PCR primers AAH78639-40 were used to amplify a gene fragment of the human  
 CC mechanically sensitive potassium channel gene. The channel is activated  
 CC by polyunsaturated fatty acids (particularly arachidonic acid (AA)) and  
 CC by riluzole. The polypeptide is designated human TWICK-related A-  
 CC activated potassium channel (hTRPAK). The hTRPAK gene is located on  
 CC chromosome 11q13. hTRPAK is involved in regulation of neuronal and muscle  
 CC excitation, cardiac rhythm and secretion of hormones. Cells that express  
 CC hTRPAK, designated to screen for modulators of hTRPAK activity. Such  
 CC modulators are potentially useful for prevention or treatment, in humans  
 CC and animals, of: cardiac and/or vascular disease; nervous system  
 CC disorders associated with ischemia and anoxia; endocrinal diseases  
 CC associated with anomalous hormone secretion or muscle diseases; and  
 CC retinal diseases. Typical examples are epilepsy, cardiac arrhythmia and  
 CC neurodegeneration

XX Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 112 GCGCGCGCGGATCCCG 129

DB 4 GCGCGCGCGGATCTTG 21

RESULT 3122

AAH62114  
 ID AAH62114 standard; DNA; 21 BP.  
 AC AAH62114;

DT 12-SEP-2001 (first entry)

XX CACNA2D2 polymorphism containing DNA fragment #15.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
 KW heart disease; paternity testing; forensic science; ds.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Variation replace(11,A)

FT /tag= a /standard\_name= "single nucleotide polymorphism"

PN WO200138576-A2.

PD 31-MAY-2001.

PE 17-NOV-2000; 2000WO-US031639.

PR 24-NOV-1999; 99US-0167334P.

PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

PI Cargill M, Ireland JS, Lander ES;

PS WPI; 2001-36705/38.

PT New nucleic acid segments of the human genome, particularly from genes

PT including polymorphic sites, for phenotype correlation, forensics,

PT paternity testing, medicine and genetic analysis.

PS Claim 1; Page 29; 80pp; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
 CC contain single nucleotide polymorphisms (SNPs). A method is included in  
 CC the invention for analysing a nucleic acid sample, which consists of  
 CC determining the base occupying any one of the polymorphic sites given in  
 CC the SNP containing sequences. The nucleotide sequences can be used in the  
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
 CC diseases, diseases of the cardiovascular system, and infection by  
 CC microorganisms. The oligonucleotides are also useful in the manufacture  
 CC of a medicament for the treatment or prophylaxis of the diseases, and as  
 CC a pharmaceutical. SNP containing oligonucleotides are useful in  
 CC applications such as phenotype correlation, forensics, paternity testing,  
 CC medicine and genetic analysis

XX Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3582 GCTGCAGAACTGCACCT 3599

DB 1 GCTGCAGAACTGCACACT 18

## RESULT 3123

AAH62539  
 ID AAH62539 standard; DNA; 21 BP.

AC AAH62539;

DT 12-SEP-2001 (first entry)

XX Arachidonate 12-lipoxygenase polymorphism containing DNA fragment #440.

KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;  
 KW heart disease; paternity testing; forensic science; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT replace(11,A)  
 FT /+tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 EN WO200138576-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PE 17-NOV-2000; 2000WO-US031639.  
 XX  
 PR 24-NOV-1999; 99US-0167334P.  
 XX  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Cargill M, Ireland JS, Lander ES;  
 XX  
 DR WPI; 2001-367705/38.  
 XX  
 DR WPI; 2001-367705/38.  
 XX  
 PT New nucleic acid segments of the human genome, particularly from genes  
 PT including polymorphic sites, for phenotype correlation, forensics,  
 PT paternity testing, medicine and genetic analysis.  
 XX  
 PS Claim 1; Page 64; 80pp; English.  
 XX  
 CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which  
 CC contain single nucleotide polymorphisms (SNPs). A method is included in  
 CC the invention for analysing a nucleic acid sample, which consists of  
 CC determining the base occupying any one of the polymorphic sites given in  
 CC the SNP containing sequences. The nucleotide sequences can be used in the  
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart  
 CC diseases, diseases of the cardiovascular system, and infection by  
 CC microorganisms. The oligonucleotides are also useful in the manufacture  
 CC of a medicament for the treatment or prophylaxis of the diseases, and as  
 CC a pharmaceutical. SNP containing oligonucleotides are useful in  
 CC applications such as phenotype correlation, forensics, paternity testing,  
 CC medicine and genetic analysis  
 XX  
 SO Sequence 21 BP; 10 A; 1 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred.No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 6216 AAAAGCTGGGAAAGGAGA 6233  
 Db 4 AAAAGCTGGGAAAGGAGA 21  
 RESULT 3124  
 AAF64065  
 ID AAF64065 standard; DNA; 21 BP.  
 XX  
 AC AAF64065;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Primer #9.  
 XX  
 KW Human; lipoprotein lipase; LPL; stenosis; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 EN WO200102606-A2.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PD 30-JUN-2000; 2000WO-US018308.

XX  
 PR 102-JUL-1999; 99US-00347114.  
 XX  
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
 XX  
 PI Taylor KD, Scheuner M, Rotter J, Yang H;  
 XX  
 DR WPI; 2001-138155/14.  
 XX  
 PT Genetic testing for determining non-responsiveness to statin drug in  
 PT patients of a coronary artery disease, involves analyzing amplification  
 PT products for homozygosity for a variant allele in the human lipoprotein  
 PT lipase gene.  
 XX  
 PS Claim 11; Page 17; 74pp; English.  
 XX  
 CC The present invention relates to detecting a genetic predisposition in a  
 CC human subject for non-responsiveness to statin drug treatment, involving  
 CC amplifying nucleic acids including a non-coding or untranslated region  
 CC within the 3' end of the human lipoprotein lipase (LPL) gene from a  
 CC tissue sample. The method is useful for determining which patients  
 CC suffering from coronary artery disease, or which coronary artery bypass  
 CC graft (CABG) patients, will likely not respond positively to statin drug  
 CC treatment with respect to stenosis of a coronary artery or bypass graft  
 XX  
 SO Sequence 21 BP; 3 A; 3 C; 5 G; 10 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred.No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 4280 GCACTCTTCTTGCAACT 4297  
 Db 4 GCACTGTTCTTGTAAGT 21  
 RESULT 3125  
 AAH78090/C  
 ID AAH78090 standard; DNA; 21 BP.  
 XX  
 AC AAH78090;  
 XX  
 DT 26-NOV-2001 (first entry)  
 XX  
 DE Primer for breast amplified G protein coupled receptor (BCA-GPCR)-2.  
 XX  
 KW Breast amplified G protein coupled receptor; BCA-GPCR; breast cancer;  
 KW chromosome 14q4; BCA-GPCR-1; BCA-GPCR-2; BCA-GPCR-3; BCA-GPCR-4;  
 KW signal transduction; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200168704-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PE 13-MAR-2001; 2001WO-US008020.  
 XX  
 PR 14-MAR-2000; 2000US-00524730.  
 PR 11-APR-2000; 2000US-00546986.  
 XX  
 PA (TULA-) TULARIK INC.  
 PA (POWER/) POWERS S.  
 PA (YANG/) YANG J.  
 PA (CUTLER/) CUTLER G.  
 XX  
 PI Powers S, Yang J, Cutler G;  
 XX  
 DR WPI; 2001-570865/64.  
 XX  
 PT Four nucleic acids encoding breast amplified G protein coupled receptors  
 PT (BCA-GPCRs), useful for identifying modulators of G-protein coupled  
 PT receptor signal transduction which can be used in the treatment of cancer

PT such as breast cancer.  
 XX  
 XX  
 PS Claim 7; Page 54; 68pp; English.  
 XX  
 CC PCR primers AAH78089-90 were used to amplify cDNA or DNA encoding breast  
 CC amplified G protein coupled receptor (BCA-GPCR)-2. BCA-GPCRs are  
 CC located at chromosome 1q44, in the following orientation (starting from  
 CC the centromere end): BCA-GPCR-1 (3'-5' orientation), BCA-GPCR-2 (5'-3'  
 CC orientation), BCA-GPCR-3 (3'-5' orientation), and BCA-GPCR-4 (5'-3'  
 CC orientation). The G protein coupled receptors are useful for assaying and  
 CC identifying modulators of G-protein coupled receptor signal transduction.  
 CC The modulators and antibodies against the G protein coupled receptors are  
 CC useful for pharmacological modulation of signalling pathways, e.g. in  
 CC cancer cells such as breast cancer  
 CC  
 SQ Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3894 CTGAGTTACTTTCATAG 3911  
 DB 18 CTGAGTTACTTCTTAG 1  
 XX  
 RESULT 3126  
 AAH89072  
 ID AAH89072 standard; DNA; 21 BP.  
 XX  
 XX AAH89072;  
 AC  
 DT 27-FEB-2002 (first entry)  
 XX  
 XX Human polymorphic oligonucleotide L21952 fragment.  
 DE  
 XX Human, single nucleotide polymorphic; SNP; forensic science;  
 KM paternity testing; phenotypic trait; genetic mapping; animal breeding;  
 KW plant breeding; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Variation /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN MO200134840-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 10-NOV-2000; 2000MO-US030766.  
 XX  
 PR 10-NOV-1999; 99US-0164596P.  
 XX  
 PA (GLAXO ) GLAXO GROUP LTD.  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Au K, Chen J, Patil N, Thomas D;  
 XX  
 DR WPI; 2001-335945/35.  
 XX  
 XX New polymorphic sites derived from the human genome are useful to  
 PT determine sites correlating with phenotypic traits, particularly disease,  
 PT and also in forensics and paternity testing.  
 XX  
 PS Claim 82; Page 13; 43pp; English.  
 XX  
 CC The present invention relates to human oligonucleotides comprising a  
 CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present  
 CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
 CC forensics, paternity testing, correlation of polymorphisms with

CC phenotypic traits, genetic mapping of phenotypic traits and marker  
 CC assisted breeding of animals and crop plants  
 CC  
 SQ Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 7408 AACATAGCAGCAGCAGC 7425  
 DB 2 AACGACGAGCTGCAGCAGC 19  
 XX  
 RESULT 3127  
 AAF89455  
 ID AAF89455 standard; DNA; 21 BP.  
 XX  
 XX AAF89455;  
 AC  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE Human genetic marker PCR primer SEQ ID NO: 44.  
 XX  
 XX Genetic marker; genetic disease diagnosis; cystic fibrosis; haemophilia;  
 KM sickle cell disease; muscular dystrophy; Huntington's disease;  
 KW retinoblastoma; PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN MO200134839-A1.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000MO-US030493.  
 XX  
 PR 12-NOV-1999; 99US-0165301P.  
 XX  
 PA (DUNLOP ) DUNLOP C L M.  
 PA (WEISL) WEISL J M.  
 XX  
 PI Dunlop CLM, Weisel JM;  
 XX  
 DR WPI; 2001-329096/34.  
 XX  
 PT Detecting multiple genetic markers in one assay, useful to simultaneously  
 PT detect a number of genetic disorders, comprises generating extension  
 PT products and separating them on the basis of melting behavior is.  
 XX  
 PS Claim 44; Page 36; 40pp; English.  
 XX  
 CC The present invention describes a method of identifying the presence of a  
 CC plurality of genetic markers in a subject, involving generating extension  
 CC products using PCR primers flanking the plurality of markers, separating  
 CC the extension products depending on their melting temperatures, and  
 CC analysing them to determine the presence or absence of each genetic  
 CC marker. This can be used in the diagnosis of genetic diseases, including  
 CC familial hypercholesterolaemia, cystic fibrosis, Tay-Sachs, thalassaemia,  
 CC sickle cell disease, phenylketonuria, galactosaemia, fragile X syndrome,  
 CC haemophilia A, myotonic dystrophy, medium chain acyl-CoA dehydrogenase,  
 CC maturity onset diabetes, cystinuria, methylmalonic acidemia, urea cycle  
 CC disorders, hereditary fructose intolerance, hereditary haemochromatosis,  
 CC neonatal thrombocytopenia, Gaucher's disease, tyrosinaemia, Wilson's  
 CC disease, acropnuria, hypolactasia, Baker's disease, argininaemia,  
 CC adenomatous polyposis coli, hereditary nonpolyposis colorectal cancer,  
 CC Huntington's disease, adult polycystic kidney disease, alpha-1-  
 CC antitrypsin deficiency, Duchenne muscular dystrophy, Marfan's syndrome,  
 CC neurofibromatosis, osteogenesis imperfecta, retinoblastoma, Friedreich's  
 CC ataxia, haemoglobinopathies, Leber's hereditary optic neuropathy, MCAD,  
 CC Canavan's disease, retinitis pigmentosa, Bloom syndrome, Fanconi anaemia  
 CC or Neuman Pick disease. The present sequence is one of the PCR primers  
 CC of the invention



SQ Sequence 21 BP; 5 A; 9 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 597 CTCGATCAAGTGCTAGC 614

Db 4 CTCGATCAAGTGCTAGC 21

RESULT 3128

AA512385/c

ID AA512385 standard; RNA; 21 BP.

XX AA512385;

XX 21-NOV-2001 (first entry)

XX Class VII ribozyme, substrate domain.

XX Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;

KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.

XX Synthetic.

XX WO200159102-A2.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-US004223.

XX 08-FEB-2000; 2000US-0181360P.

XX 31-MAR-2000; 2000US-0193646P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (UYVA ) UNIV YALE.

XX Breaker R, Beigelman L, Emlisson G;

XX WPI; 2001-536526/59.

XX New nucleic acids with endonuclease activity, such as ribozymes and

XX nucleozymes, for modulating gene expression in a plant, mammalian,

XX bacterial or fungal cell.

XX Example 1; Fig 9; 96pp; English.

XX The invention relates to nucleic acid molecules with endonuclease

XX activity, which are particularly useful for cleavage of RNA or DNA. The

XX nucleic acids are used in a pharmaceutical composition and are used to

XX modulate expression of a gene in a plant, mammalian, bacterial or fungal

XX cell. They are used to cleave a separate nucleic acid, preferably RNA.

XX The nucleic acids are used to inhibit gene expression and/or cell

XX proliferation, and can be used to treat a disease or condition. More than

XX one nucleic acid can be independently targeted to the same or different

XX sites in a cell. The nucleic acids may be used to study DNA. The

XX modifications to the nucleic acids optimises their catalytic activity and

XX can maintain or enhance their activity. They exhibit a high degree of

XX specificity for RNA. The present sequence represents the Class VII

XX ribozyme, substrate domain, used in an example which demonstrates the

XX method of the invention

RESULT 3129

AA512374/c

ID AA512374 standard; RNA; 21 BP.

XX AA512374;

XX 21-NOV-2001 (first entry)

XX Class I-XII ribozyme substrate.

XX Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;

KW gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.

XX Synthetic.

XX Key

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

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XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

XX misc\_binding

Location/Qualifiers

1. .8 /tag= a

/note= "Forms double-stranded region with bases 46 to 39

of AA512375"

1. .8 /tag= e

/note= "Forms double-stranded region with bases 20 to 28

of AA512383"

1. .8 /tag= h

/note= "Forms double-stranded region with bases 30 to 23

of AA512394"

1. .5 /tag= b

/note= "Forms double-stranded region with bases 42 to 38

of AA512377"

1. .5 /tag= c

/note= "Forms double-stranded region with bases 43 to 39

of AA512379"

1. .5 /tag= d

/note= "Forms double-stranded region with bases 29 to 25

of AA512381"

1. .5 /tag= f

/note= "Forms double-stranded region with bases 49 to 45

of AA512388"

1. .4 /tag= g

/note= "Forms double-stranded region with bases 49 to 46

of AA512392"

1. .4 /tag= i

/note= "Forms double-stranded region with bases 35 to 32

of AA512396"

8. .15 /tag= k

/note= "Forms double-stranded region with bases 8 to 1 of

AA512377"

8. .15 /tag= l

/note= "Forms double-stranded region with bases 8 to 1 of

AA512379"

8. .15 /tag= m

/note= "Forms double-stranded region with bases 8 to 1 of

AA512381"

8. .13 /tag= n

/note= "Forms double-stranded region with bases 14 to 9

of AA512388"

8. .12 /tag= j

/note= "Forms double-stranded region with bases 36 to 32

of AA512390"



AAD29834/C  
 ID AAD29834 standard; DNA; 21 BP.  
 AC AAD29834;  
 XX  
 DT 17-MAY-2002 (first entry)  
 DE Arabidopsis NADPH dependent trx reductase gene amplifying primer, STR2B.  
 XX  
 KW Transgenic plant; thioredoxin reductase; starch; protein; grain;  
 RM milling process; enzyme; PCR primer; ss.  
 XX  
 OS Arabidopsis sp.  
 PN WO200198509-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 19-JUN-2001; 2001WO-EP006918.  
 XX  
 PR 21-JUN-2000; 2000US-0058747.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI lanahan MB, Desai NM, Gasdaaka PY;  
 XX  
 DR WPI; 2002-179557/23.  
 XX  
 PT Transgenic plant coding for eukaryotic thioredoxin reductase at elevated  
 PT levels useful for separating the starch and protein components of grain  
 PT in a milling process.  
 XX  
 PS Example 4; Page 52; 86pp; English.  
 XX  
 CC The present invention relates to a transgenic plant comprising  
 CC heterologous DNA coding for eukaryotic thioredoxin reductase integrated  
 CC into its nuclear or plastid genome and use of thioredoxin reductase for  
 CC separating the starch and protein components of grain in a milling  
 CC process. Transgenic plant is used for separating the starch and protein  
 CC components of grain in a milling process. Transgenic plant may be used to  
 CC produce thioredoxin reductase at elevated levels. Delivery of thioredoxin  
 CC reductase eliminates the need to develop exogenous sources for addition  
 CC during processing. Secondly, physical disruption of seed integrity is not  
 CC necessary to bring the enzyme in contact with the storage or matrix  
 CC proteins of the seed prior to processing or as an extra processing step.  
 CC The present sequence is Arabidopsis NADPH dependent trx reductase gene  
 CC (NTR) amplifying PCR primer  
 XX  
 SQ Sequence 21 BP; 3 A; 4 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 351 CATCCCTAAGATCGACGT 368  
 Db 19 CAACCCGAAGATCGACGT 2  
 RESULT 3132  
 ABL49744  
 ID ABL49744 standard; DNA; 21 BP.  
 AC ABL49744;  
 XX  
 DT 29-MAY-2002 (first entry)  
 DE Rice PCR primer SEQ ID NO:6.  
 XX  
 KW Human; interferon alpha; interferon omega; prolamin; fusion protein;  
 KW plant; grass plant; tea; PCR primer; ss.  
 XX  
 OS Oryza sativa.

XX  
 PN JP2002017187-A.  
 XX  
 PD 22-JAN-2002.  
 XX  
 PE 07-JUL-2000; 2000JP-00207230.  
 XX  
 PR 07-JUL-2000; 2000JP-00207230.  
 XX  
 PA (NICH-) JAPAN CHEM RES CO LTD.  
 XX  
 DR WPI; 2002-263239/31.  
 XX  
 PT Plant with incorporated human interferon gene.  
 PT  
 PS Example; Page 4; 22pp; Japanese.  
 XX  
 CC The present invention describes a true grass plant in which a base  
 CC sequence encoding a human interferon protein, with a base sequence  
 CC encoding a signal amino acid sequence causing accumulation of the stored  
 CC protein of albumen to the protein body connected upstream, is recombined  
 CC expressably to a genomic DNA. The grass plant can be used for the  
 CC creation of a useful application of tea. The present sequence represents  
 CC a PCR primer which is used in an example from the present invention  
 XX  
 SQ Sequence 21 BP; 5 A; 2 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 6317 GGCTACTGTTGCTGGGAA 6334  
 Db 4 GGCTAATGTTGTTGGGAA 21  
 RESULT 3133  
 ABR70370  
 ID ABR70370 standard; DNA; 21 BP.  
 AC ABR70370;  
 XX  
 DT 15-JUL-2002 (first entry)  
 DE Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #58.  
 XX  
 KW Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;  
 KW insulin-like growth factor binding protein-2; hormone-regulated tumour;  
 KW breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;  
 KW hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;  
 KW ODN; endocrine tumour therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200222642-A1.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 13-SEP-2001; 2001WO-US028748.  
 XX  
 PR 14-SEP-2000; 2000US-0232641P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Gleave M, Satoshi K, Nelson C, Rennie PS;  
 XX  
 DR WPI; 2002-339861/37.  
 XX  
 PT Composition for treating hormone-regulated cancer, particularly of  
 PT prostate or breast, comprises oligonucleotide antisense to insulin-like  
 PT growth factor binding protein-2.  
 XX  
 PS Example 1; Page 13; 36pp; English.

XX The present invention relates to a new composition for treating hormone-  
CC regulated cancer. The composition comprises an antisense oligonucleotide  
CC that inhibits expression of IGFBP-2 (Insulin-like growth factor binding  
CC protein-2). The molecules of the invention are used to delay progression  
CC of hormone-regulated tumours, particularly of breast or prostate, to the  
CC hormone-independent state, to delay metastatic progression to the bone of  
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by  
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid  
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense  
CC IGFBP-2-oligonucleotides (ODN) that were used in the invention for  
CC prostate and other endocrine tumour therapy  
XX

Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCA 7432  
DB 4 GCACTAGCAGCAGCAGCA 21  
|||||  
|||||

RESULT 3134  
ID ABS52265 standard; DNA; 21 BP.  
XX  
AC ABS52265;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Plant vector PCR primer #29.  
XX  
XX Plant; PCR; primer; ss; plasmid; plasmid genome; antibiotic;  
KM herbicide resistance gene.  
XX  
OS Synthetic.  
XX  
PN WO200257466-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 18-JAN-2002; 2002WO-EP000481.  
XX  
PR 19-JAN-2001; 2001DE-01002389.  
XX  
PA (ICON-) ICON GENETICS AG.  
XX  
PI Ehl1 C, Huang F, Klaus S, Muehlbauer S, Herz S, Koop H;  
XX  
DR WPI; 2002-590747/63.  
XX  
XX Transforming multicellular plants, by altering the function of a plasmid  
PT gene, selecting plants expressing altered phenotype, transforming plants  
PT with a vector capable of restoring function and separating transformed  
PT plants.  
XX  
XX Example 6; Page 38; 56pp; English.  
XX  
XX The invention relates to producing multicellular plants, organs or  
CC tissues transformed on their plasmid, comprising altering/disrupting the  
CC function of a gene in a plasmid genome for producing a selectable  
CC phenotype and selecting plants with plasmids expressing the phenotype.  
CC transforming the plasmid genomes of selected plants with a transformation  
CC vector with a restoring sequence for restoring function and separating  
CC transformed plants. This method is useful for producing multicellular  
CC plants; organs or tissues transformed on their plasmid and for selection  
CC of antibiotics and herbicide resistance genes. Sequences ABS52237-  
CC ABS52269 represent PCR primers used to amplify plant vector genes of the  
CC invention  
XX  
SQ Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5072 AAAGAGAGTGTACTTAC 5089  
DB 4 AAAGAGAGGAGTCTTAC 21  
|||||  
|||||

RESULT 3135  
ID ABS51698 standard; DNA; 21 BP.  
XX  
AC ABS51698;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Human LDLB-like protein forward PCR primer #1.  
XX  
XX Human; NOVA; pathological condition; NOVA-associated disorder;  
KM Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;  
KM pancreatitis; obesity; diabetes; autoimmune disease; infertility;  
KM renal artery stenosis; interstitial nephritis; glomerulonephritis;  
KM polycystic kidney disease; cataract; Alzheimer's disease; cancer;  
KM acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;  
KM congenital heart defect; scleroderma; endometriosis; haemophilia;  
KM dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;  
KM multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;  
KM acne; wound; asthma; human disease; calpain; epain; zinc finger;  
KM low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;  
KM serine protease TSP; tyrosine activated protein kinase kinase-2;  
KM glypican-2 precursor; thymosin beta-10; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO20025702-A2.  
XX  
PD 18-JUL-2002.  
XX  
XX 26-OCT-2001; 2001WO-US050925.  
XX  
PF 26-OCT-2000; 2000US-0243320P.  
XX  
PR 26-OCT-2000; 2000US-0243592P.  
XX  
PR 26-OCT-2000; 2000US-0243642P.  
XX  
PR 27-OCT-2000; 2000US-0243681P.  
XX  
PR 27-OCT-2000; 2000US-0243863P.  
XX  
PR 31-OCT-2000; 2000US-0244443P.  
XX  
PR 01-NOV-2000; 2000US-0244995P.  
XX  
PR 01-NOV-2000; 2000US-0245029P.  
XX  
PR 02-NOV-2000; 2000US-0245293P.  
XX  
PR 02-NOV-2000; 2000US-0245315P.  
XX  
PR 02-NOV-2000; 2000US-0245316P.  
XX  
PR 19-JAN-2001; 2001US-0262994P.  
XX  
PR 15-FEB-2001; 2001US-0269056P.  
XX  
PR 02-MAR-2001; 2001US-0272923P.  
XX  
PR 15-MAR-2001; 2001US-0276565P.  
XX  
PR 07-SEP-2001; 2001US-0318119P.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Gangoli EA, Spytek KA, Gilbert J, Casman S, Blalock A, Li L,  
PI Vannoy CM, Shenoy S, Mishra V, Furtak K, Gerlach V, Edinger S;  
PI Malayankar U, Stone D, Miller I, Smithson G, Gunther E, Padigaru M;  
PI Taupier RJ, Anderson D;  
XX  
XX WPI; 2002-590673/63.  
XX  
XX Isolated NOVA polypeptides and nucleic acid molecules useful for  
PT treating, preventing, diagnosing and researching pathological conditions  
PT in humans with a NOVA-associated disorder, e.g. cancer, stroke or  
PT Alzheimer's disease.  
XX

PS Example 3; Page 170; 236pp; English.

XX The present invention relates to a new polypeptide that comprises any of

CC 17 fully defined sequences of 43-990 amino acids given in the

CC specification. The NOVX polypeptide, nucleic acid and antibody of the

CC invention are useful for treating or preventing a pathological condition

CC in humans with a NOVX-associated disorder, e.g. Von Hippel-Lindau

CC syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity,

CC diabetes, autoimmune disease, renal artery stenosis, interstitial

CC nephritis, glomerulonephritis, polycystic kidney disease, cataract,

CC Alzheimer's disease, acoustic trauma, cancer, infertility,

CC cardiomyopathies, atherosclerosis, hypertension, congenital heart

CC defects, scleroderma, endometriosis, haemophilia, dementia, stroke,

CC Parkinson's disease, Huntington's disease, epilepsy, multiple sclerosis,

CC anxiety, pain, leukemias, hypothyroidism, psoriasis, acne, wounds and

CC asthma. They are also useful for the manufacture of a medicament for

CC treating a syndrome associated with a human disease, specifically a NOVX-

CC associated disorder. They may also be useful in therapeutic applications

CC including protein therapy, as small molecule drug targets, as antibody

CC targets, as diagnostic and/or prognostic markers, in gene therapy, as

CC research tools and in tissue regeneration. The present nucleic acid

CC sequence represents a PCR primer that was used in the methods of the

CC invention to amplify one of the 17 novel proteins of the invention

XX

SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3683 GCCAGAAAGCCAGCTATT 3700

DB 1 GCCAGAAAGCCAGCTATT 18

RESULT 3136

ABK91200

ID ABK91200 standard; DNA; 21 BP.

XX

AC ABK91200;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human proteolipid, PLP, protein RT-PCR primer #1.

XX

KM Human; ss; Ulp; CRMP; collagen response mediator protein; PCR;

KM Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;

KM paraneoplastic neurodegenerative disease; PND; myelination;

KM demyelination; remyelination; myelin disorder; multiple sclerosis;

KM autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;

KM human T lymphocyte virus 1; reverse transcriptase PCR; primer;

KM

XX

OS Homo sapiens.

XX

PN US2002119944-A1.

XX

PD 29-AUG-2002.

XX

PF 09-NOV-2001; 2001US-00986632.

XX

PR 09-NOV-2000; 2000US-0246751P.

XX

PA (AGUE//) AGUERA M.

PA (BELI//) BELIN M.

PA (CHAR//) CHARRIER B.

PA (HONO//) HONORAT J.

PA (RICA//) RICARD D.

PA (ROGE//) ROGEMOND V.

XX

PI Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;

XX WPI; 2002-627172/67.

XX

PT Prevention or treatment of myelin disorders, such as multiple sclerosis,

PT by administering an agent selected from a Ulp/CRMP protein, a nucleic

PT acid coding for the protein, or an antibody directed against protein.

PS

XX Example; Page 8; 44pp; English.

XX

CC The invention relates to a new method for prevention or treatment of

CC myelin disorders, comprises administering to a patient an effective

CC amount of an agent selected from a Ulp (Unc-33-like protein/CRMP

CC (collapsin response mediator protein) protein, a nucleic acid coding for

CC Ulp/CRMP, an antisense sequence capable of specifically hybridizing with

CC the nucleic acid, an antibody directed against Ulp/CRMP, or an aptamer

CC capable of binding Ulp/CRMP, and a pharmacologically acceptable carrier.

CC Also included are methods of diagnosing a myelin disorder in a subject,

CC identifying agents useful for the prevention or treatment of myelin

CC disorders, using the Ulp/CRMP proteins/nucleic acids, agents capable of

CC modulating the function or expression of the proteins (increasing or

CC decreasing), and a method for identifying an endogenous agent as a

CC therapeutic target for the prevention or the treatment of myelin

CC disorders. The agents are useful for preventing or creating a myelin

CC disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus

CC 1) associated myelopathy and neurodegenerative diseases, Alzheimer's

CC disease, paraneoplastic neurodegenerative diseases (PND), autoimmune

CC neurodegenerative disorder. Ulp/CRMP proteins are involved in

CC the processes of myelination, demyelination and remyelination. Antibodies

CC to a Ulp/CRMP protein are useful for diagnosing a myelin disorder. The

CC present sequence is a reverse transcriptase (RT)-PCR primer for

CC proteolipid protein (PLP), an oligodeoxynucleotide marker protein used as a

CC control in an experiment to detect mRNA encoding Ulp proteins

XX

SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 692 TGCATTCGCCATGAGGC 709

DB 4 TGCATTCGCCATGAGGC 21

RESULT 3137

ABL57072/C

ID ABL57072 standard; DNA; 21 BP.

XX

AC ABL57072;

XX

DT 22-JUL-2002 (first entry)

XX

DE Molecular beacon target sequence (single mismatch).

XX

KM Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.

KM

XX

OS Synthetic.

XX

FN Key Location/Qualifiers

FT misc\_feature 9

FT /\*tag= a

FT /note= "mismatch site"

XX

PN W0200218951-A2.

XX

PD 07-MAR-2002.

XX

PF 29-AUG-2001; 2001WO-US041941.

XX

PR 29-AUG-2000; 2000US-0228728P.

PR 30-MAR-2001; 2001US-0280350P.

XX

PA (VVRQ ) UNIV ROCKEFELLER.

XX

PI Dubertret B, Calame M, Libhaber A;

```
XX WPI; 2002-404569/43.
DR
XX
XX Sensitive detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.
XX
XX Example 3; Page 62; 62pp; English.
XX
CC The present sequence is that of a single mismatch target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridized termini. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Experiments with the present
CC sequence and a perfectly-matched target (see ABL57071) showed that
CC hybridisation was very specific to the matched target. The invention
CC relates generally to the use of metal surface quenchers such as particles
CC or films for high sensitivity applications in, for example, detection and
CC diagnostic systems
XX
SQ Sequence 21 BP; 14 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4461 GACCTTTTCTTTTCTT 4478
DB 19 GAGCTTTTGTGTTT 2
RESULT 3138
AAD22716/c
ID AAD22716 standard; DNA; 21 BP.
XX
AC AAD22716;
XX
DT 26-FEB-2002 (first entry)
XX
DE Fluorescent-oligonucleotide Flu. 4 used for hybridisation.
XX
KM Oligonucleotide array; hydrophobic attachment layer; diagnosis;
KM cholesterol; genetic analysis; DNA chip; hybridisation; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Fluorescein labelled guanosine"
XX
XX WO200179544-A1.
XX
XX 25-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-KR000514.
XX
XX 14-APR-2000; 2000KR-00019557.
XX
XX (GENO-) GENOTECH CORP.
XX
XX KIm J, Cha S;
XX
XX WPI; 2002-026037/03.
XX
XX Attaching oligonucleotide on support by fluidizing hydrophobic attachment
```

```
PT layer applied on support, spotting oligonucleotide solution having one of
PT its ends bonded to hydrophobic group on layer and solidifying layer.
XX
XX Example 1; Page 12; 32pp; English.
XX
XX The invention relates to a method for attaching oligonucleotide to a
XX solid support and an oligonucleotide array. The oligonucleotide array is
XX prepared by applying hydrophobic attachment layer onto a support which
XX can be solidified under certain conditions, spotting certain portions of
XX said attachment layer with aqueous oligonucleotide solution in which
XX hydrophobic groups are bonded to 3' or 5' terminals and solidifying said
XX attachment layer. The method is useful for attaching a oligonucleotide
XX (preferably a PCR amplified product from a PCR with its 5' terminal
XX bonded to a hydrophobic group) onto support. The method is useful in the
XX area of genetic diagnosis and analysis, and DNA chips which are based on
XX hybridisation. The present sequence is fluorescent oligonucleotide useful
XX in hybridisation
XX
SQ Sequence 21 BP; 11 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2904 TGCTTGTTCCTTCCTAT 2921
DB 20 TGACTTCCTTCCTTCAT 3
RESULT 3139
ABS98296/c
ID ABS98296 standard; DNA; 21 BP.
XX
XX ABS98296;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human lactoferrin (LTF) gene polymorphic sequence #59.
XX
DE Human; db: cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
XX
XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF;
XX
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR117;
XX
XX aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS;
XX
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX
XX HMMT; kallikrein 2; KIK2; nicotinamide-N-methyl transferase; NNMT;
XX
XX NADPH quinone oxidoreductase 2; NQO2; sulfoxtransferase thermolabile; STM;
XX
XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
XX
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX
XX central nervous system; pulmonary; immunological; SNP;
XX
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200257410-A2.
XX
XX 25-JUL-2002.
XX
XX 28-NOV-2001; 2001WO-US044838.
XX
XX 28-NOV-2000; 2000US-00724389.
XX
XX (DNAS-) DNA SCI LAB INC.
XX
XX Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
```

PT Isolated nucleic acid molecules having polymorphisms in known human genes  
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
 PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.

XX Example 23; Page 149; 714pp; English.

CC This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),  
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 CC transferase (HNMT), kallikrein 2 (KIK2), nicotinamide -N-methyl  
 CC sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1  
 CC (MDR1), lactocortisterin (LRF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHRM1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,  
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered pulmonary,  
 CC immunological or haematological function, in KIK2 for altered serine  
 CC protease activity in the prostate, in LRF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention

XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 86.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6049 GTTCTCTCATGCTTTT 6066

DB 20 GTATCTCATGCTGCTT 3

RESULT 3140  
 ABL51321

ID ABL51321 standard; DNA; 21 BP.

AC ABL51321;

DT 27-JUN-2002 (first entry)

DE Bacteriophage lambda related LAMP primer SEQ ID NO:55.

KW Bacteriophage lambda: loop mediated isothermal amplification; LAMP;

KW polynucleotide synthesis; single nucleotide polymorphism; SNP;

KW identification; primer; ss.

OS Bacteriophage lambda.

OS Synthetic.

XX

PN WO200224902-A1.

XX 28-MAR-2002.

PF 19-SEP-2001; 2001WO-JP008142.

PR 19-SEP-2000; 2000JP-00283862.

PA (BIKE ) BIKEN KAGAKU KK.

PI Nagamine K;

DR WPI; 2002-315737/35.

PT Rapid isothermal polynucleotide synthesis using loop-mediated  
 PT amplification for simple detection of single nucleotide polymorphisms.

XX Example 4; Page 68; 135pp; Japanese.

CC The present invention describes a method for polynucleotide synthesis by  
 CC loop-mediated isothermal amplification (LAMP). The method comprises: (a)  
 CC identifying a target sequence on the template and a set of primers (inner  
 CC and outer primer) hybridised to it and annealed to form a single-stranded  
 CC polynucleotide with a loop at each end, followed by self-primed strand  
 CC displacement complementary chain synthesis to form a two-stranded  
 CC polynucleotide having a loop at one end and containing two copies of the  
 CC template; (b) using a second (loop) primer set to initiate complementary  
 CC chain synthesis at a different position; (c) repeating the process; and  
 CC (d) carrying out DNA polymerase catalysed complementary chain synthesis.  
 CC The method is simple and efficient for polynucleotide amplification,  
 CC allowing easy identification of the presence of single nucleotide  
 CC polymorphisms (SNP). The method is isothermal, produces a high degree of  
 CC amplification in a short time, and since it uses primers hybridising to  
 CC several different sequences on the template it is highly accurate,  
 CC without the amplification of irrelevant sequences which is a problem in  
 CC conventional methods. The present sequence represents a primer which is  
 CC used in an example from the present invention

XX Sequence 21 BP; 4 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;

Best Local Similarity 86.9%; Pred. No. 2.1e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4368 ACAAGCTGGGGAATTTTG 4385

DB 2 ACAAGCTGGCGCATTTTG 19

RESULT 3141  
 ABQ94035

ID ABQ94035 standard; DNA; 21 BP.

AC ABQ94035;

DT 21-OCT-2002 (first entry)

DE NOV15 forward PCR primer #2.

KW Human; NOV; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;

KW Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;

KW Antiaesthetic; Nephrotoxic; Hepatotoxic; Neuroprotective; Nootropic;

KW Antibacterial; Vitruice; Antiparasitic; Relaxant; Anticonvulsant;

KW Gene Therapy; NOV; cancer; heart disease; inflammation;

KW autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity;

KW asthma; IGA nephropathy; cirrhosis; arthritis; Alzheimer's disease;

KW infection; stroke; muscular dystrophy; epilepsy; wasting disorder; PCR;

OS primer; ss.

OS Homo sapiens.

OS WO200255704-A2.

XX

PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002MO-US000554.  
XX  
PR 09-JAN-2001; 2001US-0260417P.  
XX 10-JAN-2001; 2001US-0260831P.  
PR 28-FEB-2001; 2001US-0272338P.  
PR 09-MAR-2001; 2001US-0274876P.  
PR 18-APR-2001; 2001US-0284704P.  
XX  
PA (CUBA-) CUBAGEN CORP.  
XX  
PI Padigaru M., Li L., Zernusen BD, Caesman SJ, Shenoy S, Spytek KA;  
PI Phong M, Gangoli EA, Burgess CE, Patrujan M, Vernet CAM;  
PI Taylor S, Tchernev VT, Miller CE, Guo X, Bolding FC, Grose WM;  
PI Albrock JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K,  
PI MacDougall J, Malankar U, Millet I, Peyman J, Smithson G;  
PI Gunther E, Stone DJ;  
XX  
DR WPI; 2002-590674/63.  
XX  
PT NOVX polypeptides and encoding polymucleotides, useful for preventing or  
PT treating NOVX-associated disorders e.g. cancer, inflammation, or  
PT Alzheimer's disease, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
PS Example 3; Page 316; 358pp; English.  
XX  
CC The present invention relates to coding sequences for NOV proteins  
CC (ABN85578-ABN95403 and ABN94401-ABN94424). The NOV proteins and coding  
CC sequences are useful for treating or preventing NOV-associated disorders  
CC or in the manufacture of a medicament for treating the disorders, such as  
CC cancer, heart disease, inflammation, autoimmune disorders, allergies,  
CC blood disorders, AIDS, diabetes, obesity, asthma, IGA nephropathy,  
CC cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial,  
CC viral, parasitic), stroke, muscular dystrophy, epilepsy, and other  
CC wasting disorders associated with chronic diseases. The present sequence  
CC is a PCR primer for a NOV coding sequence, which was used in an example  
CC from the invention  
XX  
SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 3683 GCCAGAAAGCCAGCTATT 3700  
DB |||||  
1 GCCAGAAAGGCAACTATT 18

RESULT 3142  
ABX96561  
ID ABX96561 standard; DNA; 21 BP.  
XX  
AC ABX96561;  
XX  
DT 14-MAY-2003 (first entry)  
XX  
DE Human genomic DNA mchfr SNP primer #5.  
XX  
KW Human; allele-specific base detection; primer extension reaction;  
KW base-specific detection primer; allele-specific primer extension assay;  
KW AS; high throughput; single nucleotide polymorphism; SNP analysis;  
KW mutation detection; genetic variation; allele-specific extension; primer;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200268684-A2.  
XX  
PD 06-SEP-2002.

```

XX 22-FEB-2002; 2002MO-GB000794.
PF 23-FEB-2001; 2001IG-00004560.
XX 23-FEB-2001; 2001US-00791190.
PR 07-FEB-2002; 2002US-00071926.
XX
XX (PYRO-) PYROSEQUENCING AB.
PA (DZIE/) DZIEGLEWSKA H.
XX
XX Lundeberg J, Ahmadian A, Nyren P;
PI WPI; 2002-707012/76.
XX
XX Detecting a base at a pre-determined position in a nucleic acid molecule,
XX comprises performing primer extension reactions using base-specific
XX detection primers in the presence of a nucleotide-degrading enzyme.
XX
XX Example 1; Page 26; 59pp; English.
XX
XX The present invention relates to a method for detecting a base at a pre-
XX determined position in a nucleic acid molecule. The method comprises
XX performing primer extension reactions using base-specific detection
XX primers, each being specific for a particular base at the predetermined
XX position. The allele-specific (AS) primer extension assay method of the
XX invention is useful for detecting an allele-specific base at a pre-
XX determined position in a nucleic acid molecule, for high throughput
XX single nucleotide polymorphism (SNP) analysis, and for detecting
XX mutations and genetic variations. The new method solves the deficiencies
XX of previous methods by providing a method of allele-specific extension
XX that allows accurate discrimination between matched and mismatched
XX configurations, as well as reducing or eliminating false positive results
XX observed in prior art. The use of two allele-specific primers increases
XX the sensitivity by a factor of two because signals of two extensions are
XX obtained. The present sequence represents a primer used in the examples
XX of the present invention
XX
SQ Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+03;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 5816 CTATGTCGATGATGAATC 5833
XX |||||
XX 2 CTGCGTATGATGAATC 19
XX
RESULT 3143
ABX96562
ID ABX96562 standard; DNA; 21 BP.
XX
XX AC ABX96562;
XX
XX DT 14-MAY-2003 (first entry)
XX
XX DE Human genomic DNA mtfr SNP primer #6.
XX
XX KW Human: allele-specific base detection; primer extension reaction;
XX KW base-specific detection primer; allele-specific primer extension assay;
XX KW AS; high throughput; single nucleotide polymorphism; SNP analysis;
XX KW mutation detection; genetic variation; allele-specific extension; primer;
XX KW 88.
XX
XX OS Homo sapiens.
XX
XX PN WO200268684-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 22-FEB-2002; 2002MO-GB000794.
XX
XX PR 23-FEB-2001; 2001IG-00004560.
XX PR 23-FEB-2001; 2001US-00791190.

```



PR 07-FEB-2002; 2002US-00071926.  
XX  
XX (PYRO-) PYROSEQUENCING AB.  
PA (DZIE//) DZIELEWSKA H.  
XX  
XX  
PI Lundberg J, Ahmadian A, Nyren P;  
XX WPI; 2002-707012/76.  
DR  
XX  
XX Detecting a base at a pre-determined position in a nucleic acid molecule,  
PT comprises performing primer extension reactions using base-specific  
PT detection primers in the presence of a nucleotide-degrading enzyme.  
XX  
XX Example 1; Page 26; 59pp; English.  
XX  
XX The present invention relates to a method for detecting a base at a pre-  
CC determined position in a nucleic acid molecule. The method comprises  
CC performing primer extension reactions using base-specific detection  
CC primers, each being specific for a particular base at the predetermined  
CC position. The allele-specific (AS) primer extension assay method of the  
CC invention is useful for detecting an allele-specific base at a pre-  
CC determined position in a nucleic acid molecule, for high throughput  
CC single nucleotide polymorphism (SNP) analysis, and for detecting  
CC mutations and genetic variations. The new method solves the deficiencies  
CC of previous methods by providing a method of allele-specific extension  
CC that allows accurate discrimination between matched and mismatched  
CC configurations, as well as reducing or eliminating false positive results  
CC observed in prior art. The use of two allele-specific primers increases  
CC the sensitivity by a factor of two because signals of two extensions are  
CC obtained. The present sequence represents a primer used in the examples  
CC of the present invention  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 5816 CTATGTGATGATGAATC 5833  
DB 2 CTGCGTGTGATGAATC 19  
RESULT 3144  
AADS0224  
ID AADS0224 standard; DNA; 21 BP.  
XX  
AC AADS0224;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE Human GALT 8 specific PCR primer #2.  
XX  
XX Human; cystic fibrosis; Tay-sachs; familial hypercholesterolaemia; FH;  
KM fragile X syndrome; haemophilia A; diabetes; cystinuria; tyrosinaemia;  
KM urea cycle disorder; hereditary fructose intolerance; Baker's disease;  
KM Wilson's disease; alcaptonuria; adult polycystic kidney disease; MCAD;  
KM Huntington's disease; myotonic dystrophy; retinitis pigmentosa; cancer;  
KM Gaucher's disease; Canavan's disease; galactosaemia; thrombocytopaenia;  
KM thalassaemia; sickle cell disease; phenylketonuria; Marfan's syndrome;  
KM haemoglobinopathy; Bloom syndrome; Neimann Pick's disease; PCR; primer;  
KM haemolysis-1-phosphate uridylyl transferase; GALT; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200290374-A1.  
XX  
PD 14-NOV-2002.  
XX  
XX 06-MAY-2002; 2002WO-US014562.  
XX  
XX 08-MAY-2001; 2001US-00851501.  
XX

PA (AMBR-) AMERY GENETICS CORP.  
XX  
XX Dunlop CLM, Weisel JM;  
XX  
XX WPI; 2003-103498/09.  
DR  
XX  
XX PT Identifying the presence or absence of a mutation or polymorphism in a  
PT subject, useful for diagnosing genetic diseases, comprises generating  
PT extension products and analyzing the melting behavior of the mixed DNA  
PT sample.  
XX  
PS Claim 56; Page 45; 49pp; English.  
XX  
XX The invention relates to a method for identifying the presence or absence  
CC of a mutation or polymorphism in a plurality of genes. The method is used  
CC for identifying the presence or absence of a mutation or polymorphism in  
CC a subject, or the presence or absence of several genetic markers in a  
CC subject for diagnosing genetic diseases, e.g. cystic fibrosis, Tay-sachs,  
CC familial hypercholesterolaemia (FH), thalassaemia, sickle cell disease,  
CC phenylketonuria, galactosaemia, fragile X syndrome, haemophilia A,  
CC myotonic dystrophy, medium-chain acyl CoA dehydrogenase, maturity onset  
CC diabetes, cystinuria, methylenic aciduria, urea cycle disorders,  
CC hereditary fructose intolerance, hereditary haemochromatosis, neonatal  
CC alcaptonuria, hypolactasia, Baker's disease, argininaemia adenomatous  
CC polypsis coli (APC), adult polycystic kidney disease, Duchenne muscular  
CC dystrophy, alpha-1-antitrypsin deficiency, hereditary non-polyposis  
CC colorectal cancer, Huntington's disease, neurofibromatosis, Marfan's  
CC syndrome, osteogenesis imperfecta, retinoblastoma, Friedreich's ataxia,  
CC haemoglobinopathies, MCAD, Canavan's disease, Leber's hereditary optic  
CC neuropathy, retinitis pigmentosa, Bloom syndrome, Fanconi's anaemia, or  
CC Neimann Pick's disease. The present sequence is human galactose-1-  
CC phosphate uridylyl transferase (GALT) specific PCR primer used to  
CC illustrate the method of the invention  
XX  
SQ Sequence 21 BP; 5 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 597 CTCATCATGAGTGCTAGC 614  
DB 4 CTCATCATGAGTGCTAGC 21  
RESULT 3145  
ACDS0312  
ID ACDS0312 standard; RNA; 21 BP.  
XX  
AC ACDS0312;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV ribozyme substrate sequence #10.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KM RNA stability; RNA expression; RNA synthesis; antisense;  
KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinczyme;  
KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KM HBV reverse transcriptase; Enhancer I region; viral replication;  
KM degenerative disease state; HBV infection; HCV infection; cirrhosis;  
KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KM virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX



XX The present invention provides the protein and coding sequences of four  
CC novel human G-protein coupled receptors (GPCR) which are amplified in  
CC breast cancers. The sequences are useful in the treatment of cancers,  
CC including breast and prostate cancers. The present sequence is a PCR  
CC primer used to isolate a coding sequence for a GPCR of the invention  
XX

Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3894 CTGAGTACTTCTCTAG 3911  
Db 18 CTGAGTACTTCTCTAG 1

RESULT 3148  
ADA09668  
ID ADA09668 standard; DNA; 21 BP.  
XX  
AC ADA09668;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human G protein-coupled receptor HGRBM76 Taqman PCR probe.  
XX

88; human; HGRBM76; G protein-coupled receptor;  
KW male reproductive condition; amine disorder; testicular disorder;  
KW testicular cancer; choriocarcinoma; nonseminoma; seminoma;  
KW spermatogenesis; infertility; Klinefelter's syndrome; XX male;  
KW epididymitis; genital wart; germinal cell aplasia of the testis;  
KW cryptorchidism; varicocele; immature cilia syndrome; viral orchitis;  
KW premature puberty; incomplete puberty; Kallman syndrome;  
KW Cushing's syndrome; hyperprolactinemia; haemochromatosis;  
KW congenital adrenal hyperplasia; follicle stimulating hormone deficiency;  
KW granulomatous disease; PCR; probe; reverse transcriptase PCR; RT-PCR.  
XX  
OS Homo sapiens.  
XX  
PN US2003064381-A1.  
XX  
PD 03-APR-2003.  
XX  
PF 07-MAR-2002; 2002US-00092771.  
XX  
PR 07-MAR-2001; 2001US-0273963P.  
PR 27-MAR-2001; 2001US-0278927P.  
XX

(FEDE/) FEDER J N.  
PA (RAMA/) RAMANATHAN C S.  
PA (MINT/) MINTIER G A.  
PA (CACA/) CACACE A.  
PA (BARB/) BARBER L E.  
PI Feder JN, Ramanathan CS, Mintier GA, Cacace A, Barber LE;  
XX WPI; 2003-555589/52.  
XX

New human G-protein coupled receptor HGRBM76 polypeptides and nucleic  
PT acids, useful for preventing, treating or ameliorating e.g. testicular  
PT disorder, choriocarcinoma, infertility, viral orchitis, or Cushing's  
PT syndrome.  
XX  
PS Example 4; Page 78; 149pp; English.  
XX

The invention relates to an isolated nucleic acid molecule encoding a G  
CC protein-coupled receptor HGRBM76. The nucleotide sequence comprises  
CC sequential nucleotide deletions from either the C-terminus or the N-  
CC terminus. Also included are an isolated polypeptide encoded by the  
CC nucleic acid, a recombinant vector comprising the nucleic acid, making a  
CC recombinant host cell comprising the nucleic acid, diagnosing a

CC pathological condition or a susceptibility to a pathological condition in  
CC testicular tissue of a subject, identifying a compound that modulates the  
CC biological activity of a human G-protein coupled receptor HGRBM76 (and  
CC a member consisting of NFAT/CRE or NFAT G alpha 15, all undefined), and  
CC screening for candidate compounds capable of modulating activity of the  
CC HGRBM76 polypeptide. The HGRBM76 polypeptides, polynucleotides,  
CC compounds or pharmaceutical preparations comprising HGRBM76 are useful  
CC for preventing, treating or ameliorating a male reproductive condition;  
CC an amine disorder or a condition where G-protein coupled receptors are  
CC (in)directly involved in disease progression, a testicular disorder,  
CC testicular cancer, choriocarcinoma, nonseminoma, seminoma,  
CC spermatogenesis, infertility, Klinefelter's syndrome, XX male,  
CC epididymitis, genital warts, germinal cell aplasia of the testis,  
CC cryptorchidism, varicocele, immature cilia syndrome, viral orchitis,  
CC premature puberty, incomplete puberty, Kallman syndrome, Cushing's  
CC syndrome, hyperprolactinemia, haemochromatosis, congenital adrenal  
CC hyperplasia, follicle stimulating hormone (FSH) deficiency and  
CC granulomatous disease. The present sequence is a reverse transcriptase  
CC (RT)-PCR probe used to determine the tissue expression profile of  
CC HGRBM76 mRNA.  
XX  
XX

Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 954 CCTCAGGACTCTCAGCG 971  
Db 1 CCCACGAGCTCCACGG 18

RESULT 3149  
AD16552/C  
ID AD16552 standard; RNA; 21 BP.  
XX  
AC AD16552;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Short interfering double-stranded RNA oligonucleotide SEQ ID NO:277.  
XX

expression interference; expression inhibition; target gene;  
KW short interfering double stranded RNA; cytosolic; gene therapy;  
KW proliferative disease; cancer; ds.  
XX  
OS Synthetic.  
XX  
PN WO2003012052-A2.  
XX  
PD 13-FEB-2003.  
XX  
PF 30-JUL-2002; 2002WO-US024226.  
XX  
PR 30-JUL-2001; 2001US-0308640P.  
PR 08-APR-2002; 2002US-0370970P.  
XX

(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (CARN-) CARNEGIE INST WASHINGTON.  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX

Caplen NJ, Morgan RA, Fire A, Parrish S, Mousaes S,  
PI Kallionemi O, Cornelison JR, Alton EW, Griesenbach U;  
XX WPI; 2003-248169/24.  
XX

New RNA comprising double stranded RNA and a 3' or 5' overhang having a  
PT length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse  
PT genetic and/or therapeutic tools for interfering or inhibiting expression  
PT of a target gene.  
XX  
PS Claim 71; SEQ ID NO 277; 176pp; English.  
XX

CC The present invention describes an RNA (I) used for the interference or  
 CC inhibition of expression of a target gene, where (I) comprises double  
 CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang  
 CC having a length of 0-nucleotide to 5-nucleotides on each strand, where  
 CC the sequence of the double stranded RNA is substantially identical to a  
 CC portion of a mRNA or transcript of the target gene. Also described: (1)  
 CC interfering with or inhibiting the expression of a target gene in a cell  
 CC by exposing the cell to an amount of (1); (2) a gene silencing array  
 CC comprising a substantially flat substrate, and addressably arrayed  
 CC different double-stranded RNAs; (3) an array-based method of assessing a  
 CC phenotypic effect of a double-stranded RNA on a target gene; (4)  
 CC validating a gene as a potential drug target for a disease or condition;  
 CC (5) selecting an optimised sequence of a double-stranded RNA for  
 CC interference with or inhibition of expression of a target gene in a cell;  
 CC and (6) a short double-stranded RNA effective for interfering with or  
 CC inhibiting expression of a target gene comprising any of 311 20-78  
 CC nucleotide sequences (see ADCl6276 to ADCl6586). (I) has cytostatic  
 CC activity, and can be used in gene therapy. The RNAs are useful as reverse  
 CC genetic and/or therapeutic tools for interfering or inhibiting expression  
 CC of a target gene. They are useful for treating proliferative diseases,  
 CC e.g. cancer.

XX  
 SQ Sequence 21 BP; 4 A; 6 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4926 GACTGTTGAGTAAGTCTCT 4943  
 |||||  
 Db 20 GACTGCTGAGGAACTCTCT 3

RESULT 3150  
 ADD14587  
 ID ADD14587 standard; DNA; 21 BP.  
 XX  
 AC ADD14587;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human src biomarker reverse PCR primer SEQ ID NO:776.  
 XX  
 KM predictor set; protein tyrosine kinase activity modulator;  
 KM protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;  
 KM gene therapy; drug sensitivity; genetic profile; cancer; human;  
 KM PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003062395-A2.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 17-JAN-2003; 2003WO-US001981.  
 XX  
 PR 18-JAN-2002; 2002US-0350061P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Huang F, Fairchild CR, Lee FY, Shaw P;  
 XX  
 DR WPI; 2003-636735/60.  
 XX  
 PT New polynucleotides and polypeptides for predicting the activity of  
 PT compounds that interact with protein tyrosine kinases and/or protein  
 PT tyrosine kinase pathways.  
 XX  
 PS Example 2; SEQ ID NO 776; 139pp; English.  
 XX  
 CC The present invention describes a predictor set comprising a plurality of  
 CC polynucleotides or polypeptides whose expression pattern is predictive of

CC the response of cells to treatment with a compound that modulates protein  
 CC tyrosine kinase activity or members of the protein tyrosine kinase  
 CC pathway. Also described: (1) predicting whether a compound is capable of  
 CC modulating the activity of cells, comprising obtaining a sample of cells,  
 CC determining whether the cells express a plurality of markers, and  
 CC correlating the expression of the markers to the compound's ability to  
 CC modulate the activity of the cells; (2) a plurality of cell lines for  
 CC identifying polynucleotides and polypeptides whose expression levels  
 CC correlate with compound sensitivity or resistance of cells associated  
 CC with a disease state; and (3) identifying polynucleotides and  
 CC polypeptides that predict compound sensitivity or resistance of cells  
 CC associated with a disease state, comprising subjecting the plurality of  
 CC cell lines to one or more compounds, analysing the expression pattern of  
 CC a microarray of polynucleotides or polypeptides, and selecting  
 CC polynucleotides or polypeptides that predict the sensitivity or  
 CC resistance of cells associated with a disease state by using the  
 CC expression pattern of the microarray. The polynucleotides and  
 CC polypeptides have cytostatic activities, and can be used in gene therapy.  
 CC The polynucleotides and polypeptides are useful in predicting the  
 CC activity of compounds that interact with protein tyrosine kinases and/or  
 CC protein tyrosine kinase pathways. These may be used in determining drug  
 CC sensitivity in patients to allow the development of individualized  
 CC genetic profiles which aid in treating diseases and disorders (e.g.  
 CC cancer) based on patient response at a molecular level. The present  
 CC sequence is used in the exemplification of the present invention.

XX  
 SQ Sequence 21 BP; 2 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4219 TCCTTCCTCTGTCAGAT 4236  
 |||||  
 Db 2 TCCTGCTCTGTCAGAT 19

RESULT 3151  
 ADD14405/C  
 ID ADD14405 standard; DNA; 21 BP.  
 XX  
 AC ADD14405;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human src biomarker reverse PCR primer SEQ ID NO:594.  
 XX  
 KM predictor set; protein tyrosine kinase activity modulator;  
 KM protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;  
 KM gene therapy; drug sensitivity; genetic profile; cancer; human;  
 KM PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003062395-A2.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 17-JAN-2003; 2003WO-US001981.  
 XX  
 PR 18-JAN-2002; 2002US-0350061P.  
 XX  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 PI Huang F, Fairchild CR, Lee FY, Shaw P;  
 XX  
 DR WPI; 2003-636735/60.  
 XX  
 PT New polynucleotides and polypeptides for predicting the activity of  
 PT compounds that interact with protein tyrosine kinases and/or protein  
 PT tyrosine kinase pathways.  
 XX

PS Example 2; SEQ ID NO 594; 139pp; English.

XX The present invention describes a predictor set comprising a plurality of  
 CC polynucleotides or polypeptides whose expression pattern is predictive of  
 CC the response of cells to treatment with a compound that modulates protein  
 CC tyrosine kinase activity or members of the protein tyrosine kinase  
 CC pathway. Also described: (1) predicting whether a compound is capable of  
 CC modulating the activity of cells, comprising obtaining a sample of cells,  
 CC determining whether the cells express a plurality of markers, and  
 CC correlating the expression of the markers to the compound's ability to  
 CC modulate the activity of the cells; (2) a plurality of cell lines for  
 CC identifying polynucleotides and polypeptides whose expression levels  
 CC correlate with compound sensitivity or resistance of cells associated  
 CC with a disease state; and (3) identifying polynucleotides and  
 CC polypeptides that predict compound sensitivity or resistance of cells  
 CC associated with a disease state, comprising subjecting the plurality of  
 CC cell lines to one or more compounds, analysing the expression pattern of  
 CC a microarray of polynucleotides or polypeptides, and selecting  
 CC polynucleotides or polypeptides that predict the sensitivity or  
 CC resistance of cells associated with a disease state by using the  
 CC expression pattern of the microarray. The polynucleotides and  
 CC polypeptides have cytoskeletal activities, and can be used in gene therapy.  
 CC The polynucleotides and polypeptides are useful in predicting the  
 CC activity of compounds that interact with protein tyrosine kinases and/or  
 CC protein tyrosine kinase pathways. These may be used in determining drug  
 CC sensitivity in patients to allow the development of individualized  
 CC genetic profiles which aid in treating diseases and disorders (e.g.  
 CC cancer) based on patient response at a molecular level. The present  
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 6 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6555 GCTGTTGGACAGCTTTG 6572  
 |||||  
 Db 20 GCAGTGGGAAAGTTTG 3

RESULT 3152  
 ADE27642/C  
 ID ADE27642 standard; RNA; 21 BP.  
 AC ADE27642;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:586.  
 XX  
 KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;  
 KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;  
 KW antiarteriosclerotic; cytoskeletal; virucide; obesity; diabetes;  
 KW atherosclerosis; cancer; viral infection; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003070885-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 13-FEB-2003; 2003WO-US004317.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 20-SEP-2002; 2002US-0412304P.  
 PR 15-JAN-2003; 2003US-0440129P.

XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PA Mcswigen J, Beigelman L, Thompson J;  
 P1 WPI; 2003-721687/68.  
 XX  
 DR  
 XX  
 PT New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of obesity or diabetes, downregulates expression of the  
 PT stearoyl-CoA desaturase gene.  
 XX  
 PS Example 3; SEQ ID NO 586; 139pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene  
 CC by RNA interference. Also described: (1) modulating expression of SCD  
 CC genes in cells, tissue explants or organisms by introduction of siNA; (2)  
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
 CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytoskeletal and  
 CC virucide activities. The siNAs can be used to modulate expression of SCD  
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;  
 CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
 CC They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents an SCD siNA, which is  
 CC used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 5 A; 2 C; 8 G; 2 T; 4 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 7232 TCCCTCAAGTCCAGCA 7249  
 |||||  
 Db 18 TCCATCTCATGTCCAGCA 1

RESULT 3153  
 ADE47931/C  
 ID ADE47931 standard; DNA; 21 BP.  
 AC ADE47931;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOVX reverse PCR primer SEQ ID NO:293.  
 XX  
 KW human; cardiac; antiarteriosclerotic; hypotensive; immunosuppressive;  
 KW dermatological; anorectic; cytoskeletal; antidiabetic; haemostatic;  
 KW anti-IV; antiasthmatic; antibacterial; virucide; neuroprotective;  
 KW nootropic; antiparinsonian; antilipemic; gene therapy; vaccine; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003076642-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024459.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0309511P.  
 PR 08-AUG-2001; 2001US-0310951P.  
 PR 09-AUG-2001; 2001US-0311282P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 14-AUG-2001; 2001US-0312203P.  
 PR 17-AUG-2001; 2001US-0313156P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 20-AUG-2001; 2001US-0313702P.

PR 21-AUG-2001; 2001US-0314031P.  
 PR 23-AUG-2001; 2001US-0314466P.  
 PR 28-AUG-2001; 2001US-0315403P.  
 PR 29-AUG-2001; 2001US-0315853P.  
 PR 31-AUG-2001; 2001US-0316508P.  
 PR 21-SEP-2001; 2001US-0323936P.  
 PR 03-DEC-2001; 2001US-0338078P.  
 PR 05-FEB-2002; 2002US-0354655P.  
 PR 05-MAR-2002; 2002US-0361764P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 15-MAY-2002; 2002US-0380971P.  
 PR 15-MAY-2002; 2002US-0380980P.  
 PR 16-MAY-2002; 2002US-0381039P.  
 PR 28-MAY-2002; 2002US-0383761P.  
 PR 29-MAY-2002; 2002US-0383887P.  
 PR 01-AUG-2002; 2002US-00210130.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Zernusen BD, Paturajan M, Kekuda R, Miller CE, Rieger DK;  
 PI Pena CE, Shimeles RA, Li L, Berghs C, Zhong M, Caeman SU, Voss EZ;  
 PI Bolido FL, Padigaru M, Smithson G, Shenoy SG, Ji W, German L;  
 PI Verneet CM, Lette MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;  
 PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Raselli L, Agee ML;  
 PI Chaudhuri A, Chant JS, DiPippo VA, Edinger SR, Eisen A, Gangolli EA;  
 PI Glot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;  
 PI Tsaplier RJ, Catterton E;  
 XX  
 DR WPI; 2003-779062/73.  
 XX  
 PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, diabetes,  
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing  
 PT or pharmacogenomics.  
 PT  
 PS Example 49; SEQ ID NO 293; 562bp; English.  
 XX  
 CC The invention relates to a novel (NOVX) human polypeptide. A polypeptide  
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,  
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,  
 CC haemostatic, anti-HIV, antiasthmatic, antibacterial, virucide,  
 CC neuroprotective, nootropic, antiparkinsonian, and antilipaeic activity.  
 CC A polynucleotide encoding a polypeptide of the invention may have a use  
 CC in gene therapy and as a vaccine. A polypeptide of the invention is  
 CC useful in the manufacture of a medicament for treating a syndrome  
 CC associated with a human disease, the disease selected from a pathology  
 CC associated with the polypeptide. These may also be used in diagnosing,  
 CC treating or preventing NOVX-associated disorders such as cardiomyopathy,  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,  
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,  
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's  
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting  
 CC disorders associated with chronic diseases. The nucleic acids are also  
 CC used as hybridisation probes, in chromosome mapping, tissue typing,  
 CC preventive medicine, and pharmacogenomics. The polypeptides are also  
 CC useful as vaccines. The present sequence represents a PCR primer used in  
 CC the invention.  
 CC  
 XX  
 SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 21;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 7384 TGTACAGTTCCTCTGAA 7401  
 Db 19 TGTCCAGTTCCTCTGAA 2  
 RESULT 3154  
 AAT78996  
 ID AAT78996 standard; DNA; 22 BP.

XX  
 AC AAT78996;  
 XX  
 DT 13-JAN-1998 (first entry)  
 XX  
 DE Human Huntington's disease gene intron 1 3' acceptor site.  
 XX  
 KW Huntington's disease; animal model; transgenic animal; human; therapy;  
 KW drug screening; Hdh gene; ss.  
 OS Homo sapiens.  
 XX  
 PN CA2178022-A.  
 XX  
 PD 02-DEC-1996.  
 XX  
 PF 03-JUN-1996; 96CA-02178022.  
 XX  
 PR 01-JUN-1995; 95US-00457273.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Hayden M, Lin B, Nasir J;  
 XX  
 DR WPI; 1997-298677/28.  
 XX  
 PT Mouse Huntington's Disease Gene - useful for generating transgenic mice  
 PT as a model of Huntington's Disease.  
 PT  
 PS Disclosure; Page 60; 69pp; English.  
 PS  
 CC This oligonucleotide comprises the 5' acceptor site of intron 1 of the  
 CC human Huntington's disease (HD) gene. The splice site sequences for the  
 CC first 5 exons of the mouse HD gene (see AAT78997) and the human HD gene  
 CC were compared (see AAT78985-T79002). Targeted disruption of the murine HD  
 CC gene, e.g. at exon 5, can be used to examine the function of the HD gene  
 CC and its role in development. Transgenic mice can be used as models of HD  
 CC  
 XX  
 SQ Sequence 22 BP; 2 A; 3 C; 1 G; 16 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4463 CTTTCTTTTCTTTTCTTTT 4480  
 Db 3 CTTCTTTTCTTTTCTTTT 20  
 RESULT 3155  
 AAT94992/C  
 ID AAT94992 standard; DNA; 22 BP.  
 XX  
 AC AAT94992;  
 XX  
 DT 02-APR-1998 (first entry)  
 XX  
 DE Primer 6 for sequencing of human leukocyte antigen class I genes.  
 XX  
 KW Human leukocyte antigen-C class I gene; HLA-C; exon 1; exon 5;  
 KW locus specific nucleic acid amplification; HLA typing; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9731126-A1.  
 XX  
 PD 28-AUG-1997.  
 XX  
 PF 20-FEB-1996; 96WO-US002408.  
 XX  
 PR 20-FEB-1996; 96WO-US002408.  
 XX

PA (PEKE ) PERKIN-ELMER CORP.  
 XX Johnston-Dow L, Chadwick RB, Parham P;  
 XX WPI; 1997-435175/40.  
 DR WPI; 1997-435175/40.  
 XX Amplification and sequencing primers specific for HLA class I genes -  
 PT useful for locus specific nucleic acid amplification for HLA typing.  
 XX Claim 10; Page 57; 105pp; English.  
 XX  
 CC Sequencing primers AAT94987-92 were used to sequence PCR amplified human  
 CC leukocyte antigen (HLA) class I genes. The primers are designed to  
 CC hybridise to exon-intron borders of exons 2, 3 and 4 of the HLA genes.  
 CC PCR primers were used for locus specific nucleic acid amplification for  
 CC HLA typing. Typing HLA-A, -B or -C class I genes comprises providing a  
 CC sample DNA containing a HLA-A, -B or -C class I gene having a 1st and 2nd  
 CC exon and a target sequence, contacting the sample DNA with an  
 CC amplification primer including sequence complementary to sequence located  
 CC in exon 1 of the HLA-A, -B or -C gene, and a second amplification primer  
 CC sequence complementary to sequence located in exon 5 of the HLA-A, -B or  
 CC -C gene. The PCR product is sequenced using the above primers and the  
 CC determined DNA sequence compared with the DNA sequences of known HLA  
 CC types  
 XX  
 SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 942 GCAGCCCAAGCCCTCAG 959  
 DB 21 GCTGCCGAAGCCCTCAG 4  
 RESULT 3156  
 AAT95005/C  
 ID AAT95005 standard; DNA; 22 BP.  
 XX  
 AC AAT95005;  
 XX  
 DT 02-APR-1998 (first entry)  
 XX  
 DE Primer for sequencing exon 4 sense strand of HLA class I genes.  
 XX  
 KW Human leukocyte antigen-C class I gene; HLA-C; exon 1; exon 5;  
 KW locus specific nucleic acid amplification; HLA typing; exon 4; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09731126-A1.  
 XX  
 PD 28-AUG-1997.  
 XX  
 PF 20-FEB-1996; 96WO-US002408.  
 XX  
 PR 20-FEB-1996; 96WO-US002408.  
 XX  
 PA (PEKE ) PERKIN-ELMER CORP.  
 XX  
 PI Johnston-Dow L, Chadwick RB, Parham P;  
 DR WPI; 1997-435175/40.  
 XX  
 PT Amplification and sequencing primers specific for HLA class I genes -  
 XX useful for locus specific nucleic acid amplification for HLA typing.  
 XX Claim 29; Page 62; 105pp; English.  
 XX  
 PS The present sequencing primer was used to sequence PCR amplified human  
 CC leukocyte antigen (HLA) class I genes. The primer is designed to sequence

CC the sense strand of exon 4, from the 5' exon-intron border. PCR primers  
 CC were used for locus specific nucleic acid amplification for HLA typing.  
 CC Typing HLA-A, -B or -C class I genes comprises providing a sample DNA  
 CC containing a HLA-A, -B or -C class I gene having a 1st and 2nd exon and a  
 CC target sequence, contacting the sample DNA with an amplification primer  
 CC including sequence complementary to sequence located in exon 1 of the HLA  
 CC -A, -B or -C gene, and a second amplification primer sequence  
 CC complementary to sequence located in exon 5 of the HLA-A, -B or -C gene.  
 CC The PCR product is sequenced using the above primers and the determined  
 CC DNA sequence compared with the DNA sequences of known HLA types  
 CC  
 XX  
 SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 942 GCAGCCCAAGCCCTCAG 959  
 DB 21 GCTGCCGAAGCCCTCAG 4  
 RESULT 3157  
 AAX59677/C  
 ID AAX59677 standard; DNA; 22 BP.  
 XX  
 AC AAX59677;  
 XX  
 DT 22-JUL-1999 (first entry)  
 XX  
 DE PCR primer p1 used to amplify termamyl-like alpha-amylase DNA.  
 XX  
 KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;  
 KW saccharifier; ethanol; starch; textile desizing; starch liquefaction;  
 KW saccharification process; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX  
 PN W09923211-A1.  
 XX  
 PD 14-MAY-1999.  
 XX  
 PF 30-OCT-1998; 98WO-DK000471.  
 XX  
 PR 30-OCT-1997; 97DK-00001240.  
 PR 14-JUL-1998; 98DK-00000936.  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;  
 PI Kjaerulf S;  
 XX  
 DR WPI; 1999-326987/27.  
 XX  
 PT New Termamyl-like alpha-amylase variants.  
 XX  
 PS Example 10; Page 58; 115pp; English.  
 XX  
 CC The specification describes termamyl-like alpha-amylase variants that  
 CC have altered amino acid sequences to improve properties. The variants are  
 CC produced by creating one or more of the following mutations in amino acid  
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,  
 CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,  
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,  
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,  
 CC K311, E346, K385, G456, M457, K458, P459, G460, T461, V462, T463. The  
 CC variants can be used for washing and/or dishwashing. They can also be  
 CC used in the production of sweeteners and ethanol from starch, and/or for  
 CC textile desizing, and in starch liquefaction and/or saccharification  
 CC processes. The present PCR primer was used to construct the variants of  
 CC the invention  
 XX  
 SQ Sequence 22 BP; 6 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1919 TTGGTGGCATTAAACACA 1936  
 |||||  
 19 TTGGCGGCATTAAATACCA 2

Db

RESULT 3158  
 AAA64619  
 ID AAA64619 standard; DNA; 22 BP.  
 XX  
 AC AAA64619;  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX  
 DE PCR primer used to assess frequency of expression of MAGE-A10 gene.  
 XX  
 KM MAGE-A10; MAGE-A5; MAGE-A8; MAGE-A9; MAGE-A11; tumour rejection antigen;  
 KM human leukocyte antigen; HLA; T cell response; region q28; X chromosome;  
 KM cancer; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200052163-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 01-MAR-2000; 2000MO-US005346.  
 XX  
 PR 02-MAR-1999; 99US-00260978.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Serrano A, Lethe B, Lurquin C, De Plaen E, Rimoldi D;  
 PI Boon-Falleur T;  
 XX  
 DR WPI; 2000-579285/54.  
 XX  
 PT Complementary polynucleotide of MAGE family, useful in the diagnosis of  
 PT cancer in a patient.  
 XX  
 PS Example 1; Page 4; 72pp; English.  
 XX  
 CC PCR primers AAA64618-19 were used in reverse transcription PCR reactions  
 CC to assess the frequency of expression of MAGE-A10 gene. The specification  
 CC describes MAGE-A5, MAGE-A8, MAGE-A9, MAGE-A10 and MAGE-A11. The MAGE  
 CC genes encode tumour rejection antigens which complex to human leukocyte  
 CC antigens (HLAs), and provoke response by autologous, cytolytic T cells.  
 CC The genes are located in region q28 of the X chromosome. The MAGE  
 CC polynucleotides are useful for diagnosis of cancer in a patient  
 XX  
 SQ Sequence 22 BP; 4 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1738 ACCTACTCAGGGCTGCAG 1755  
 |||||  
 3 ACCTCCTCAGGGGTGCAG 20

Db

RESULT 3159  
 AAA90556/c  
 ID AAA90556 standard; DNA; 22 BP.  
 XX  
 AC AAA90556;  
 XX  
 DT 11-JAN-2001 (first entry)  
 XX

DE HLA class I gene sequencing primer #6.  
 XX  
 KM Human leukocyte Antigen class I; HLA-A; antigen presentation; HLA typing;  
 KM organ transplantation; autoimmune disease; sequencing primer;  
 KM infectious disease susceptibility; chromosome 6p21.3; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6103465-A.  
 XX  
 PD 15-AUG-2000.  
 XX  
 PF 03-OCT-1995; 95US-00538666.  
 XX  
 PR 14-FEB-1995; 95US-00390251.  
 XX  
 PA (PEKE ) PERKIN-ELMER CORP.  
 XX  
 PI Parham P, Johnston-Dow L, Chadwick RB;  
 XX  
 DR WPI; 2000-542544/49.  
 XX  
 PT Typing HLA class I genes for organ transplantation, involves contacting  
 PT the sample DNA containing HLA class I gene comprising two exons and a  
 PT target sequence, with amplification primers and detecting the amplicon.  
 XX  
 PS Claim 40; Col 36; 60pp; English.  
 XX  
 CC The present sequence is a sequencing primer for Human Leukocyte Antigen  
 CC (HLA) class I gene. The HLA class I genes are found on chromosome 6p21.3.  
 CC HLA class I proteins are found on the surface of almost all nucleated  
 CC cells and are involved in antigen presentation to immune system cells.  
 CC This primer can be used to type HLA class I genes; by carrying out PCR on  
 CC a sample DNA, comprising HLA class I gene, and detecting the amplicon  
 CC formed using a sequence-specific detection method e.g. DNA sequencing  
 CC (using the present sequence). The present sequence is useful for  
 CC discriminating among the HLA-A, HLA-B, and HLA-C genes and other related  
 CC class I genes and pseudogenes. In addition, the present sequence is  
 CC useful for organ transplantation studies, for the study of autoimmune  
 CC disease and for the determination of susceptibility to infectious disease  
 XX  
 SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

942 GCAGCCCAAGCCCTCAG 959  
 |||||  
 21 GCTGCCGAAGCCCTCAG 4

Db

RESULT 3160  
 AAA90562/c  
 ID AAA90562 standard; DNA; 22 BP.  
 XX  
 AC AAA90562;  
 XX  
 DT 11-JAN-2001 (first entry)  
 XX  
 DE HLA class I gene sequencing primer #12.  
 XX  
 KM Human leukocyte Antigen class I; HLA-A; antigen presentation; HLA typing;  
 KM organ transplantation; autoimmune disease; sequencing primer;  
 KM infectious disease susceptibility; chromosome 6p21.3; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6103465-A.  
 XX  
 PD 15-AUG-2000.  
 XX  
 PF 03-OCT-1995; 95US-00538666.  
 XX



```
XX 14-FEB-1995; 95US-00390251.
PR
XX (PEXE ) PERKIN-ELMER CORP.
XX
XX Parham P, Johnston-Dow L, Chadwick RB;
PI
XX WPI; 2000-542544/49.
DR
XX
XX Typing HLA class I genes for organ transplantation, involves contacting
PT the sample DNA containing HLA class I gene comprising two exons and a
PT target sequence, with amplification primers and detecting the amplicon.
XX
XX Claim 10; Col 35; 60pp; English.
XX
XX The present sequence is a sequencing primer for Human Leukocyte Antigen
CC (HLA) class I gene. The HLA class I genes are found on chromosome 6p21.3.
CC HLA class I proteins are found on the surface of almost all nucleated
CC cells and are involved in antigen presentation to immune system cells.
CC This primer can be used to type HLA class I genes: by carrying out PCR on
CC a sample DNA, comprising HLA class I gene, and detecting the amplicon
CC formed using a sequence-specific detection method e.g. DNA sequencing
CC (using the present sequence). The present sequence is useful for
CC discriminating among the HLA-A, HLA-B, and HLA-C genes and other related
CC class I genes and pseudogenes. In addition, the present sequence is
CC useful for organ transplantation studies, for the study of autoimmune
CC disease and for the determination of susceptibility to infectious disease
CC
XX
SQ Sequence 22 BP; 3 A; 5 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 942 GCAGCCCAAGCCCTCACC 959
DB 21 GCTGCCGAGAGCCCTCAC 4

RESULT 3161
AAZ91959
ID AAZ91959 standard; DNA; 22 BP.
XX
XX AAZ91959;
AC
XX 08-JUN-2000 (first entry)
DT
XX Mahogany protein gene exon 10 primer Celegel17.
DE
XX
XX Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;
KW weight regulation; cell therapy; body weight disorder; cachexia;
KW anorexia; hyperpigmentation; increased metabolic rate disorder;
KW hyperphagia; Antiobesity; anti-anorexic; anticachectic; PCR primer; ss.
XX
XX Mammalia.
OS
XX
XX WO200005373-A2.
PN
XX
XX 03-FEB-2000.
PD
XX
XX 21-JUL-1999; 99WO-US016484.
PF
XX
XX 21-JUL-1998; 98US-0093630P.
PR
XX 20-OCT-1998; 98US-0104978P.
PR
XX 05-FEB-1999; 99US-00245041.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX
XX Moore K, Nagle DL;
PI
XX
XX WPI; 2000-195103/17.
DR
XX
XX New human and murine mahogany genes, useful, e.g. for diagnosis and
PT
```

```
PT treatment of body weight disorders.
XX
XX Example; Fig 5; 189pp; English.
PS
XX
XX This sequence represents a PCR primer for a mahogany gene of the
CC invention. The mahogany genes are used: (i) to produce recombinant
CC mahogany (mg) proteins (ii); (ii) as a source of antisense, ribozyme or
CC triplex-forming therapeutics; (iii) as a source of diagnostic probes and
CC primers for detecting expression of mg genes or mutations, regulatory
CC defects, in this gene, or for isolation of related sequences; and (iv) in
CC (cell-based) gene therapy. (ii) are used to raise specific antibodies
CC (Ab); to identify other (extra)cellular products involved in weight
CC regulation, and to screen for agents that disrupt interaction between
CC (ii) and other macromolecules. The Ab are used to detect abnormal levels
CC (or function) of (ii) (for diagnosis, prognosis or monitoring of
CC treatment); to evaluate (ii)-expressing cells intended for cell therapy,
CC and as therapeutic mg inhibitors. Cells that express the mg gene (or
CC contain the mg polypeptide) are used to identify agents (A) that modulate
CC mg activity. (A) are potentially useful for the treatment of body weight
CC disorders, particularly obesity, cachexia or anorexia, or other
CC conditions associated with the mg gene such as hyperpigmentation,
CC hyperphagia and disorders that result in increased metabolic rate
CC
XX
SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7072 TGAATGACAGAGCCCT 7089
DB 1 TGAATGACAGAGCCCT 18

RESULT 3162
AAC58261/c
ID AAC58261 standard; DNA; 22 BP.
XX
XX AAC58261;
AC
XX 29-JAN-2001 (first entry)
DT
XX
XX Human PRO212 hybridisation probe SEQ ID NO:80.
DE
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; PCR primer;
KW hybridisation; probe; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic;
KW leukaemia; lymphoid malignancy; neuronal disorder; glial disorder;
KW astrocytal disorder; hypothalamic disorder; glandular disorder;
KW macrophagal disorder; epithelial disorder; stromal disorder;
KW blastocoelec disorder; inflammatory disorder; angiogenic;
KW immunologic disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200053755-A2.
PN
XX
XX 14-SEP-2000.
PD
XX
XX 06-JAN-2000; 2000WO-US000376.
PF
XX
XX 08-MAR-1999; 99WO-US005028.
PR
XX 02-JUN-1999; 99WO-US012252.
PR
XX 23-JUN-1999; 99US-0141037P.
PR
XX 07-JUL-1999; 99US-0143048P.
PR
XX 26-JUL-1999; 99US-0145698P.
PR
XX 30-NOV-1999; 99WO-US028313.
PR
XX 20-DEC-1999; 99WO-US030911.
PR
XX 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH ) GENENTECH INC.
PA
XX
```

PI Aekhenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Watanabe CK, Wood WI;  
XX WPI; 2000-572270/53.  
XX  
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer.  
XX  
PS Example 23; Page 133; 286pp; English.  
XX  
XX The present invention describes an isolated antibody that binds to one of  
CC the human PRO proteins designated PRO232, PRO290, PRO341, PRO353, PRO619,  
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,  
CC PRO1060, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,  
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO2094, PRO245 OR  
CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The  
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis  
CC and prevention of cancer. The antibodies and other anti-tumour compounds  
CC maybe used to treat various conditions, including those characterised by  
CC overexpression and/or activation of the amplified PRO genes. Exemplary  
CC conditions or disorders to be treated with such antibodies and other  
CC compounds include benign or malignant tumours (e.g., renal, liver,  
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,  
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, and  
CC glioblastomas, and various head and neck tumours), leukemias and  
CC lymphoid malignancies, other disorders such as neuronal, glial,  
CC astrocytal, hypochalamic and other glandular, macropapagal, epithelial,  
CC stromal and blastocoeleic disorders, and inflammatory, angiogenic and  
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and  
CC hybridisation probes used in the isolation of the human PRO sequences.  
CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO  
CC polynucleotide and protein sequences given in the exemplification of the  
CC present invention  
XX  
SQ Sequence 22 BP; 2 A; 10 C; 5 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 5210 GGCGTAGATCAGGGCAG 5227  
DB 22 GGCGCAGATCAGTGCAC 5  
XX  
RESULT 3163  
XX ABA82014/C  
XX ID ABA82014 standard; DNA; 22 BP.  
XX  
XX ABA82014;  
XX  
XX 25-JAN-2002 (first entry)  
XX  
XX Mouse wound healing related PCR primer SEQ ID NO 83.  
XX  
XX Human; mouse; vulnery; dermatological; skin disorder; wound healing;  
XX gene therapy; PCR primer; ss.  
XX  
XX Mus musculus.  
XX  
XX CA2325226-A1.  
XX  
XX 17-MAY-2001.  
XX  
XX 16-NOV-2000; 2000CA-02325226.  
XX  
XX 17-NOV-1999; 99DB-01055349.  
XX  
XX 17-DEC-1999; 99US-0172511P.  
XX  
XX 20-JUN-2000; 2000DE-01030149.  
XX  
XX (SWIT-) SWITCH BIOTECH AG.  
XX  
XX Regenbogen J, Wolf E, Goppelt A, Werner S, Halle J;

XX  
XX WPI; 2001-433142/47.  
XX  
XX  
XX Use of novel polypeptide or its variant or nucleic acid encoding the  
PT polypeptide for diagnosing and/or preventing and/or treating skin  
PT disorders and/or treatment in wound healing or for identifying active  
PT substances.  
XX  
XX  
PS Example 8; Page 64; 265pp; English.  
XX  
XX The invention relates to the use of a polypeptide (ABA44544-ABA44601,  
CC ABA44606-ABA44623) or its variant or encoding nucleic acid (ABA11990-  
CC ABA81995, ABA82016-ABA82032) with vulnery and/or dermatological  
CC activity for the diagnosis, prevention and treatment of skin disorders  
CC and treatment in wound healing or for the identification of  
CC pharmacologically active substances. The nucleic acids are useful in gene  
CC therapy. The present sequence is that of a PCR primer, useful to the  
CC invention. Note: The printed sequence listing for this specification was  
CC incomplete, terminating part way through SEQ ID NO 106. The remaining  
CC data was obtained from EPO data for an equivalent patent (EP1114862)  
XX  
SQ Sequence 22 BP; 3 A; 6 C; 5 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 5912 TTCCCGAAGCCGAGAT 5929  
DB 22 TTCCCGAAGCAGAGAT 5  
XX  
RESULT 3164  
XX AAF84350  
XX ID AAF84350 standard; DNA; 22 BP.  
XX  
XX AAF84350;  
XX  
XX 20-JUN-2001 (first entry)  
XX  
XX Human CYP2C18i PCR primer #6.  
XX  
XX Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.  
XX  
XX Homo sapiens.  
XX  
XX JF2001017185-A.  
XX  
XX 23-JAN-2001.  
XX  
XX 10-DEC-1999; 99JP-00351610.  
XX  
XX 19-MAR-1999; 99JP-00076592.  
XX  
XX 06-MAY-1999; 99JP-00125918.  
XX  
XX (SAKA ) OTSUKA PHARM CO LTD.  
XX  
XX WPI; 2001-285409/30.  
XX  
XX  
XX Detection of gene polymorphism of drug-metabolising enzymes useful for  
PT diagnosis and testing comprises carrying out polymerase chain reaction.  
XX  
XX Example 1; Page 13; 27pp; Japanese.  
XX  
XX The present invention relates to a kit and method for the detection of  
CC gene polymorphisms of drug-metabolising enzyme genes. The kit contains a  
CC polymerase chain reaction (PCR) buffer solution containing DNA polymerase  
CC and NTP, a normal forward primer, a mutated forward primer, a reverse  
CC primer and a fluorescence-labelling probe. The method involves carrying  
CC out PCR on sample DNA, containing a drug-metabolising enzyme gene,  
CC together with PCR buffer, the normal forward primer, the reverse primer  
CC and the fluorescence-labelling probe (step A); and carrying out PCR on  
CC the sample DNA together with PCR buffer, the mutated forward primer, the

CC reverse primer and the fluorescence-labelling probe (step B), and a step  
CC of comparing the result of step a with that of step b. The present  
CC sequence is a primer for human CYP2C18i, which was used to illustrate the  
CC present invention

XX Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;

Best Local Similarity 88.9%; Pred. No. 2.2e+03; Mismatches 2; Indels 0; Gaps 0;

Qy 5289 GCCTTACTCCGACGAC 5306  
Db 5 GCCTGTATCCGACGAC 22

RESULT 3165

AA165435

ID AA165435 standard; DNA; 22 BP.

XX AA165435;

DT 10-DEC-2001 (first entry)

DE Reverse transcription primer for maize.

KM Plant androgenesis marker; maize; androgenesis; quantitative trait loci;  
KM cereal; plant breeding; primer; ss.

OS Zea mays.

PN FR2806419-A1.

PD 21-SEP-2001.

PF 14-MAR-2000; 2000FR-00003245.

PR 14-MAR-2000; 2000FR-00003245.

PA (LIMA-) LIMAGRAIN GENETICS GRANDES CULTURES.

PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.

PI Dufour P, Murigneux A, Beckert M;

DR WPI; 2001-573132/65.

PT New markers for plant androgenesis, useful for evaluating androgenic  
PT potential, cloning of androgenesis genes and genetic analysis.

PS Example; Page 13; 49pp; French.

XX The present sequence represents a primer used to produce maize cDNA. The  
CC specification describes plant androgenesis markers, which are derived  
CC from maize. Maize androgenesis markers are used to evaluate the  
CC androgenic potential of plants and derived cultures of microspores. The  
CC markers are also used to clone genes involved in androgenesis, and for  
CC genetic analysis to identify quantitative trait loci involved in  
CC androgenesis, particularly in cereals, specifically maize. Varieties  
CC capable of androgenesis are useful in plant breeding programs

XX Sequence 22 BP; 3 A; 1 C; 2 G; 15 T; 0 U; 1 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;

Best Local Similarity 88.9%; Pred. No. 2.2e+03; Mismatches 2; Indels 0; Gaps 0;

Qy 4461 GACCTTTTTTTTTTTT 4478  
Db 4 GAATCTTTTTTTTTTT 21

RESULT 3166

AAH37409/C

ID AAH37409 standard; DNA; 22 BP.

XX AAH37409;

DT 14-AUG-2001 (first entry)

DE SNP specific upper PCR primer SEQ ID 205.

KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KM SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-016096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polymorphic nucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 51; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNP) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence

XX Sequence 22 BP; 3 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;

Best Local Similarity 88.9%; Pred. No. 2.2e+03; Mismatches 2; Indels 0; Gaps 0;

Qy 2411 CAGTGAACCCACATCA 2428  
Db 20 CAGTGTACCAACATCA 3

RESULT 3167

AAH40497  
ID AAH40497 standard; DNA; 22 BP.  
XX  
AC AAH40497;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific upper PCR primer SEQ ID 3293.  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KM SNE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KM Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC00129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polymorphic polymorphism in a nucleic  
PT acid sample.  
XX  
PS Claim 1; Page 66; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNP) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 22 BP; 7 A; 10 C; 1 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4832 CAAACATCTATCCGAG 4849  
DB 2 CACACACTCTATCCGAG 19

RESULT 3168  
AAS14520  
ID AAS14520 standard; DNA; 22 BP.  
XX  
AC AAS14520;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human GSTT1\*0 3187bp fragment PCR primer GST-TR9n.  
XX  
XX Human; PCR primer; ss; GSTT1; Glutathione-S-transferase theta;  
KM skin cancer; GSTT1\*0 allele; oxidative stress; genotyping; GST-TR9n.  
XX  
OS Homo sapiens.  
XX  
PN EP1130112-A1.  
XX  
PD 05-SEP-2001.  
XX  
PF 24-FEB-2000; 2000EP-00103844.  
XX  
PR 24-FEB-2000; 2000EP-00103844.  
XX  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX  
PI Sprenger R, Schlagenhauer R, Brinkmann U, Kerb R;  
XX  
DR WPI; 2001-591524/67.  
XX  
PT PCR assay to detect presence of single allele e.g., glutathione S-  
PT transferase chetaasterisk0 allele, of deletion mutant involves performing  
PT PCR with primers derived from sequences upstream and downstream of  
PT deletion area.  
XX  
PS Disclosure; Page 17; 24pp; English.  
XX  
XX The invention relates to a PCR assay for detecting presence of at least a  
CC single allele of deletion mutant GSTT1\*0 (glutathione S-transferase theta  
CC allele) involves performing PCR with two primers, of which one is from  
CC the sequence upstream of the deletion area and the other is from the  
CC sequence downstream of the deletion area, and checking the corresponding  
CC DNA fragment produced in PCR. The method is useful for detecting presence  
CC of at least GSTT1\*0 allele, for diagnostic testing of individuals to  
CC check whether they are susceptible to toxins or resistant to certain  
CC therapeutic agents or belonging to risk groups (e.g. UV-mediated skin  
CC damage, skin cancer and cancers associated with oxidative stress. The  
CC method allows the characterisation and mechanism of the GSTT1 deletion  
CC and identifies 18 kb homology regions flanking GSTT1 which are involved  
CC in the deletion event that produced the \*0 allele. The method permits the  
CC unambiguous discrimination of all GSTT1 genotypes (\*A/A, \*0/0 (both  
CC homozygous), \*/0 (heterozygous)). The technique allows the reproducible  
CC simultaneous discrimination of all the genotypes. The three GSTT1  
CC genotypes detected by these procedures correlated highly significant with  
CC enzyme activity in erythrocytes. The trimodular distribution of  
CC phenotypes at high-, intermediate- and null- activity in homo- and  
CC heterozygotes for the \*A allele and \*0/0 homozygotes, respectively  
CC indicate a gene dose effect. The present sequence is a PCR primer for  
CC amplifying a 3187bp fragment from the human GSTT1\*0 allele  
XX  
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2965 ACCAGCCAGAAATCTCTG 2982  
DB 3 ATCAGCCAGAGATCTCTG 20  
RESULT 3169  
ABS59077/c  
ID ABS59077 standard; DNA; 22 BP.

XX AC ABS59077;  
 XX DT 05-NOV-2002 (first entry)  
 XX DE Human G-protein coupled receptor, reverse primer #75.  
 XX  
 KM Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;  
 KM diabetes; cell signal processing; metabolic pathway modulation; cancer;  
 KM adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;  
 KM immune response; neurodegenerative disorder; inflammatory disorder;  
 KM Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;  
 KM primer; PCR; ss.  
 XX  
 OS Homo sapiens.  
 XX MO200259313-A2.  
 XX PD 01-AUG-2002.  
 XX PF 18-DEC-2001; 2001WO-US049394.  
 XX PR 18-DEC-2000; 2000US-0256635P.  
 PR 21-DEC-2000; 2000US-0257876P.  
 PR 04-JAN-2001; 2001US-0259743P.  
 PR 10-JAN-2001; 2001US-0260718P.  
 PR 12-JAN-2001; 2001US-0261498P.  
 PR 24-JAN-2001; 2001US-0263689P.  
 PR 08-FEB-2001; 2001US-0267464P.  
 PR 22-FEB-2001; 2001US-0271021P.  
 PR 14-MAR-2001; 2001US-0275946P.  
 PR 23-MAR-2001; 2001US-0278150P.  
 PR 18-APR-2001; 2001US-0284591P.  
 PR 23-APR-2001; 2001US-0285718P.  
 PR 19-JUN-2001; 2001US-0293227P.  
 PR 16-AUG-2001; 2001US-0312902P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;  
 Pi Caeman SJ, Vernhet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;  
 Pi Gerlach V, Smithson G, Stone DJ, Sciore P, MacDougall JR, Gunther B;  
 PI Peyman JA, Ellerman K, Gangolli EA, Millet I;  
 XX WPI; 2002-599789/64.  
 DR  
 XX  
 PT New G protein coupled receptor polypeptides and polynucleotides, useful  
 PT in gene therapy, particularly for treating or preventing cardiomyopathy,  
 PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer  
 PT in humans.  
 XX  
 PS Claim 1; Page 455; 685pp; English.  
 XX  
 CC The invention relates to novel isolated G-protein coupled receptor (GPCR)  
 CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid  
 CC and antibody, are useful for treating, preventing or alleviating a GPCR-  
 CC associated disorder or a pathological state in a subject, particularly a  
 CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,  
 CC diabetes, or a disorder related to cell signal processing and metabolic  
 CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful  
 CC for diagnosing the presence of or predisposition to a disease associated  
 CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid  
 CC and polypeptide are especially useful in therapeutic or prophylactic  
 CC applications for disorders associated with aberrant GPCR expression or  
 CC activity. The DNA encoding the protein is useful in gene therapy for  
 CC treating the above conditions. Furthermore, the nucleic acids and  
 CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate  
 CC cancer, uterus cancer, immune response, neurodegenerative disorders,  
 CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or  
 CC Albright hereditary osteodystrophy. These are also useful in developing a  
 CC powerful assay system for functional analysis of various human disorders,  
 CC as well as in diagnostic applications. ABS58747-ABS59231 represent human  
 CC GPCR coding sequences, primers and probes of the invention

XX SQ Sequence 22 BP; 10 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.24; Score 14.8; DB 1; Length 22;  
 XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 OY 5705 TTGCTTTTCTCTTCTCT 5722  
 DB 21 TTGCTTTTCTCTCTCT 4  
 XX  
 RESULT 3170  
 ABK33445/C  
 ID ABK33445 standard; DNA; 22 BP.  
 XX  
 AC ABK33445;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Human TNF-receptor I exon Pro12Pro (A/G) FAM probe (G allele).  
 XX  
 KM Human; anti-tumour necrosis factor receptor II; TNF receptor II;  
 KM TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder;  
 KM inflammatory disorder; chronic disease; receptor; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1172444-A1.  
 XX  
 PD 16-JAN-2002.  
 XX  
 PF 10-JUL-2000; 2000EP-00114786.  
 XX  
 PR 10-JUL-2000; 2000EP-00114786.  
 PR  
 XX (CONA-) CONARIS RES INST GMBH.  
 PA  
 XX  
 PI Schreiber S, Hampe J, Mascheretti S;  
 XX WPI; 2002-156651/21.  
 DR  
 XX  
 PT Detecting non-responders to anti-human necrosis factor therapy, comprises  
 PT testing an individual for homozygosity for a single nucleotide  
 PT polymorphism in the gene coding for the tumor necrosis factor receptor  
 PT II.  
 XX  
 PS Disclosure; Page 6; 45pp; English.  
 XX  
 CC The present invention relates to a method for detecting non-responders to  
 CC anti-tumour necrosis factor (TNF) therapy. The method involves testing an  
 CC individual for homozygosity for at least one single nucleotide  
 CC polymorphism (SNP) in the gene coding for TNF receptor II, which is  
 CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168  
 CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and  
 CC Met196Arg respectively, are also described. The method of the invention  
 CC is useful for detecting non-responders to anti-TNF therapy such as  
 CC infliximab therapy, or therapy of Crohn's disease. The genes containing  
 CC the 2 novel polymorphisms are useful for diagnostic purposes in  
 CC inflammatory, malignant or other chronic diseases. The present sequence  
 CC represents a TaqMan probe used in the methods of the present invention  
 XX  
 SQ Sequence 22 BP; 2 A; 7 C; 8 G; 5 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.24; Score 14.8; DB 1; Length 22;  
 XX Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 OY 7412 TCAGCAGCAGCAGCAGCA 7429  
 DB 18 TCACGACGCGCAGCAGCA 1

RESULT 3171  
 ABK69044/c  
 ID ABK69044 standard; DNA; 22 BP.  
 XX  
 AC ABK69044;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Rat ARP RT PCR probe.  
 XX  
 KM Alpha related protein; Beta related protein; ARP; BRP; hypothyroidism;  
 KM glycoprotein hormone; reproductive disorder; cell proliferative disorder;  
 KM ovulatory disease; fertility related disorder; metabolic disorder;  
 KM pituitary disorder; spermatogenesis; lung fibrosis; liver fibrosis;  
 KM reperfusion injury; systemic cytokine damage; inflammatory condition;  
 KM septic shock; sepsis; systemic inflammatory response syndrome; SIRS;  
 KM ischaemia; endotoxin lethality; arthritis; nephritis; Crohn's disease;  
 KM complement-mediated hyperacute rejection; chemokine-induced lung injury;  
 KM inflammatory bowel disease; anaphylaxis; hypersensitivity; ss; probe;  
 KM reverse transcriptase; PCR.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200214348-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 10-AUG-2001; 2001WO-US025240.  
 XX  
 PR 11-AUG-2000; 2000US-0225035P.  
 PR 08-MAY-2001; 2001US-00851465.  
 XX  
 PA (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.  
 XX  
 PI Campbell RK, El Tayar N, He C, Kelton CA;  
 XX  
 DR WPI; 2002-339445/37.  
 XX  
 PT Novel beta subunits of glycoprotein, termed as beta related protein, are  
 useful for treating or preventing a reproductive disorder in a subject.  
 XX  
 PS Example 5; Page 91; 158pp; English.  
 XX  
 CC The invention relates to an isolated beta-related protein (BRP) a novel  
 CC glycoprotein hormone, its fragment, derivative, analogue, homologue or  
 CC naturally occurring allelic variant and the nucleic acid encoding it.  
 CC Also disclosed are novel alpha related proteins (ARP) and their nucleic  
 CC acids. Also included are a nucleic acid vector comprising BRP, a host  
 CC cell comprising the vector, a protein multimer comprising BRP or ARP  
 CC polypeptide, and a second polypeptide, an antibody that selectively binds  
 CC to BRP or the multimer, screening for a modulator of activity, or of  
 CC latency or predisposition to a reproductive disorder comprising  
 CC administering a test compound to an animal at risk from a pathology  
 CC associated with BRP, where the animal recombinantly expresses an ARP/BRP  
 CC polypeptide, measuring the activity of the polypeptide and comparing it  
 CC to a control level, determining the presence of, or predisposition to, a  
 CC reproductive disorder in a subject by measuring the amount of an ARP/BRP  
 CC nucleic acid in a sample and comparing it to a control and expressing an  
 CC ARP/BRP polypeptide as a product of an endogenous gene in a cell. The  
 CC BRP/ARP proteins, nucleic acids, antibodies and multimers are useful for  
 CC treating, preventing or diagnosing reproductive and cell proliferative  
 CC disorders including ovulatory diseases, fertility related disorders,  
 CC hypothyroidism and metabolic disorders affecting pituitary function or  
 CC pituitary target organs e.g. adrenal gland, thyroid, gonad and liver,  
 CC they are also useful for stimulating spermatogenesis, increasing the  
 CC function of the thyroid glandular cells, regulating gonadal function,  
 CC regulating gonadal hormone production, and promoting or suppressing  
 CC fertility, gut protection or regeneration and treatment of lung or liver  
 CC fibrosis, reperfusion injury in various tissues and conditions resulting  
 CC from systemic cytokine damage, for promoting or inhibiting  
 CC differentiation of tissues from precursor tissues or cells, inhibiting  
 CC the growth of tissues, for treating inflammatory conditions including  
 CC chronic or acute conditions, e.g. inflammation associated with infection

CC (such as septic shock, sepsis or systemic inflammatory response syndrome  
 CC (SIRS)) ischaemia-reperfusion injury, endotoxin lethality, arthritis,  
 CC complement-mediated hyperacute rejection, nephritis, cytokine or  
 CC chemokine-induced lung injury, inflammatory bowel disease, Crohn's  
 CC disease, anaphylaxis and hypersensitivity, and disorders resulting from  
 CC over production of cytokines. The present sequence is an ARP or BRP  
 CC reverse transcriptase (RT)-PCR probe  
 XX  
 SO Sequence 22 BP; 3 A; 10 C; 4 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 5275 GGGAGCAGGTGGCAGCCT 5292  
 DB 19 GGGTGCAGTGGCAGCCT 2  
 XX  
 RESULT 3172  
 ABK68344  
 ID ABK68344 standard; DNA; 22 BP.  
 XX  
 AC ABK68344;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Mouse HYPLIP1 locus specific primer 354K16S #1.  
 XX  
 KM Mouse; primer; antilipemic; cardiant; hypotensive; anorectic; HYPLIP1;  
 KM FCHL1; lipid disorder; familial combined hyperlipidaemia;  
 KM coronary artery disease; atherogenic lipoprotein phenotype; cancer;  
 KM hyperapobetalipoproteinaemia; hypertriglyceridaemia; obesity; ss;  
 KM familial dyslipidaemic hypertension; syndrome X; insulin resistance;  
 KM hypercholesterolaemia; chromosome 3.  
 KM  
 OS Mus sp.  
 XX  
 PN WO200220847-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US028181.  
 XX  
 PR 08-SEP-2000; 2000US-0231322P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Bodnar JS, Caesteclani LW, Chatterjee A, De Jong P, Luis AJ;  
 PI Ohmen J, Ross D, Tafari S, Wu C;  
 XX  
 DR WPI; 2002-339808/37.  
 XX  
 XX  
 PT Novel HYPLIP1 and FCHL1 genes and their sequence variations associated  
 with lipid disorder and cancer, useful for prognosis, diagnosis and  
 treatment of lipid disorders.  
 XX  
 PS Claim 11; Page 77; 102pp; English.  
 XX  
 CC This invention relates to the cDNA and protein sequences of novel  
 CC proteins HYPLIP1 or FCHL1 and to sequence variations within these genes  
 CC that have been shown to be associated with lipid disorders.  
 CC Oligonucleotide probes that hybridise to the cDNA sequence are useful for  
 CC analysing the expression of FCHL1 by detecting the expression of the mRNA  
 CC transcript in the sample. A host cell transformed with the cDNA of the  
 CC invention is useful for producing the protein by recombinant means.  
 CC Pharmaceutical compositions based on the sequences of the invention are  
 CC useful for treating or preventing a lipid disorder associated with  
 CC expression of FCHL1 such as familial combined hyperlipidaemia, coronary  
 CC artery disease, atherogenic lipoprotein phenotype, familial  
 CC hyperapobetalipoproteinaemia, hypertriglyceridaemia, familial  
 CC dyslipidaemic hypertension, syndrome X, obesity, insulin resistance and  
 CC hypercholesterolaemia. The cDNA sequence is useful in the diagnosis or

CC prognosis of predisposition to lipid disorders and cancers, and also to  
 CC identify a molecule which enhances or decreases the HYPPLP1 or FCHL1  
 CC activity. The present sequence represents an oligonucleotide primer  
 CC specific for the mouse HYPPLP1 locus of the invention. The mouse HYPPLP1  
 CC locus is situated on chromosome 3

XX Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGCAGCTTGAAGTGACA 561  
 DB 4 GTGCAGCTTGAAGTGACA 21

RESULT 3173  
 ABQ88519  
 ID ABQ88519 standard; DNA; 22 BP.

XX AC ABQ88519;  
 XX DT 23-SEP-2002 (first entry)

DE Human GPCR reverse PCR primer SEQ ID NO:231.

XX Human, G protein coupled receptor; GPCR; GPCR; neuroprotective;  
 KW nootropic; anti-HIV; antiallergic; antidiabetic; cytostatic;  
 KW immunomodulator; antidiabetic; anorectic; haemostatic;  
 KW antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic;  
 KW cardiant; antitumor; antiallergic; hepatotropic; antiparkinsonian; HIV;  
 KW vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes;  
 KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;  
 KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;  
 KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;  
 KW systemic lupus erythematosus; PCR primer; ss.

XX Homo sapiens.  
 OS Synthetic.

XX WO200250276-A2.

XX PD 27-JUN-2002.

XX PE 18-DEC-2001; 2001WO-US049347.

XX 18-DEC-2000; 2000US-0256635P.  
 PR 21-DEC-2000; 2000US-0257876P.  
 PR 04-JAN-2001; 2001US-0259743P.  
 PR 10-JAN-2001; 2001US-0260718P.  
 PR 12-JAN-2001; 2001US-0261498P.  
 PR 24-JAN-2001; 2001US-0263689P.  
 PR 08-FEB-2001; 2001US-0267464P.  
 PR 22-FEB-2001; 2001US-0271021P.  
 PR 14-MAR-2001; 2001US-0275946P.  
 PR 23-MAR-2001; 2001US-0278150P.  
 PR 18-APR-2001; 2001US-0284591P.  
 PR 23-APR-2001; 2001US-0285718P.  
 PR 19-JUN-2001; 2001US-0299327P.  
 PR 16-AUG-2001; 2001US-0312902P.

XX (CURA-) CURAGEN CORP.

XX Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Scioire P,  
 PI Smithson G, Peyman JA, Macdougall JR, Stone D, Verneet CAM, Shenoy S;  
 PI Gunther E, Millet I, Tcherny VT, Anderson D, Gusev V, Malyankar UM,  
 PI Zhong H, Ellerman KE, Wolenc A;

XX WPI; 2002-557660/59.

XX New isolated human G-protein coupled receptor X (GPCRX) polypeptide,  
 PT useful for treating or preventing GPCR-associated disorders e.g.

PT diabetes, atherosclerosis, cancer or obesity.

XX \*Example 3; Page 217; 354pp; English.

XX ABQ88519 to ABQ88417 represent human G protein coupled receptor (GPCR)  
 CC CDNA sequences, and ABP51624 represent human GPCR proteins  
 CC from the present invention. GPCR sequences can have neuroprotective,  
 CC nootropic, anti-HIV, antiallergic, antidiabetic, anorectic, haemostatic,  
 CC immunomodulator, antifungal, antiparkinsonian, antiparasitic, cytostatic,  
 CC antibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic,  
 CC cardiant, antitumor, antiallergic, hepatotropic and antiparkinsonian  
 CC activities, and can be used in vaccines and gene therapy. GPCR proteins,  
 CC nucleic acid molecules, and antibodies from the present invention can be  
 CC used for manufacturing a medicament for treating or preventing a GPCR-  
 CC associated disorder or syndrome related to cell signal processing and  
 CC metabolic pathway modulation, such as cardiomyopathy, atherosclerosis,  
 CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or  
 CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,  
 CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus  
 CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be  
 CC used diagnostically to monitor protein levels in tissues as part of a  
 CC clinical testing procedure such as in determining the efficacy of a given  
 CC treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes  
 CC for the human GPCRs of the present invention

XX Sequence 22 BP; 6 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1750 CTGCAGCTCATTTATGTC 1767  
 DB 5 CAGCAGCTCATTTATGTC 22

RESULT 3174

ABX09454  
 ID ABX09454 standard; DNA; 22 BP.

XX AC ABX09454;

XX DT 22-JAN-2003 (first entry)

DE Arteriosclerosis-detecting probe from HCF2.

XX Arteriosclerosis; diagnosis; hybridisation; synergism; gene therapy;  
 KW mutation; probe; ss.

XX Homo sapiens.

XX WO200272882-A2.

XX PD 19-SEP-2002.

XX PE 13-MAR-2002; 2002WO-EP002780.

XX PR 13-MAR-2001; 2001DE-01011925.

XX (OGHA-) OGHAM GMBH.

XX Cullen P, Seedorf U;

XX WPI; 2002-723374/78.

XX Determining genetic risk of arteriosclerosis, for clinical diagnosis,  
 PT comprises hybridizing patient nucleic acid with an array of probes  
 PT derived from risk-associated reference genes and their mutations.

XX Example 1; Page 126; 146pp; German.

XX This invention describes a novel method for determining the genetic risk  
 CC of arteriosclerosis both for clinical diagnosis and for population

CC studies. The method comprises: (i) selecting risk-associated reference  
 CC nucleic acid sequences, including their functionally characterizing  
 CC mutations; (ii) applying probes from these sequences, or their  
 CC complements, to a carrier; (iii) hybridising the probes with a nucleic  
 CC acid from (or synthesised from) a patient sample; and (iv) detecting and  
 CC evaluating the hybridisation pattern. The method provides a quick,  
 CC inexpensive and informative diagnosis, and makes possible a  
 CC multifactorial analysis for detecting e.g. synergism between different  
 CC mutations or mutations that when present alone carry no risk but are risk  
 CC -associated in presence of other mutations. The results may be combined  
 CC with known risk-assessment methods to provide a more reliable diagnosis,  
 CC especially important with new therapeutic methods (e.g. gene therapy)  
 CC that are directed against specific genes. All relevant mutations in a  
 CC reference sequence can be screened for in a single test and the method is  
 CC well suited to automation. ABX09147-ABX09676 represent probes used to  
 CC illustrate the method of the invention

XX  
 SQ Sequence 22 BP; 2 A; 9 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5703 CCTTCCTTTCTCTCTCT 5720  
 |||||  
 Db 4 CCTTCCTTTCTCTCATCT 21

RESULT 3175  
 ABS97168/c  
 ID ABS97168 standard; DNA, 22 BP.  
 XX  
 AC ABS97168;  
 XX  
 DT 23-DEC-2002 (first entry)  
 DX  
 XX Human CYP4501A2 promoter 1B sequencing primer #2.

XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002E1; LTF;  
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTS;  
 KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
 KM HNMT; kallikrein 2; KLR2; nicotinamide-N-methyl transferase; NMNT;  
 KM NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;  
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
 KM multidrug resistance 1; lactoferrin; orphan nuclear receptor;  
 KM multidrug resistance associated protein 3; cancer; prostate;  
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KM altered drug metabolism; cardiovascular function; colorectal tumour;  
 KM central nervous system; pulmonary; immunological; sequencing.

XX  
 OS Homo sapiens.  
 XX  
 XX MO200257410-A2.  
 XX  
 XX PD 25-JUL-2002.  
 XX  
 XX PF 28-NOV-2001; 2001WO-US044838.  
 XX  
 XX PR 28-NOV-2000; 2000US-00724389.  
 XX  
 XX PA (DNAS-) DNA SCI LAB INC.  
 XX  
 XX PI Guida M, Hall J;  
 XX  
 XX DR WPI; 2002-698522/75.  
 XX  
 XX PT Isolated nucleic acid molecules having polymorphisms in known human genes  
 e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers

PT for locating, identifying and characterizing the genes responsible for  
 PT disorder-related traits.

XX  
 XX Example 2; Page 101; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid  
 CC molecule comprising at least one base variation from that of a known  
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
 CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1),  
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 CC (ARNT), cathepsin S (CTS), cyclooxygenase 2 (COX2), diazepam binding  
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 CC transferase (HNMT), kallikrein 2 (KLR2), nicotinamide-N-methyl  
 CC transferase (NMNT), NADPH quinone oxidoreductase 2 (NQO2), transferase 2B4  
 CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 1  
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1  
 CC (MDR1), lactoferrin (LTF), multidrug resistance associated protein 3  
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterizing the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related  
 CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1, AHR,  
 CC ARNT, EPHX2, GST12, NMNT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered pulmonary,  
 CC immunological or haematological function, in KLR2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC sequencing primer used to sequence the polymorphic genes of the invention

XX  
 SQ Sequence 22 BP; 13 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4459 TGGACCTTTTCTTTT 4476  
 |||||  
 Db 18 TGAACATTTTCTTTT 1

RESULT 3176  
 ABK71248  
 ID ABK71248 standard; DNA, 22 BP.  
 XX  
 XX AC ABK71248;  
 XX  
 XX DT 15-JUL-2002 (first entry)  
 XX  
 XX DE Mouse HYPLIP1 locus PCR primer #321.  
 XX  
 XX KM Human; mouse; HYPLIP1, FCHL1, familial combined hyperlipidaemia; cancer;  
 KM lipid disorder; PCR; primer; ss.  
 XX  
 XX OS Mus SP.  
 XX  
 XX XX MO200220848-A2.  
 XX  
 XX PD 14-MAR-2002.  
 XX  
 XX XX



```
PF 07-SEP-2001; 2001WO-US028182.
XX
XX 08-SEP-2000; 2000US-0231322P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Bodnar JS, Castellani LM, Chatterjee A, De Jong P, Lusie AV,
PI Ohmen J, Ross D, Tafuri S, Wu C,
XX WPI; 2002-329882/36.
XX
XX New mouse HYPLIP1 and human FCHL1 (familial combined hyperlipidemia)
PT genes and their sequence variations, useful for diagnosing, treating or
PT preventing lipid disorders and cancers.
XX
XX Claim 11; Page 77; 102pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC variation of a mouse HYPLIP1 cDNA or a human FCHL1 (familial combined
CC hyperlipidaemia) gene. The FCHL1 polynucleotide, the FCHL1 polypeptide or
CC antibody immunoreactive to the FCHL1 polypeptide are useful for treating
CC or preventing cancer associated with expression of FCHL1, as well as for
CC treating lipid disorder. The mouse HYPLIP1 cDNA or human FCHL1 gene are
CC also useful for diagnosing or prognosing a predisposition to lipid
CC disorder and cancer. ABK70902-ABK71303 represent mouse HYPLIP1, human
CC FCHL1 coding sequences and PCR primers of the invention
XX
XX Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 544 GTCGACCTTGAGTGACA 561
DB 4 GTCGACATTTAGTGACA 21
RESULT 3177
ABK15346
ID ABK15346 standard; DNA; 22 BP.
XX
XX ABK15346;
AC
XX 08-MAY-2002 (first entry)
DT
XX Cyclooxygenase-2 (COX-2) sense PCR primer DNA sequence.
DE
XX Mouse; cyclooxygenase-2; COX-2; PCR; primer; sepsis; pancreatitis; burn;
KM trauma; blood loss; penetrating injury; septic shock; pneumonia;
KM septicemia; bacteraemia; urinary tract infection; wound infection;
KM drug reaction; systemic inflammatory response syndrome; PGE_2;
KM prostaglandin E_2; receptor; ss.
XX
XX Mus sp.
OS
XX
XX US2002006915-A1.
PN
XX 17-JAN-2002.
PD
XX 14-FEB-2001; 2001US-00782936.
PF
XX 15-FEB-2000; 2000US-0182524P.
PR
XX (STRO/) MACK STRONG V B.
PA (STAP/) STAPLETON P P.
PA (DALY/) DALY J M.
XX
XX Mack Strong VE, Stapleton PP, Daly JM;
PI
XX WPI; 2002-179019/23.
DR
XX Treating a patient at risk for systemic inflammatory response syndrome
PT
```

```
PT e.g. trauma involves administering cyclooxygenase-2 inhibitor or a drug.
XX
XX Example 1; Page 5; 39pp; English.
XX
XX The present invention relates to a new method of treating a patient at
CC risk for systemic inflammatory response syndrome. The method involves
CC administering a selective cyclooxygenase-2 inhibitor or a drug which
CC stimulates at least one prostaglandin E 2 (PGE 2) receptor or a drug
CC which interferes with binding of PGE 2 to at least one of PGE 2
CC receptors. The invention can be used for treating a patient at risk for
CC systemic inflammatory response syndrome e.g. sepsis, pancreatitis, burns,
CC trauma, life threatening blood loss from penetrating injury, or a patient
CC who has undergone surgery, septic shock, infections such as pneumonia,
CC septicemia, bacteraemia, urinary tract infection, wound infection or
CC drug reaction and can also be used for beneficial immune modulation. The
CC inhibitor or the drugs selectively modulate the immune response after
CC trauma, reduce the incidence of infectious complications and improve
CC survival after traumatic injury. The present nucleic acid sequence
CC represents the mouse cyclooxygenase-2 (COX-2) sense PCR primer that was
CC used in the invention with the COX-2 antisense PCR primer (ABK15347) for
CC the isolation and determination of COX-2 mRNA
XX
XX Sequence 22 BP; 7 A; 11 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1575 CGCACCCCAAAACAGTG 1592
DB 2 CCACACCCCAAAACAGTG 19
RESULT 3178
ACA54762
ID ACA54762 standard; DNA; 22 BP.
XX
XX ACA54762;
AC
XX 05-JUN-2003 (first entry)
DT
XX Human NF-kappaB associated polynucleotide PCR primer #19.
DE
XX
XX Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
KM inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
KM haematopoietic tumour; hyper-IGM syndrome; viral infection; asthma;
KM hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
KM X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
KM influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB;
KM experimental allergic encephalomyelitis; autoimmune disorder; wound;
KM hyper immune activity; acute phase response; hypercongenital condition;
KM birth defect; necrotic lesion; organ transplant rejection; pancreas;
KM signal transduction; hyperproliferative disorder; diabetes mellitus;
KM vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
KM Turner's syndrome; bacterial infection; cardiovascular disorder;
KM infertility; psoriasis; haemolytic anaemia; anti-inflammatory; anti-HIV;
KM cytostatic; hepatotropic; virucide; antineumatic; antiarthritic;
KM antiaesthetic; immunomodulator; antidiabetic; antiallergic;
KM neuroprotective; immunosuppressive; vulnery; antibacterial;
KM antifertility; antihaemic; antiporiatic; cerebroprotective; cardiac;
KM antiarteriosclerotic; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200286076-A2.
PN
XX 31-OCT-2002.
PD
XX 19-APR-2002; 2002WO-US012636.
PF
XX 19-APR-2001; 2001US-0284962P.
PR 26-APR-2001; 2001US-0286645P.
PT
```

PR 09-JAN-2002; 2002US-0346986P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA Carman J, Feder J, Nadler S;  
 PI WPI; 2003-093119/08.  
 XX  
 DR Novel NF-kappaB-associated polypeptides and polynucleotides useful for  
 PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant  
 PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.  
 XX  
 PS Example 3; Page 341; 608pp; English.  
 XX  
 CC The present invention relates to the isolation of human nuclear factor-  
 CC kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-  
 CC kappaB associated polypeptide and polynucleotide sequences are useful for  
 CC preventing, treating or ameliorating various disorders including immune  
 CC disorders, inflammatory disorders, cancers, disorders relating to  
 CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,  
 CC hematopoietic tumors, hyper-IGM syndromes, hypohidrotic ectodermal  
 CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al  
 CC inconitinentia pigmenti, viral infections (e.g. those caused by human  
 CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),  
 CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),  
 CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,  
 CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental  
 CC allergic encephalomyelitis (EAE), autoimmune disorders, disorders related  
 CC to hyper immune activity, disorders related to aberrant acute phase  
 CC responses, hypercongenital conditions, birth defects, necrotic lesions,  
 CC wounds, organ transplant rejection, disorders related to aberrant signal  
 CC transduction, hyperproliferative disorders, diseases of the pancreas  
 CC (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological  
 CC disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial  
 CC infections, cardiovascular disorders, Turner's syndrome, bacterial  
 CC hemolytic anaemia. The present sequence represents a PCR primer used in  
 CC the examples of the present invention  
 XX  
 CC Sequence 22 BP; 3 A; 2 C; 7 G; 10 T; 0 U; 0 Other;  
 XX  
 SQ  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 683 TGCAGCCTCGATGTCG 700  
 |||||  
 Db 2 TGCAGCCTCGATGTCG 19  
 RESULT 3179  
 ADA05936  
 ID ADA05936 standard; DNA; 22 BP.  
 XX  
 AC ADA05936;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human NOX reverse PCR primer SEQ ID NO:296.  
 XX  
 KW human; NOX; antidiabetic; anorectic; antibacterial; virucide;  
 KW immunomodulator; cyostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; antilipemic; gene therapy; human disease;  
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW immune disorder; haematopoietic disorder; dyslipidaemia; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003029424-A2.  
 XX  
 PD 10-APR-2003.  
 XX

PF 02-OCT-2002; 2002WO-US031373.  
 XX  
 PR 02-OCT-2001; 2001US-0326483P.  
 PR 05-OCT-2001; 2001US-0327435P.  
 PR 05-OCT-2001; 2001US-0327449P.  
 PR 09-OCT-2001; 2001US-0327917P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328044P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328849P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330309P.  
 PR 18-OCT-2001; 2001US-0341058P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 17-APR-2002; 2002US-037360P.  
 PR 19-APR-2002; 2002US-0373815P.  
 PR 19-APR-2002; 2002US-0373817P.  
 PR 19-APR-2002; 2002US-0373826P.  
 PR 19-APR-2002; 2002US-0373844P.  
 PR 22-APR-2002; 2002US-0374977P.  
 PR 16-MAY-2002; 2002US-0381037P.  
 PR 16-MAY-2002; 2002US-0381038P.  
 PR 16-MAY-2002; 2002US-0381042P.  
 PR 17-MAY-2002; 2002US-0381642P.  
 PR 28-MAY-2002; 2002US-0383656P.  
 PR 29-MAY-2002; 2002US-0383631P.  
 PR 25-JUN-2002; 2002US-0391335P.  
 PR 01-OCT-2002; 2002US-00262511.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 PA Smitthson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;  
 PI Paturajan M, Spytek KA, Edinger SR, Billeman K, Malyanar UW;  
 PI Ort-T, Gorman L, Zerkunen BD, Anderson DW, Zhong M, Catterton E;  
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;  
 PI Shimkete RA, Rothenberg ME, Leach MD, Agree ML, Bergs C, DiPippo VA;  
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;  
 XX  
 DR WPI; 2003-381626/36.  
 XX  
 PT New NOX polypeptides and nucleic acids, useful for diagnosing,  
 PT preventing or treating NOX-associated disorders, e.g. diabetes, obesity,  
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Example C; Page 384; 586pp; English.  
 XX  
 CC The present invention describes NOX proteins, where X can be 1 to 55  
 CC (e.g. NOX1). Also described: (1) a composition comprising a polypeptide  
 CC described above and a carrier; (2) a kit comprising, in one or more  
 CC containers, the composition described above; (3) an isolated nucleic acid  
 CC molecule which encodes a NOX protein of the invention; (4) a vector  
 CC comprising the nucleic acid molecule described above; (5) a cell  
 CC comprising the above vector; (6) an antibody that immunospecifically  
 CC binds to the polypeptide described above; (7) methods for determining the  
 CC presence or amount of the above polypeptide or nucleic acid molecule in a  
 CC sample; (8) methods for determining the presence of or predisposition to  
 CC a disease associated with altered levels of expression of the above  
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a  
 CC method of identifying an agent that binds to the polypeptide described  
 CC above; (10) a method for identifying a potential therapeutic agent for  
 CC use in treating a pathology that is related to an aberrant expression or  
 CC aberrant physiological interactions of the polypeptide; (11) a method of  
 CC screening for a modulator of activity or of latency or predisposition to  
 CC a pathology associated with the polypeptide; (12) a method for modulating  
 CC the activity of the polypeptide described above; (13) methods of treating  
 CC or preventing a pathology associated with the above polypeptide in a  
 CC mammal; and (14) a method for producing the above polypeptide. NOX  
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,

CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian  
CC and antilipase activities, and can be used in gene therapy. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease. The polypeptide or the nucleic  
CC acid molecule may be used to diagnose, treat or prevent metabolic  
CC disorders such as diabetes or obesity, infections, cachexia, cancer,  
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's  
CC disease, immune disorders, haematopoietic disorders and various  
CC dyslipidaemias. The nucleic acids can also be used as hybridisation  
CC probes, in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The present sequence represents a PCR primer for a  
CC human NOV sequence, which is used in an example from the present  
CC invention.  
XX  
SQ Sequence 22 BP; 3 A; 6 C; 4 G; 9 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5654 GCCTCATCTCTTACTTG 5671  
Db 3 GCCTCATCTCTTACTG 20  
RESULT 3180  
ACD02547 ACD02547 standard; DNA; 22 BP.  
XX ACD02547;  
XX  
XX 31-JUN-2003 (first entry)  
DE PCR primer #2 for perennial ryegrass construct pPZP21LpLTI6Baense.  
XX  
XX Perennial ryegrass; salt-inducible; salt responsive; ES13; CSA; LTI6;  
XX glutathione peroxidase homologue; low-temperature-inducible protein;  
XX salt-stress induced protein; SALT; WSR5; ALDP; plant tolerance;  
XX early salt-responding glucose 6 phosphate 1 dehydrogenase; salt shock;  
XX plastidic fructose 1,6-bisphosphate aldolase homologue; osmotic stress;  
XX environmental stress; sodium compartmentalisation; salt stress; PCR;  
XX sodium ion influx; sodium ion efflux; plant metabolism; primer; ss.  
XX  
OS Lolium perenne.  
XX  
XX  
XX WO2003031631-A1.  
XX  
XX 17-APR-2003.  
XX  
XX 04-OCT-2002; 2002WO-AU001346.  
XX  
XX 05-OCT-2001; 2001AU-00008112.  
XX  
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
XX (AGRE-) AGRSEARCH LTD.  
XX  
XX Spengenberg G, Sawbridge TI, Ong EK, Emmerling M;  
XX WPI; 2003-381721/36.  
XX  
XX New substantially purified or isolated nucleic acid or nucleic acid  
XX fragment encoding a salt-inducible or salt responsive protein, useful as  
XX genetic markers for modifying plant tolerance to environmental and/or  
XX osmotic stress.  
XX  
XX Example 6; Page 38; 297pp; English.  
XX  
XX The present invention relates to the isolation of perennial ryegrass  
XX (Lolium perenne) nucleic acids and nucleic acid fragments encoding salt-  
XX inducible or salt responsive proteins. The salt-inducible or salt  
XX responsive proteins include salt-inducible proteins (ES13), glutathione  
XX peroxidase homologues (CSA), low-temperature-inducible proteins (LTI6),  
XX salt-stress induced proteins (SALT), early salt-responding glucose 6

CC phosphate 1 dehydrogenase (WSR5), and plastidic fructose 1,6-bisphosphate  
CC aldolase homologues (ALDP). The nucleic acids and nucleic acid fragments  
CC are useful as genetic markers. The nucleic acids, nucleic acid fragments,  
CC constructs, and vectors containing them are useful for modifying plant  
CC tolerance to environmental stress and/or osmotic stress, plant capacity  
CC to survive salt shock, compartmentalisation of sodium in a plant, sodium  
CC ion influx and/or efflux in a plant, plant recovery after exposure to  
CC salt stress, or plant metabolism under salt stress. The present sequence  
CC represents a PCR primer used in the examples of the present invention  
XX  
SQ Sequence 22 BP; 8 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 22;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5500 ACTTGAAATACCCCGA 5517  
Db 4 ACTTGAAATACCCCGA 21  
RESULT 3181  
ADA15387  
ID ADA15387 standard; DNA; 22 BP.  
XX  
XX ADA15387;  
XX  
XX 06-NOV-2003 (first entry)  
DE Mouse HYPLIP1 locus PCR primer #327.  
XX  
XX  
XX Mouse; PCR; primer; ss; HYPLIP1; FCHL1 variation; lipid disorder;  
XX allele; anti-lipid disorder; anti-cancer therapy; gene therapy;  
XX familial combined hyperlipidaemia; coronary artery disease;  
XX atherogenic lipoprotein phenotype; hyperobesity; hypercholesterolaemia;  
XX hypertriglyceridaemia; low density lipoprotein subclass B; LDL;  
XX familial dyslipidaemia; hypertension; syndrome X; hypercholesterolaemia;  
XX obesity; insulin resistance; cancer; cytostatic; antilipase;  
XX hypotensive; anorectic.  
XX  
OS Mus sp.  
XX  
XX  
XX US2003064372-A1.  
XX  
XX  
XX 03-APR-2003.  
XX  
XX 07-SEP-2001; 2001US-00949428.  
XX  
XX 22-JUN-2000; 2000US-0213322P.  
XX  
XX (BODN/) BODNAR J S.  
XX (CAST/) CASTELLANI L W.  
XX (CHAT/) CHATTERJEE A.  
XX (JONG/) JONG P D.  
XX (LUST/) LUSTS A J.  
XX (OHME/) OHMEN J.  
XX (ROSS/) ROSS D.  
XX (TAFU/) TAFURI S.  
XX (WUCC/) WU C.  
XX  
XX Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusst AJ;  
XX Ohmen J, Ross D, Tafuri S, Wu C;  
XX WPI; 2003-540780/51.  
XX  
XX Novel isolated polynucleotide comprising a mouse or human familial  
XX combined hyperlipidaemia 1 gene having a variation that is associated with  
XX a lipid disorder, useful for identifying susceptibility to the lipid  
XX disorder.  
XX  
XX Claim 11; Page 40; 63pp; English.  
XX  
XX The invention discloses isolated polynucleotides comprising mouse HYPLIP1

CC cDNA sequence, mouse HYPLIP1 genomic DNA, or the homologous human  
 CC familial combined hyperlipidaemia 1 (FCHL1) gene, where a variation in  
 CC the sequence is associated with a lipid disorder. Also claimed is an  
 CC isolated polypeptide comprising a variant form of the mouse HYPLIP1 amino  
 CC acid sequence, or a variant form of a fully defined human FCHL1 amino  
 CC acid sequence, where the variant is associated with the lipid disorder,  
 CC an isolated polynucleotide having at least 12 contiguous nucleotides of  
 CC the isolated polynucleotides, where the 12 contiguous nucleotides span  
 CC the variation position, an isolated polypeptide comprising 4 contiguous  
 CC amino acids of the encode polypeptides, where the 4 contiguous amino  
 CC acids span the variation position, a kit for the detection of the FCHL1  
 CC locus comprising, an isolated antibody, identifying susceptibility to a  
 CC lipid disorder which comprises comparing the nucleotide sequence of the  
 CC suspected FCHL1 allele with a wild-type FCHL1 nucleotide sequence, where  
 CC the difference between the suspected allele and the wild-type sequence  
 CC identifies a sequence variation of FCHL1 nucleotide sequence and a  
 CC pharmaceutical composition. Also disclosed is a transgenic animal which  
 CC carries an altered HYPLIP1 or FCHL1 allele and a method for screening  
 CC drugs for inhibition or restoration of FCHL1 gene function as an anti-  
 CC lipid disorder or anti-cancer therapy. The polynucleotides, polypeptides  
 CC and antibodies are useful for treating or preventing (e.g. gene therapy)  
 CC a lipid disorder associated with expression of FCHL1, for diagnosis or  
 CC prognosis of predisposition to lipid disorder, and cancer and for  
 CC treating a lipid disorder such as familial combined hyperlipidaemia,  
 CC coronary artery disease, atherogenic lipoprotein phenotype,  
 CC hyperapoproteinemia, hypertriglyceridaemia, low density  
 CC lipoprotein (LDL) subclass B, familial dyslipidemic hypertension,  
 CC syndrome X, hypercholesterolemia, obesity, insulin resistance and  
 CC cancer. The sequence presented is a PCR primer which was used to amplify  
 CC part of the mouse HYPLIP1 locus.

XX  
 SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGACCTTGAGTGACA 561  
 |||||  
 Db 4 GTGCACATTGAGTGACA 21

#### RESULT 3182

ID ADB95949 standard; DNA; 22 BP.

XX AC ADB95949;

XX DT 04-DEC-2003 (first entry)

XX DE Mouse HYPLIP1 PCR primer #327.

XX KW cytostatic; antilipemic; gene therapy; peptide therapy; HYPLIP1; FCHL1;  
 KW cancer; metabolic pathway; cellular mechanism; lipid disorder;  
 KW familial combined hyperlipidaemia; mouse; PCR; primer; ss.

XX OS Mus sp.

XX PN US2003054418-A1.

XX PD 20-MAR-2003.

XX PF 07-SEP-2001; 2001US-00949427.

XX PR 08-SEP-2000; 2000US-0231322P.

XX PA (BODN/) BODNAR J S.

XX PA (CAST/) CASTELLANI L W.

XX PA (CHAT/) CHATTERJEE A.

XX PA (JONG/) JONG P D.

XX PA (LUSI/) LUSIS A J.

XX PA (OHME/) OHMEN J.

XX PA (ROSS/) ROSS D.

PA (TAFU/) TAFURI S.  
 XX (WUCC/) WU C.  
 PI Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusis AJ;  
 PI Ohmen J, Rose D, Tafuri S, Wu C;  
 XX WPI; 2003-695901/66.

PT Novel human FCHL1 or mouse HYPLIP1 polypeptide, useful for drug  
 PT screening, peptide therapy of lipid disorder or cancer.

XX Claim 11; Page 39; 56pp; English.

XX The invention describes an isolated polypeptide (I) comprising a variant  
 CC form of a mouse HYPLIP1 polypeptide sequence (S1) or a human FCHL1  
 CC polypeptide sequence (S2), not given in the specification, where the  
 CC variant form is associated with cancer, or an amino acid sequence having  
 CC at least 65 % sequence identity to (S1) or (S2). A composition comprising  
 CC DNA encoding (I) is useful for treating or preventing cancer associated  
 CC with expression of FCHL1. FCHL1 gene or HYPLIP1 gene and its product are  
 CC useful for the study of metabolic pathway and cellular mechanism to  
 CC identify other genes, receptors and relationships that contribute to  
 CC lipid disorder and cancer. FCHL1 gene or its fragments are useful in gene  
 CC therapy to increase the amount of the expression products of the gene for  
 CC the treatment of lipid disorder or cancerous cells. The sequence  
 CC variation of FCHL1 gene or HYPLIP1 gene is also useful in the diagnosis  
 CC and prognosis of predisposition to lipid disorder and cancer. Antisense  
 CC polynucleotide sequences are useful in preventing or diminishing the  
 CC expression of HYPLIP1 or FCHL1 locus. This sequence represents a primer  
 CC used in the analysis of the mouse HYPLIP1 gene.

XX  
 SQ Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 544 GTGACCTTGAGTGACA 561  
 |||||  
 Db 4 GTGCACATTGAGTGACA 21

#### RESULT 3183

ID ADC84386/c standard; DNA; 22 BP.

XX AC ADC84386;

XX DT 01-JAN-2004 (first entry)

XX DE Human papillomavirus type MW8 detection oligonucleotide #9.

XX KW probe; human papilloma virus; HPV; detection; identification; ss.

XX OS Human papillomavirus.

XX PN EP1302550-A1.

XX PD 16-APR-2003.

XX PF 10-OCT-2001; 2001EP-00123379.

XX PR 10-OCT-2001; 2001EP-00123379.

XX PA (KING-) KING CAR FOOD IND CO LTD.

XX PI Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Fan C;

XX PI Hau H, Shin C, Yeh C, Kao Y, Pan C, Chan P;

XX DR WPI; 2003-432398/41.

XX Detector for identifying human papilloma virus subtypes, comprises  
 PT carrier having two parts carrying first and second oligonucleotides that

PT respectively hybridize with DNA contained in first and second subtypes of  
 PT the virus.  
 XX  
 PS Claim 4; SEQ ID NO 616; 221bp; English.  
 CC The invention comprises oligonucleotides for detecting and identifying  
 CC subtypes of human papilloma virus (HPV) contained in a sample. The  
 CC oligonucleotides of the invention are useful for simultaneously detecting  
 CC and identifying subtypes of HPVs. The present DNA sequence represents an  
 CC HPV detection oligonucleotide of the invention.  
 XX  
 SQ Sequence 22 BP; 2 A; 10 C; 9 G; 1 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 40 AGGCTCCGCGCGCGCGC 57  
 22 AGGCTTGGCGCGCGCGC 5  
 RESULT 3184  
 ADC98229  
 ID ADC98229 standard; DNA; 22 BP.  
 AC  
 AC ADC98229;  
 DT 15-JAN-2004 (first entry)  
 DE Mouse type I hair keratin Ha3 PCR primer mHa3 247R.  
 XX  
 KW Mouse; murine; hard keratin; type I hair keratin; Ha3; Bg8;  
 KW hard keratin expression; hair loss; hair shaft injury; hair growth;  
 KW skin disease; tongue disease; nail disease; hair disease;  
 KW dot keratoderm; dermatological; trichological; Tagman analysis;  
 KW expression analysis; PCR; primer; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003087362-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 02-APR-2003; 2003WO-JP004236.  
 XX  
 PR 03-APR-2002; 2002JP-00100843.  
 PR 20-DEC-2002; 2002JP-00369385.  
 XX  
 PA (BANY ) BANYU PHARM CO LTD.  
 XX  
 PI Inoue S, Nambu T, Shimomura T, Itadani H, Tanaka K;  
 DR WPI; 2003-833733/77.  
 XX  
 PT Protein for treatment and prevention of diseases associated with the  
 PT function of hard keratin producing cells, such as hair loss, hair shaft  
 PT injury, abnormal or insufficient hair growth, diseases of the skin,  
 PT tongue, nails and hair.  
 XX  
 PS Example 5; SEQ ID NO 11; 67bp; Japanese.  
 XX  
 CC The invention relates to a human G protein coupled receptor (GPCR). Bg8  
 CC (ADC98222), and nucleic acids encoding it (ADC98221). The human Bg8 gene  
 CC is located on chromosome 12p12. Bg8 is involved in controlling the  
 CC expression of hard keratin such as the type I hair keratins Ha3 and Ha4.  
 CC The invention also relates to antibodies against Bg8, a drug screening  
 CC method using the antibodies, the compounds identified, and a method for  
 CC detecting and controlling functional abnormalities in cells producing  
 CC hard keratin. The invention provides for the treatment and prevention of  
 CC diseases associated with the function of hard keratin-producing cells,  
 CC such as hair loss, hair shaft injury, abnormal or insufficient hair  
 CC growth, diseases of the skin, tongue, nails and hair, and abnormal

CC formation of hard keratin such as dot keratoderm. Sequences ADC98228-  
 CC ADC98229 represent mouse type I hair keratin Ha3 PCR primers used with  
 CC probe ADC98227) in Tagman expression analysis of Bg8-mediated expression  
 CC of type I hair keratin Ha3 in mouse hair follicle tissue.  
 XX  
 SQ Sequence 22 BP; 5 A; 8 C; 4 G; 5 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 1892 ACCTGCGCTCAAGATCA 1909  
 1 ACCTGTGCTTCAGATCA 18  
 RESULT 3185  
 ADE47875  
 ID ADE47875 standard; DNA; 22 BP.  
 AC  
 AC ADE47875;  
 DT 29-JAN-2004 (first entry)  
 DE Human NOVX forward PCR primer SEQ ID NO:237.  
 XX  
 KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;  
 KW dermatological; anorectic; cytosstatic; antidiabetic; haemostatic;  
 KW anti-HIV; antiaesthetic; antibacterial; antiviral; neuroprotective;  
 KW noctropic; antiparkinsonian; antilipemic; gene therapy; vaccine; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003076642-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024459.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0310291P.  
 PR 08-AUG-2001; 2001US-0310951P.  
 PR 09-AUG-2001; 2001US-0311232P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 14-AUG-2001; 2001US-0312203P.  
 PR 17-AUG-2001; 2001US-0313156P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 20-AUG-2001; 2001US-0313702P.  
 PR 21-AUG-2001; 2001US-0314031P.  
 PR 23-AUG-2001; 2001US-0314466P.  
 PR 28-AUG-2001; 2001US-0315403P.  
 PR 29-AUG-2001; 2001US-0315853P.  
 PR 31-AUG-2001; 2001US-0316508P.  
 PR 21-SEP-2001; 2001US-0323936P.  
 PR 03-DEC-2001; 2001US-0338078P.  
 PR 05-FEB-2002; 2002US-0354655P.  
 PR 05-MAR-2002; 2002US-0361764P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 15-MAY-2002; 2002US-0380971P.  
 PR 15-MAY-2002; 2002US-0380980P.  
 PR 16-MAY-2002; 2002US-0381039P.  
 PR 28-MAY-2002; 2002US-0383761P.  
 PR 29-MAY-2002; 2002US-0383887P.  
 PR 01-AUG-2002; 2002US-00210130.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Zexhuen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;  
 PI Pena CE, Shimkets RA, Li L, Berghs C, Zhong M, Casman ST, Voss EZ;  
 PI Boljod FL, Padigar M, Mitchson G, Shenoy SG, Ji W, Gorman L;  
 PI Vernet CM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;  
 PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;

PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eissen A, Gangolli EA,  
 PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;  
 PI Taupier RJ, Catterton E;  
 XX WPI; 2003-779062/73.  
 XX  
 PT New NOXV polypeptides and nucleic acids, useful for preventing or  
 PT treating NOXV-associated disorders, e.g. cancer, diabetes,  
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing  
 PT or pharmacogenomics.  
 PS  
 XX Example 49; SEQ ID NO 237; 562bp; English.  
 CC The invention relates to a novel (NOXV) human polypeptide. A polypeptide  
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,  
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,  
 CC haemostatic, anti-HIV, antiaesthetic, antibacterial, virucide,  
 CC neuroprotective, nootropic, antiparkinsonian, and antilipase activity.  
 CC A polynucleotide encoding a polypeptide of the invention may have a use  
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is  
 CC useful in the manufacture of a medicament for treating a syndrome  
 CC associated with a human disease. The disease selected from a pathology  
 CC associated with the polypeptide. These may also be used in diagnosing,  
 CC treating or preventing NOXV-associated disorders such as cardiomyopathy,  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,  
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,  
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's  
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting  
 CC disorders associated with chronic diseases. The nucleic acids are also  
 CC used as hybridisation probes, in chromosome mapping, tissue typing,  
 CC preventive medicine, and pharmacogenomics. The polypeptides are also  
 CC useful as vaccines. The present sequence represents a PCR primer used in  
 CC the invention.  
 CC  
 XX  
 SQ Sequence 22 BP; 1 A; 11 C; 0 G; 10 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5318 CTCCTCTTCTCTCTT 5335  
 Db 3 CTCCTCTTCTCTCTCT 20  
 RESULT 3186  
 ADE47878  
 ID ADE47878 standard; DNA; 22 BP.  
 XX  
 AC ADE47878;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human NOXV forward PCR primer SEQ ID NO:240.  
 XX  
 KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;  
 KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;  
 KW anti-HIV; antiaesthetic; antibacterial; virucide; neuroprotective;  
 KW nootropic; antiparkinsonian; antilipase; gene therapy; vaccine; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003076642-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024459.  
 XX  
 PR 02-AUG-2001; 2001US-0309501P.  
 PR 03-AUG-2001; 2001US-0310291P.  
 PR 08-AUG-2001; 2001US-0310951P.

PR 09-AUG-2001; 2001US-0311292P.  
 PR 13-AUG-2001; 2001US-0311979P.  
 PR 14-AUG-2001; 2001US-0312203P.  
 PR 17-AUG-2001; 2001US-0313156P.  
 PR 17-AUG-2001; 2001US-0313201P.  
 PR 20-AUG-2001; 2001US-0313702P.  
 PR 21-AUG-2001; 2001US-0314031P.  
 PR 23-AUG-2001; 2001US-0314466P.  
 PR 28-AUG-2001; 2001US-0315403P.  
 PR 29-AUG-2001; 2001US-0315853P.  
 PR 31-AUG-2001; 2001US-0316508P.  
 PR 21-SEP-2001; 2001US-0323936P.  
 PR 03-DEC-2001; 2001US-0338078P.  
 PR 05-FEB-2002; 2002US-0354655P.  
 PR 05-MAR-2002; 2002US-0361764P.  
 PR 19-APR-2002; 2002US-0373825P.  
 PR 15-MAY-2002; 2002US-0380971P.  
 PR 15-MAY-2002; 2002US-0380980P.  
 PR 16-MAY-2002; 2002US-0381039P.  
 PR 28-MAY-2002; 2002US-0383761P.  
 PR 29-MAY-2002; 2002US-0383887P.  
 PR 01-AUG-2002; 2002US-00210130.  
 XX  
 XX (CURAGEN CORP.  
 XX  
 PI Zarnhusen BD, Paturajan M, Kekuda R, Miller CE, Rieger DK;  
 PI Pena CE, Shinkels RA, Li L, Berghe C, Zhong M, Casman SD, Voas EZ;  
 PI Boldog FI, Patigaru M, Smithson G, Shenoy SG, Ji W, Gorman L;  
 PI Verne CM, Lettice MW, Guo X, Anderson DM, Szytel KA, Gerlach VJ;  
 PI Burgess CE, Kirtamsov NV, Ort T, Ellerman K, Raetelli L, Agee ML;  
 PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eissen A, Gangolli EA;  
 PI Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalte T, Liu X;  
 PI Taupier RJ, Catterton E;  
 XX WPI; 2003-779062/73.  
 XX  
 DR  
 XX  
 PT New NOXV polypeptides and nucleic acids, useful for preventing or  
 PT treating NOXV-associated disorders, e.g. cancer, diabetes,  
 PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing  
 PT or pharmacogenomics.  
 PS  
 XX Example 49; SEQ ID NO 240; 562bp; English.  
 CC The invention relates to a novel (NOXV) human polypeptide. A polypeptide  
 CC of the invention has cardiant, antiarteriosclerotic, hypotensive,  
 CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,  
 CC haemostatic, anti-HIV, antiaesthetic, antibacterial, virucide,  
 CC neuroprotective, nootropic, antiparkinsonian, and antilipase activity.  
 CC A polynucleotide encoding a polypeptide of the invention may have a use  
 CC in gene therapy, and as a vaccine. A polypeptide of the invention is  
 CC useful in the manufacture of a medicament for treating a syndrome  
 CC associated with a human disease. The disease selected from a pathology  
 CC associated with the polypeptide. These may also be used in diagnosing,  
 CC treating or preventing NOXV-associated disorders such as cardiomyopathy,  
 CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,  
 CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,  
 CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,  
 CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's  
 CC disease), haematopoietic disorders, dyslipidaemias and other wasting  
 CC disorders associated with chronic diseases. The nucleic acids are also  
 CC used as hybridisation probes, in chromosome mapping, tissue typing,  
 CC preventive medicine, and pharmacogenomics. The polypeptides are also  
 CC useful as vaccines. The present sequence represents a PCR primer used in  
 CC the invention.  
 CC  
 XX  
 SQ Sequence 22 BP; 1 A; 11 C; 0 G; 10 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.8; DB 1; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5318 CTCCTCTTCTCTCTT 5335  
 Db 3 CTCCTCTTCTCTCTCT 20

```

Db          3  CTCCTCCTTTTACACTCTCT 20

RESULT 3187
AAAN70276/C
ID  AAAN70276 standard; DNA; 26 BP.
XX
XX
AC  AAAN70276;
XX
DT  03-OCT-2002 (revised)
DT  26-MAY-1991 (first entry)
XX
DE  Sequence of scissile link probe MRC060 (HL).
XX
XX  Hybridisation; probe; ss.
XX
OS  Synthetic.
XX
PN  EP227976-A.
XX
PD  08-JUL-1987.
XX
PF  04-DEC-1986; 86RP-00116906.
XX
PR  05-DEC-1985; 85US-00805279.
XX
PA  (MEIO-) MEIOGENICS INC.
XX
PI  Duck P, Bender R, Crosby W, Robertson JG;
XX
XX  WPI; 1987-186567/27.
DR
XX
XX  Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT  linked by a scissile linkage.
XX
XX  Example; p29; 46pp; English.
PS
XX
XX  The patent claims a new molecule of formula (NA1---S---NA2)n. NA1 and
CC  NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC  linkage; n 1 or 1,000, which is used for the detection of specific DNA
CC  or RNA sequences in a test soln. The scissile link probes may be PL
CC  (Permanent Linkage to Solid Support) or HL (Hydrolyzable Linkage to Solid
CC  Support). The differential liability of DNA and RNA may be exploited in a
CC  heterogeneous system when the scissile linkage is an RNA molecule. In the
CC  examples, counter probe molecules 9 through 16 were used to determine
CC  suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC  OS field.)
CC
SQ  Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match          0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0.

QY          4012 AAATGAGAAAAAGAGAAACAA 4037
Db          26 AAAAAAAAAAAAAAAAAAAAAA 1
      ||| | | | | | | | | | | | | | | |
      ||| | | | | | | | | | | | | | | |

RESULT 3188
AAAN70275/C
ID  AAAN70275 standard; DNA; 26 BP.
XX
XX
AC  AAAN70275;
XX
DT  03-OCT-2002 (revised)
DT  26-MAY-1991 (first entry)
XX
DE  Sequence of scissile link probe MRC059 (HL).
XX
XX  Hybridisation; probe; ss.
XX
OS  Synthetic.
XX

```

```

XX      EP227976-A.
XX      08-JUL-1987.
XX
XX      04-DEC-1986;    86EP-00116906.
XX
XX      PF      05-DEC-1985;    85US--00805279.
XX
XX      PR      (MEIO-) MEIOGENICS INC.
XX
XX      PA
XX
XX      PI      Duck P, Bender R, Crosby W, Robertson JG;
XX
XX      DR      WPJ; 1987-186567/27.
XX
XX      PT      Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX      linked by a scissile linkage.
XX
XX      PS      Example; p29; 46pp; English.
XX
XX      CC      The patent claims a new molecule of formula (NA1----S-----NA2)n. NA1 and
XX      CC      NA2 are noncomplementary nucleic acid sequences; --S--- = a scissile
XX      CC      linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX      CC      or RNA sequences in a test soln. The scissile link probes may be PL
XX      CC      (Permanent Linkage to Solid Support) or HL (Hydrolyzable Linkage to Solid
XX      CC      Support). The differential liability of DNA and RNA may be exploited in a
XX      CC      heterogeneous system when the scissile linkage is an RNA molecule. In the
XX      CC      examples, counter probe molecules 9 through 16 were used to determine
XX      CC      suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
XX      CC      OS field.)
XX
XX      SQ      Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
XX
XX      Query Match          0.2%; Score 14.8; DB 1; Length 26;
XX      Best Local Similarity 73.1%; Pred. No. 2.6e+03;
XX      Matches   19; Conservative   0; Mismatches    7; Indels     0; Gaps     0.
XX
XX      QY      4012 AAAATGAGAAAAAAGAGAAAACAA 4037
XX           ||||| | | | | | | | | | | | | | |
XX      DB      26 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX      RESULT 3189
XX      ID      AAN92241/C
XX      AC      AAN92241 standard; DNA; 26 BP.
XX
XX      AC      AAN92241;
XX
XX      DT      25-MAR-2003 (revised)
XX      DT      31-OCT-2002 (revised)
XX      DT      25-APR-1990 (first entry)
XX
XX      SS      Probe MRCO59.
XX
XX      KW      Probe MRCO59; solid support; ribonuclease.
XX
XX      OS      Synthetic.
XX
XX      FH      Key Location/Qualifiers
XX      FT      misc_feature 1..10
XX      FT      /tag= a
XX      FT      /note= "deoxyribonucleotides."
XX      FT      11..14
XX      FT      /*tag= b
XX      FT      /notes= "ribonucleotides."
XX      FT      misc_feature 15..26
XX      FT      /tag= c
XX      FT      /note= "deoxyribonucleotides."
XX
XX      PN      WO8910415-A.
XX
XX      PD      02-NOV-1989.
XX

```

PF 29-APR-1988; 88US-00187814.  
XX  
XX 29-APR-1988; 88US-00187814.  
XX  
XX (MEIO-) MEIOGENICS INC.  
XX  
XX Duck P, Bender R;  
XX WPI; 1989-339977/46.  
XX  
XX  
XX Detecting target nucleic acid molecules - using excess complementary  
PT nucleic acid probes and nicking to complete a cycling sequence.  
XX  
XX  
XX Disclosure; Page 24; 34pp; English.  
XX  
XX Probe MRC059 is bound by a hydrolysable linkage to a solid support at its  
CC 3' end. It is used by reacting excess probe with a target nucleic acid;  
CC nicking hybridised probe at least once within a predetermined sequence to  
CC form 2 or more probe fragments hybridised to the target sequence, which  
CC results in the probe fragments becoming hybridised to another probe; and  
CC identifying probe fragments, so detecting the target sequence. The probe  
CC can react with target sequence to complete a cycling sequence. Using this  
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can  
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg  
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;  
SQ  
Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 3190  
AAN92242/c  
ID AAN92242 standard; DNA; 26 BP.  
XX  
XX AAN92242;  
AC  
XX 25-MAR-2003 (revised)  
DT 31-OCT-2002 (revised)  
DT 25-APR-1990 (first entry)  
XX  
XX SS probe MRC060.  
DE  
XX  
XX Probe MRC060; solid support; ribonuclease.  
KM  
XX  
XX Synthetic.  
OS  
XX  
XX Key  
FH Location/Qualifiers  
FT 1..12  
FT /\*tag= a  
FT /note= "deoxyribonucleotides."  
FT 13..16  
FT /\*tag= b  
FT /note= "ribonucleotides."  
FT 17..26  
FT /\*tag= C  
FT /note= "deoxyribonucleotides."  
XX  
XX W08910415-A.  
XX  
XX 02-NOV-1989.  
PD  
XX 29-APR-1988; 88US-00187814.  
PF  
XX 29-APR-1988; 88US-00187814.  
PR  
XX 29-APR-1988; 88US-00187814.  
CC

PA (MEIO-) MEIOGENICS INC.  
XX  
XX Duck P, Bender R;  
XX  
XX WPI; 1989-339977/46.  
XX  
XX  
XX Detecting target nucleic acid molecules - using excess complementary  
PT nucleic acid probes and nicking to complete a cycling sequence.  
XX  
XX  
XX Disclosure; Page 24; 34pp; English.  
XX  
XX Probe MRC060 is bound by a hydrolysable linkage to a solid support at its  
CC 3' end. It is used by reacting excess probe with a target nucleic acid;  
CC nicking hybridised probe at least once within a predetermined sequence to  
CC form 2 or more probe fragments hybridised to the target sequence, which  
CC results in the probe fragments becoming hybridised to another probe; and  
CC identifying probe fragments, so detecting the target sequence. The probe  
CC can react with target sequence to complete a cycling sequence. Using this  
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can  
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg  
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;  
SQ  
Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 3191  
AAF77536/c  
ID AAF77536 standard; DNA; 26 BP.  
XX  
XX AAF77536;  
AC  
XX 23-MAY-2001 (first entry)  
DT  
XX  
XX CDNA library production method related oligonucleotide SEQ ID NO: 5.  
DE  
XX  
XX CDNA library production; SCLA; gene chip technology;  
KM differential screening; pathological diagnosis; genetic identification;  
KM single-cell CDNA library amplification; de.  
XX  
XX Synthetic.  
OS  
XX  
XX US6197554-B1.  
PN  
XX  
XX 06-MAR-2001.  
PD  
XX  
XX 20-NOV-1998; 98US-00197951.  
PF  
XX 20-NOV-1998; 98US-00197951.  
PR  
XX  
XX (LINS/) LIN S.  
PA (CHUO/) CHUDONG C.  
PA (YING/) YING S.  
XX  
XX Lin S, Chuong C, Ying S;  
PI  
XX  
XX WPI; 2001-243448/25.  
DR  
XX  
XX Generating a complete full-length CDNA library from single cells for use  
PT in gene chip technology, involves reverse transcribing intracellular  
PT mRNAs, adding polynucleotide tail and amplifying formed cDNAs.  
XX  
XX Disclosure; Col 11-12; 11pp; English.  
PS  
XX  
XX The present invention describes a method of producing full-length CDNA  
CC



CC libraries from single cells, designated single-cell cDNA library  
CC amplification (SGLA). The method is useful in gene chip technology,  
CC differential screening, pathological diagnosis, physiological prognosis  
CC and genetic identification. No further information about this sequence is  
CC given in the specification  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 3192  
AAD03682/C  
ID AAD03682 standard; DNA; 26 BP.  
AC AAD03682;  
XX  
XX  
DT 19-JUN-2001 (first entry)  
XX  
XX Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.  
DE Human; phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;  
KW antipruritic; cytoskeletal; antiatherosclerotic; antiinfectivity;  
KW cardiant; antiinflammatory; dermatological; wound healing; antiviral;  
KW antibacterial; therapy; inflammatory bowel disease; diverticulitis;  
KW spermatogenesis; sperm capacitation; immunosuppressive; vaccine;  
KW cancer; reperfusion ischemia; psoriasis; melanoma; myocarditis; PID;  
KW pelvic inflammatory disease; eczema; scleroderma; vasooconstriction;  
KW heart arrhythmia; congestive heart disease; muscle spasm; fatigue;  
KW chromosomal abnormality; gene therapy; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200125444-A2.  
PN  
XX  
XX 12-APR-2001.  
PD  
XX  
XX 06-OCT-2000; 2000WO-US027734.  
PE  
XX  
XX 07-OCT-1999; 99US-00414025.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Preenell SR, Novak JE, Gao Z;  
PI  
XX  
XX WPI; 2001-266312/27.  
DR  
XX  
XX Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide  
PT encoding it, for detecting human chromosomal abnormalities, identifying  
PT modulators and treating inflammatory and cardiovascular diseases.  
XX  
XX Example 1C; Page 118; 122pp; English.  
PS  
XX  
XX The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA  
CC and its corresponding protein. Zcytor13 protein is used to promote wound  
CC healing in tissues, to exhibit anti-bacterial and anti-viral effects and  
CC to identify modulators (e.g. agonists or antagonists). Zcytor13, its  
CC agonists or antagonists are useful in the treatment of inflammatory heart  
CC or cardiovascular conditions, muscle inflammation, inflammation during  
CC and after surgery, arthritis, asthma, inflammatory bowel disease or  
CC diverticulitis, for modulating spermatogenesis, sperm capacitation, as  
CC immunosuppressive or anti-fertility vaccine and for treating male  
CC infertility. Zcytor13 protein and its antibodies are used to diagnose  
CC cancer, reperfusion ischemia, asthma, psoriasis and melanoma. Zcytor13  
CC proteins are used to enhance fertilisation. Zcytor13 antagonists are used  
CC to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),  
CC psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13

CC sequences and/or its antibodies are useful for treatment of disorders  
CC associated with vasoconstriction, heart arrhythmia, congestive heart  
CC disease, muscle spasms and fatigue. They are used for detecting human  
CC chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.  
CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins  
CC are useful for enhancing in vivo killing of target tissue. The present  
CC sequence is a polyA PCR primer, ZC7764b which is used to isolate full  
CC length zcytor13 cDNA by screening human placental cDNA library  
XX  
XX  
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 4011 TAAATGAGAAAAAGAGAAACAA 4036  
Db 26 TAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 3193  
AAF23526/C  
ID AAF23526 standard; DNA; 26 BP.  
AC AAF23526;  
XX  
XX  
XX 22-MAR-2001 (first entry)  
DT  
XX  
XX Primer #4.  
DE  
XX  
XX Primer; mRNA; amplification; ss.  
KW  
XX  
XX Unidentified.  
OS  
XX  
XX WO200075356-A1.  
PN  
XX  
XX 14-DEC-2000.  
PD  
XX  
XX 04-JUN-1999; 99WO-US012461.  
PE  
XX  
XX 04-JUN-1999; 99WO-US012461.  
PR  
XX  
XX (LINS//) LIN S.  
PA (YING//) YING S.  
PA (CHUO//) CHUONG C.  
PA (WIDE//) WIDELITZ R B.  
XX  
XX Lin S, Ying S, Chuong C, Widelitz RB;  
PI  
XX  
XX WPI; 2001-061734/07.  
DR  
XX  
XX Generating amplified messenger RNA sequences from single cells, involves  
PT cycling steps of reverse transcription, denaturation, double-stranded DNA  
PT sequences and in vitro transcription.  
XX  
XX Disclosure; Page 17; 31pp; English.  
PS  
XX  
XX The present invention relates to generating amplified messenger RNAs with  
CC polymerase reaction activity, comprising cycling steps of reverse  
CC transcription, denaturation, double-stranded cDNA synthesis and in vitro  
CC transcription. The invention is used for generating amplified mRNAs from  
CC limited mRNAs from single cells  
XX  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

```
RESULT 3194
AAS20596/c
ID AAS20596 standard; DNA; 26 BP.
XX
XX AAS20596;
AC
XX
XX 23-APR-2002 (first entry)
DE Human zsig63 cDNA sequencing primer ZC7764a.
XX
XX Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KM microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KM gastrointestinal disease; urinary tract infection; vaginal infection;
KM skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KM acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KM chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX
XX Homo sapiens.
OS
XX US6331413-B1.
PN
XX 18-DEC-2001.
PD
XX 17-MAR-2000; 2000US-00527345.
PF
XX 17-MAR-1999; 99US-0124820P.
PR
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX PI Adler DA, Shepard PO;
XX WPI; 2002-096707/13.
DR
XX Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
PT
XX
XX Example 1; Col 53; 29pp; English.
PS
XX The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
CC
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 4011 TAAATGAGAAAAAGAGAAAAACA 4036
Db 26 TAAAAAAAAAAAAAAAAAAAAA 1
RESULT 3195
AAS2638/c
ID AAS2638 standard; DNA; 26 BP.
XX
XX AAS2638;
AC
XX
XX 15-NOV-2002 (first entry)
DE Human secreted salivary protein zsig63 PCR primer ZC7764a.
XX
XX Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
```

```
KM antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KM fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KM tooth decay; periodontal disease; thrush; gastrointestinal disease;
KM urinary tract infection; vaginal infection; skin infection; microflora;
KM epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KM chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KM incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KM chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KM digestion; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX US2002081701-A1.
PN
XX 27-JUN-2002.
PD
XX 03-AUG-2001; 2001US-00922480.
PF
XX 17-MAR-1999; 99US-0124820P.
PR
XX 17-MAR-2000; 2000US-00527345.
PA
XX (ADLER) ADLER D A.
PA (SHEP) SHEPPARD P O.
PI
XX PI Adler DA, Shepard PO;
XX WPI; 2002-635468/68.
DR
XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
PT
XX
XX Example 1; Page 29; 33pp; English.
PS
XX The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
CC
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 4011 TAAATGAGAAAAAGAGAAAAACA 4036
Db 26 TAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 3196  
AAD45055/C  
ID AAD45055 standard; DNA; 26 BP.  
XX  
XX AAD45055;  
AC  
XX  
XX 27-DEC-2002 (first entry)  
DT  
XX ZC7764a primer used in the identification of human zsi63 DNA.  
DE  
XX  
XX Human; secreted salivary proteain; zsi63 protein; host defense protein;  
KW immune modulating factor; antipathogenic; cell-cell signalling molecule;  
KW growth factor; cytokine; growth factor hormone activity; dental carries;  
KW infection; tooth decay; periodontal disease; gastrointestinal disease;  
KW thrush; urinary tract infection; vaginal infection; diabetes; obesity;  
KW anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;  
KW gene therapy; salivary gland dysfunction; prostate gland dysfunction;  
KW forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; 88.  
OS Homo sapiens.  
XX  
XX US2002090677-A1.  
PN  
XX 11-JUL-2002.  
PD  
XX 03-AUG-2001; 2001US-00923236.  
XX  
XX 17-MAR-1999; 99US-0124820P.  
PR 17-MAR-2000; 2000US-00527345.  
XX  
XX (ADLE/) ADLER D A.  
PA (SHEP/) SHEPPARD P O.  
XX  
XX Adler DA, Sheppard PO;  
PI WPI; 2002-642378/69.  
XX  
XX Novel secreted salivary polypeptide, zsi63, useful as antimicrobial  
PT agent for treating microbial infection, dental carries, periodontal  
XX disease, thrush gastrointestineal disease, and for aiding digestion.  
XX  
XX Example 1; Page 30; 33pp; English.  
PS  
XX  
XX The invention relates to human secreted salivary polypeptide designated  
CC as zsi63 and nucleic acid molecules encoding such polypeptides. zsi63  
CC can be used in detecting agonists and antagonists of its activity, and is  
CC also useful as a host defense polypeptide, immune modulating factor,  
CC antipathogenic polypeptide, cell-cell signalling molecule, growth factor,  
CC cytokine, or as secreted extracellular matrix associated proteins with  
CC growth factor hormone activity. It is useful for treating conditions  
CC associated with pathological microbes, including bacterial, fungal and  
CC viral infections, for treating dental carries (tooth decay), periodontal  
CC disease, thrush and gastrointestinal disease, for treating urinary tract  
CC infection, vaginal infection and for preventing infection in skin and  
CC other epithelial wounds. zsi63 is useful for establishing normal  
CC microflora and protect against pathogenic colonisation and invasion, for  
CC treating chronic tissue damage e.g. damage in extremities associated with  
CC diabetes and useful as anti-inflammatory agents. It is useful as a marker  
CC of lung dysfunction, salivary gland dysfunction, or dysfunction of  
CC prostate gland. It is also therapeutically useful for aiding digestion.  
CC Polynucleotides of the invention are used in gene therapy for increasing  
CC or inhibiting zsi63 activity, for detecting abnormalities on human  
CC chromosome 4 associated with disease or other human traits and as  
CC diagnostics in forensic DNA profiling. Sequences of the invention are  
CC useful for stimulating proliferation or differentiation of cardiac  
CC myocytes, for proliferation or differentiation of adipocytes and for  
CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The  
CC present sequence is a primer used in the identification of human zsi63  
CC DNA  
XX  
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
XX

Query Match	0.2%;	Score 14.8;	DB 1;	Length 26;
% Best Local Similarity	73.1%;	Pred. No. 2.6e+03;		
% Matches' 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0
Db	4011 TAAATGAGAAAAAAGAGAGAAAACA	4036		
	26 TAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1		
RESULT 3197				
AAS20671/C				
ID AAS20671 standard; DNA; 26 BP.				
XX AAS20671;				
AC AAS20671;				
DT 09-APR-2002 (first entry)				
DE Human zalphall ligand sequencing primer ZC77664a.				
XX				
KM Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;				
KW natural killer cell proliferation; T-cell proliferation;				
KM B-cell proliferation; anti-tumour response; immune system;				
KW immunostimulant; cyclostatic; human; sequencing primer; ss.				
XX				
OS Homo sapiens.				
XX				
PN US6307024-B1.				
PD 23-OCT-2001.				
PF 09-MAR-2000; 2000US-00522217.				
PR 09-MAR-1999; 99US-0123547P.				
PR 11-MAR-1999; 99US-0123904P.				
PR 01-JUL-1999; 99US-0142013P.				
PA (Zymo ) ZYMOGENETICS INC.				
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;				
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;				
XX				
DR WPI; 2002-040208/05.				
XX				
PT New zalphall ligand polypeptides and polynucleotides, useful for				
PT stimulating proliferation, activation, differentiation and/or induction				
PT of inhibition of specialized cell function, or for stimulating an				
PT antigenic response.				
PS Example 7; Col 139; 105bp; English.				
XX				
CC The present invention relates to the isolation of a novel cytokine,				
CC zalphall ligand and the polynucleotide encoding it. The invention also				
CC gives the sequence for the zalphall receptor and the polynucleotide				
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of				
CC natural killer (NK) cells or NK cell progenitors, the activation of NK				
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with				
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and				
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The				
CC zalphall ligand polypeptide is also useful in preparing antibodies that				
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can				
CC be used as probes or primers to clone regions of a zalphall ligand gene,				
CC and in gene therapy. Zalphall ligand may also be used to identify				
CC inhibitors of its activity, to enhance the generation of anti-tumour				
CC responses with or without the infusion of donor lymphocytes, and to				
CC activate or stimulate the immune system. The present sequence represents				
CC a sequencing primer used to sequence cDNA clones in the isolation of				
CC human zalphall ligand				
XX				
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;				
Query Match	0.2%;	Score 14.8;	DB 1;	Length 26;
% Best Local Similarity	73.1%;	Pred. No. 2.6e+03;		
% Matches' 19; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

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QY      4011 TAAATGAGAAAAAGAGAAAAACA 4036
      ||||| ||||| ||||| |||||
DB      26 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3198
AAD43853/C
ID      AAD43853 standard; DNA; 26 BP.
XX
AC      AAD43853;
XX
DT      14-NOV-2002 (first entry)
XX
DE      Primer #2 used to illustrate the method of the invention.
XX
KM      Single stranded polynucleotide tag; cleavage agent; gene expression;
KM      primer; ss.
XX
OS      Unidentified.
XX
PN      WO200259357-A2.
XX
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-DK000052.
XX
PR      24-JAN-2001; 2001DK-00000126.
PR      12-FEB-2001; 2001US-0267704P.
XX
PA      (GENO-) GENOMIC EXPRESSION APS.
XX
PI      Pedersen ML;
XX
DR      WPI; 2002-636542/68.
XX
PT      Obtaining single stranded polynucleotide tags from a biological sample,
PT      for analyzing gene expression or diagnosing clinical conditions,
PT      comprises employing nicking endonucleases that cleave complementary
PT      strands.
XX
PS      Example; Page 294; 302pp; English.
XX
CC      The invention relates to a method for obtaining a single stranded
CC      polynucleotide tag from a biological sample by cleaving one of the
CC      complementary strands of a double stranded polynucleotide with a cleavage
CC      agent capable of recognising a double stranded polynucleotide comprising
CC      complementary strands and cleaving only one of the strands of the
CC      polynucleotide in the process of generating a single stranded
CC      polynucleotide tag. The method is useful for separating, analyzing,
CC      quantifying or obtaining single stranded polynucleotides comprising tags
CC      originating partly, and preferably wholly from a source of DNA and/or RNA
CC      in a sample comprising biological cells. The method is particularly for
CC      analyzing gene expression (expression profiling or differential gene
CC      expression), or in diagnosing clinical conditions. The present sequence
CC      is a primer used in the exemplification of the invention
XX
SQ      Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
QY      Query Match      0.2%; Score 14.8; DB 1; Length 26;
      Best Local Similarity 73.1%; Pred. No. 2.6e+03;
      Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY      4012 AAAATGAGAAAAAGAGAAAAACA 4037
      ||||| ||||| ||||| |||||
DB      26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3199
AB224784/C
ID      AB224784 standard; DNA; 26 BP.
XX
AC      AB224784;
XX

```

```

XX
DT      07-APR-2003 (first entry)
XX
DE      Oligodeoxynucleic acid molecule ODN 24.
XX
KM      Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KM      ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..26
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "thiophosphate backbone"
XX
PN      WO200295027-A2.
XX
PD      28-NOV-2002.
XX
PF      17-MAY-2002; 2002WO-EP005448.
XX
PR      21-MAY-2001; 2001AT-0000805.
XX
PA      (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA      (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI      Lingnau K, Schellack C, Schmidt W;
XX
DR      WPI; 2003-183880/18.
XX
PT      New oligodeoxynucleic acid molecules useful for the preparation of
PT      vaccine.
XX
PS      Example 8; Page 32; 57pp; English.
XX
CC      The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC      (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
CC      invention is based on the discovery that ODNs containing deoxyuridine
CC      residues (U-ODNs) have an immunostimulatory effect comparable to, or in
CC      many instances greater than, ODNs containing Cpg motifs, producing higher
CC      numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC      the systemic production of pro-inflammatory cytokines and, in contrast to
CC      Cpg ODNs, are not dependent on a specific motif or a palindromic
CC      sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC      Combining the U-ODN with an antigen strongly increases the potential of
CC      the antigen to raise the protection/immune response of a vaccinated
CC      individual. An example of the invention demonstrated the generation of a
CC      specific immune response against a melanoma-derived peptide (see
CC      APP58360) by injection of mice with the peptide in combination with ODN
CC      24
XX
SQ      Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
QY      Query Match      0.2%; Score 14.8; DB 1; Length 26;
      Best Local Similarity 73.1%; Pred. No. 2.6e+03;
      Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY      4012 AAAATGAGAAAAAGAGAAAAACA 4037
      ||||| ||||| ||||| |||||
DB      26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3200
ABX93599/C
ID      ABX93599 standard; DNA; 26 BP.
XX
AC      ABX93599;
XX
DT      28-MAY-2003 (first entry)
XX
DE      Human zsig63 PCR/sequencing primer ZC7764a.
XX

```

KM ss; PCR; zsig63; adhesin; salivary gland; dental carries;  
 KM periodontal disease; thrush; gastrointestinal disease; epithelial wound;  
 KM urinary tract infection; vaginal infection; skin infection; primer; AIDS;  
 KM pro-inflammatory; chronic tissue damage; vascular system; diabetes;  
 KM lung infection; cystic fibrosis; lung dysfunction; digestive;  
 KM salivary gland carcinoma; Pneumocystis carinii infection; emphysema;  
 KM chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;  
 KM cell culture media; gene therapy; human chromosome 4q12-4q13;  
 KM dentinogenesis imperfecta; dentin dysplasia type II.  
 OS Synthetic.  
 PN US2002173027-A1.  
 PD 21-NOV-2002.  
 PF 03-AUG-2001; 2001US-00922469.  
 PR 17-MAR-1999; 99US-0124820P.  
 PR 17-MAR-2000; 2000US-00527345.  
 PA (ADLER/) ADLER D A.  
 PA (SHEP/) SHEPPARD P O.  
 PI Adler DA, Sheppard PO;  
 DR WPI; 2003-328428/31.  
 XX Novel isolated zsig63 polypeptide, member of the adhesin family, useful  
 PT for treating dental carries, periodontal disease, thrush,  
 PT gastrointestinal disease, urinary tract infections, vaginal infections,  
 PT skin infections.  
 PS Example 1; Page 29; 32pp; English.  
 XX The invention relates to an isolated zsig63 polypeptide comprising at  
 CC least 90% identity to an amino acid sequence which comprises domain 1 of  
 CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also  
 CC included are the polynucleotide encoding zsig63, a zsig63 expression  
 CC vector, a cultured cell comprising the vector and expressing the protein,  
 CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-  
 CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a  
 CC zsig63 reporter gene construct to identify zsig63 agonists, and producing  
 CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is  
 CC useful for detecting in a test sample, the presence of antagonist of  
 CC zsig63 protein activity. Zsig63 has antimicrobial activity and since  
 CC exhibits high expression in salivary gland, can be used for treating  
 CC dental carries, periodontal disease, thrush, and gastrointestinal  
 CC disease, urinary tract infections, vaginal infections, skin infections  
 CC and other epithelial wounds. The polypeptides can be used to establish  
 CC normal microflora and protect against pathogenic colonization and  
 CC invasion. Zsig63 can also be used for providing pro-inflammatory activity  
 CC for treating chronic, tissue damage particularly in areas having limited  
 CC or damaged vascular system, e.g. in diabetes, and for treating  
 CC immunocompromised AIDS patients or in individuals that have undergone  
 CC chemotherapy, radiation treatment, for treating lung infections e.g. in  
 CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high  
 CC levels in the trachea may indicate that such polypeptides may serve as a  
 CC marker of lung dysfunction. Zsig63 is also useful in diagnosing  
 CC conditions associated with salivary gland or lung dysfunction including  
 CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,  
 CC chronic bronchitis, prostate dysfunctions such as prostate  
 CC adenocarcinoma, aiding digestion, and as components of defined cell  
 CC culture media and may be used to replace serum that is commonly used in  
 CC culture. The DNA is useful in gene therapy applications to increase or  
 CC inhibit zsig63 activity, and for detecting abnormalities on human  
 CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,  
 CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The  
 CC present sequence is a primer used to isolate and sequence nucleic acids  
 CC encoding human zsig63  
 XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
 Matches, 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 4011 TAAATGAGAAAAGAGAAAACA 4036  
 Db 26 TAAAAA 1  
 RESULT 3201  
 ID ACA62282/c  
 XX ACA62282 standard; DNA; 26 BP.  
 AC ACA62282;  
 XX 12-AUG-2003 (first entry)  
 DT 12-AUG-2003 (first entry)  
 DE Oligo (dt) primer #1.  
 XX ss; PCR; primer; antisense therapy; mRNA expression profile;  
 KM promoter containing primer.  
 OS Synthetic.  
 PN US2003022318-A1.  
 PD 30-JAN-2003.  
 PF 07-SEP-2001; 2001US-00949305.  
 PR 25-JAN-2000; 2000US-00494212.  
 PA (EPIC-) EPICLONE INC.  
 PI Lin S, Ying S;  
 DR WPI; 2003-479488/45.  
 XX Improved polymerase thermocycling reaction for nucleic acid  
 PT amplification, by thermal cycling of promoter-linked nucleic acid  
 PT template synthesis and in vitro transcriptional amplification of nucleic  
 PT acid sequences.  
 PS Example 4; Page 14; 28pp; English.  
 XX The invention relates to an improved polymerase thermocycling reaction  
 CC (M1) for linear amplification of nucleic acid sequences, involves  
 CC denaturing a number of nucleic acid templates (I1), combining the  
 CC denatured (I1) with a promoter-containing primer (P1), a primer (P2), a  
 CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,  
 CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA  
 CC polymerase, contacting P1 with (I1) to generate a number of promoter-  
 CC containing templates, denaturing the promoter-containing templates,  
 CC contacting P2 with the denatured promoter-containing templates to  
 CC generate a number of promoter-containing double-stranded DNA templates,  
 CC where the double-stranded nucleic acid templates are flanked by P1 in one  
 CC end and P2 in the other end of the other orientation, transcribing the  
 CC promoter-containing double-stranded DNA templates to form a number of  
 CC amplified RNA sequences, including the primer region of the promoter-  
 CC containing double-stranded DNA templates, contacting the amplified RNA  
 CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA  
 CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method  
 CC is useful for improved polymerase thermocycling reaction for linear  
 CC amplification of nucleic acid sequences, and thus for producing mRNA  
 CC expression profile of a cell by M1 to generate multiple copies of the  
 CC mRNA. M1 is also useful for determining aberrant protein production of  
 CC cells in a diseased state, by generating an expression profile by the  
 CC above method, of cells in both normal and diseased states, comparing the  
 CC expression profile of the cells in the normal and diseased states,  
 CC determining the differences in mRNA composition of the cell(s) in the  
 CC diseased state, isolating the mRNA sequences of cell(s) in the diseased  
 CC state that differ from mRNA in cell(s) in non-diseased state, amplifying  
 CC the isolated mRNA by M1, and determining aberrant protein function of the

protein coded for by the isolated mRNA. M1 is also useful for treating a cell in a diseased state caused by aberrant protein production, by determining protein expression of a cell in a diseased state, determining the mRNA sequence for the aberrant proteins, synthesizing an antisense sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and delivering a pharmaceutically effective dosage of a composition comprising the anti-sense mRNA and a compatible lipid based biological carrier. M1 is also useful for predicting the efficacy of a proposed drug targeted against an aberrant protein, by determining aberrant protein production of cell in a diseased state by the above method, amplifying the aberrant protein by M1 and using recombinant techniques to determine the effect of proposed drug on the aberrant protein. M1 is also useful for differential screening of tissue-specific gene expression at a cellular level, for preparing labeled RNA/DNA probes for a gene chip technology, and for determining the efficacy of a drug regimen against a gene or its cDNAs. The present sequence is an Oligo (dt) primer used to produce second strand cDNA in the method of the invention

SO Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 26;  
Best Local Similarity 73.1%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAACAA 4037  
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3202  
AAV71935/c  
ID AAV71935 standard; DNA; 27 BP.  
AC AAV71935;  
XX 18-FEB-1999 (first entry)  
XX Anchored poly T RT-PCR primer.  
DE Normalised; cDNA library; mRNA cloning; reverse transcription;  
XX Immobilise; screening; hybridisation; nucleic acid amplification;  
KM expression pattern; drug development; PCR primer; RT-PCR; ss.  
XX Synthetic.  
OS  
XX WO9851789-A2.  
PN 19-NOV-1998.  
PD 13-MAY-1998; 98MO-DK000186.  
XX 13-MAY-1997; 97DK-00000547.  
PR 19-MAY-1997; 97US-00871030.  
PR 27-MAR-1998; 98DU-00000432.  
XX (DISP-) DISPLAY SYSTEMS BIOTECH APS.  
PA  
XX Marchoe PR;  
PI  
XX WPI; 1999-009772/01.  
XX  
XX Preparation of normalised, subdivided cDNA libraries from mRNA - by  
PT reverse transcription and amplification, used to screen for new genes and  
PT intersecting proteins, potential drugs, and for diagnosis.  
XX  
XX Example 1; Page 29; 71pp; English.  
XX The invention relates to preparation of a normalised, subdivided library  
CC of amplified cDNA from the coding regions of mRNA in a sample. The method  
CC involves reverse transcription, with at least one cDNA primer of formula  
CC 5'-Con1-dtn2-Vn3-Nn4 to form first strand cDNA where Con1 = any sequence  
CC of 1-100 nucleotides; dt = deoxythymidyl; n2 is at least 1; n3 and n4  
CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand

cDNA synthesis using the first strand as template and a second cDNA primer of a similar formula, in the presence of DNA polymerase I (or its Klenow fragment) and amplification of double-stranded cDNA with a set of amplification primers. Comparison of cDNA in the prepared library with a database (a computer-generated list of molecular weights of restricted cDNA fragments of known sequence) is used to determine presence of an expressed protein in a cell, also to detect changes in such expression (particularly for diagnosis of disease). Surfaces (chip) having amplified cDNA stably immobilised on it, obtained by a similar method, are used to screen for genes of a particular family, by hybridisation with nucleic acid from the family (to identify new genes) and to detect differences in expression patterns between cells. The polypeptides expressed by the cDNA libraries can be used for drug development. Sequences AAV71935 to CCAAV71946 represent primers used to exemplify the method of the invention

SO Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 27;  
Best Local Similarity 73.1%; Pred. No. 2.7e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4011 TAAATGAGAAAAAGAGAAACAA 4036  
Db 26 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3203  
AAA40358/c  
ID AAA40358 standard; DNA; 28 BP.  
XX AAA40358;  
XX 10-NOV-2000 (first entry)  
XX pBluescriptSK+ phagemid primer SEQ ID NO: 8.  
DE Primer; cloning; ligation; ss.  
XX  
XX Synthetic.  
OS  
XX WO200036088-A1.  
PN 22-JUN-2000.  
PD 17-DEC-1999; 99MO-US030277.  
XX 17-DEC-1998; 98US-00213834.  
PR 17-DEC-1998; 98US-00213834.  
XX (ROMA/) ROMANTCHIKOV Y.  
PA  
XX Romanchikov Y;  
PI  
XX WPI; 2000-442381/38.  
XX  
XX Inserting a nucleic acid into a circular vector comprising joining their  
PT ends, melting, and reannealing ends at two different concentrations,  
PT useful for cloning small amounts of nucleic acids and forming genomic  
PT libraries.  
XX  
XX Example 3; Page 67; 71pp; English.  
XX This invention describes a novel method (M1) for inserting a nucleic acid  
CC (M1) into a circular vector (V1) comprising joining ends of M1 and V1  
CC under a first nucleic acid concentration, melting hybridized cohesive  
CC circularization ends, and reannealing the ends at a second concentration.  
CC The methods are useful for the cloning small amounts of nucleic acids and  
CC forming genomic libraries of complex populations of DNA or cDNA. The  
CC methods allow the cloning of minute amounts of nucleic acids efficiently  
CC and avoids the size selection problems of prior art systems. Larger  
CC nucleic acid fragments are just as easily cloned, allowing highly  
CC representative libraries to be made. Vector to vector ligation is avoided  
CC using the methods. AAA40351-A40366 represents primers used to illustrate  
CC the method of the invention

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XX      SQ      Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
Query Match      0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012  AAAATGAGAAAAAGAGAAAAACA 4037
Db      27  AAAAAAAAAAAAAAAAAAAAACTA 2

RESULT 3204
AA57856/C
ID  AA57856 standard; DNA; 28 BP.
XX
AC  AA57856;
XX
DT  11-OCT-2000 (first entry)
XX
DE  Deoxy-T22-tagged substrate oligonucleotide.
XX
KW  Ribozyme; catalytic RNA; analyte detection; effector molecule;
KM  nucleic acid substrate; in vitro selection; ribozyme ligase;
XX  conformation dependent activity; allosteric activation; ss.
OS  Synthetic.
XX
XX  Key      Location/Qualifiers
FH  misc_RNA 23..28
FT  /*tag= a
FT  misc_binding 24..28
FT  /*tag= b
FT  /bound_molecy= "Bases 13-17 of N90 RNA pool (AA57851)"

XX      WO200024931-A2.
XX
XX      04-MAY-2000.
XX
XX      PD  22-OCT-1999; 99WO-IL000557.
XX
XX      PR  23-OCT-1998; 98IL-00126731.
XX
XX      PA  (INTE-) INTELIGENE LTD.
XX
XX      PI  Nachan A, Ellington A;
XX
XX      WIPI; 2000-350763/30.
XX
XX      DR  Detecting an analyte in a sample comprises providing nucleic acid
PT  sequence which is catalytically active in presence of analyte, contacting
PT  catalytic nucleic acid with substrate and amplifying catalytic product.
XX
XX      Disclosure; Page; 36pp; English.
XX
XX      The invention relates to a method of detecting an analyte in a sample.
CC  The method comprises providing a nucleic acid sequence which is initially
CC  catalytically inactive, but which becomes catalytically active in the
CC  presence of an analyte (the effector); providing a nucleic acid substrate
CC  for the catalytic activity of the nucleic acid sequence; and contacting
CC  the nucleic acid sequence and the substrate with the sample under
CC  conditions allowing catalytic activity of nucleic acid sequences. The
CC  catalytic nucleic acid sequence will be able to convert the nucleic acid
CC  substrate into a nucleic acid product only if the analyte of interest is
CC  present. The nucleic acid catalytic product is then amplified, and a
CC  significant increase in the amount of product indicates the presence of
CC  the analyte in the sample. The method is useful for the qualitative or
CC  quantitative determination of an analyte in a sample in diagnostic
CC  assays. The invention describes the in vitro selection of a ribozyme
CC  ligase (L1; AA57859, AA57860) which is catalytically active only in the
CC  presence of an oligonucleotide effector (AA57854). The L1 ribozyme
CC  ligase was selected from a pool of RNA molecules comprising a central
CC  randomised region 90 nucleotides in length flanked on both sides by

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CC  constant sequence regions (the N90 RNA pool; AA57851). In the presence
CC  of the effector, selection was performed using one of the tagged
CC  substrate molecules AA57855-A57857. RNAs with ligase activity (i.e.,
CC  those which have become ligated to the substrate molecule) were reverse
CC  transcribed using the effector oligo, and then PCR amplified using the
CC  effector and a DNA primer identical in sequence to the substrate used for
CC  the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC  can only adopt its active conformation (AA57859) in the presence of the
CC  effector oligo (analyte). In the absence of the effector, L1 adopts an
CC  inactive conformation (AA57860). The present sequence represents the
CC  deoxy-T22-tagged substrate oligonucleotide. The dt22 tag enables
CC  successfully ligated products to be isolated using oligo (dt) cellulose
CC  Type 7. Note: The present sequence is not given in the specification, but
CC  is created from the information given on page 11
XX
XX      SQ      Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;
Query Match      0.2%; Score 14.8; DB 1; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4014  AATGAGAAAAAGAGAAAAACA 4039
Db      28  AGTCAGAAAAAAGAAAAA 3

RESULT 3205
AAF60450
ID  AAF60450 standard; DNA; 28 BP.
XX
AC  AAF60450;
XX
DT  27-APR-2001 (first entry)
XX
DE  RNA oligonucleotide #7.
XX
XX  Protein-RNA fusion; ss.
XX
XX  Unidentified.
XX
XX  Key      Location/Qualifiers
FH  modified_base 1
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "C6-psoralen-2-Ome-U"
FT  modified_base 28
FT  /*tag= b
FT  /mod_base= OTHER
FT  /note= "A-TBG2"

XX      WO200107657-A1.
XX
XX      PD  01-FEB-2001.
XX
XX      PF  19-JUL-2000; 2000WO-US019653.
XX
XX      PR  27-JUL-1999; 99US-0145834P.
XX
XX      PA  (PHYL-) PHYLLOS INC.
XX
XX      PI  Kurz M, Lohse P, Wagner R;
XX
XX      WIPI; 2001-182803/18.
XX
XX      DR  Affixing a peptide acceptor to an RNA molecule useful for producing
PT  fusion proteins for isolating proteins or nucleic acids with desired
PT  properties through attachment of a peptide acceptor to the 3' end of an
PT  RNA molecule.
XX
XX      Example 6; Page 29; 56pp; English.
XX
XX      The present invention relates to a method for affixing a peptide acceptor
CC  to an RNA molecule through the formation of a covalent bond, noncovalent

```

CC bond, or by chemical ligation. The method is useful for producing RNA-  
CC protein fusions which can be used for the isolation of proteins or  
CC nucleic acids with desired properties from large pools of partially or  
CC completely random amino acid or nucleic acid sequences. The present  
CC sequence is an RNA oligonucleotide used in the present invention

XX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 28;  
Best Local Similarity 65.4%; Pred. No. 2.7e+03;  
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6159 TAGGGATGACATTAAGAAAAGA 6184  
:|||||:|||||  
Db 1 UAGCGGAGUGCAAAAAAAAAAAAAA 26

## RESULT 3206

AA45359  
ID AAL45359 standard; RNA; 28 BP.

XX AAL45359;

DT 06-JUN-2002 (first entry)

DE Puromycin linker DNA sequence.

XX Peptide cleavage; chemical active ingredient targeted release; diagnosis;  
KM antidiabetic; osteoporotic; cytostatic; asthma; osteoporosis; cancer;  
KM stroke; neuronal disease; arthritis; pancreatitis; hypertension;  
KM thrombosis; infection; schistosomiasis; herbicide; insecticide;  
KM fungicide; cerebroprotective; neurological; antithrombotic; pancreatic;  
KM hypotensive; antithrombotic; virucide; protozoacide; ds.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1

FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "modified by psoralen and 2'-O-methyl"

FT modified\_base 28

FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "modified by (PBG) 2 CC (Puromycin linker)"

XX WO200216574-A2.

XX 28-FEB-2002.

XX 07-AUG-2001; 2001WO-EP009102.

XX 22-AUG-2000; 2000DE-01041238.

XX (XZIL-) XZILION GMBH & CO KG.

XX Reimholz R, Ploeger F;

XX WPI; 2002-269356/31.

PT Identifying specifically cleavable peptide, useful for targeted drug  
PT delivery and developing protease inhibitors, by incubating test compound  
PT with peptide-nucleic acid fusion.

XX Example 1; Page 19; 38pp; German.

CC The present invention relates to the identification of specific  
CC proteolytically cleavable peptides by incubating a library of fusion  
CC molecules, comprising a peptide and nucleic acid encoding said peptide,  
CC with a proteolytically active sample, then isolating the cleavage  
CC fragments and determining the coding sequences in the separated fusion  
CC molecules. The coding sequences identified by the method are used for  
CC production of specifically proteolytically cleavable substances, which

CC are useful in the treatment of asthma, osteoporosis, cancer, stroke,  
CC neuronal diseases, arthritis, pancreatitis, hypertension, thrombosis,  
CC viral infections and schistosomiasis. Also contemplated are similar  
CC compounds designed to release herbicides, insecticides and fungicides,  
CC when cleaved. The present sequence is a puromycin linker described in the  
CC exemplification of the invention

XX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.2%; Score 14.8; DB 1; Length 28;  
Best Local Similarity 65.4%; Pred. No. 2.7e+03;  
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 6159 TAGGGATGACATTAAGAAAAGA 6184  
:|||||:|||||  
Db 1 UAGCGGAGUGCAAAAAAAAAAAAAA 26

## RESULT 3207

AAF26222/C  
ID AAF26222 standard; DNA; 30 BP.

XX AAF26222;

DT 26-APR-2001 (first entry)

DE APC binding protein associated primer ON-AT- SEQ ID 7.

XX ABC binding protein; cell proliferation; adenomatous polyposis coli;  
KM tumor cell detection; primer; ss.

XX Unidentified.

XX DE19933237-A1.

XX 18-JAN-2001.

XX 15-JUL-1999; 99DE-01033237.

XX 15-JUL-1999; 99DE-01033237.

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Mueller O;

XX WPI; 2001-148321/16.

PT Determining proliferative capacity of cells, useful e.g. for detecting  
PT tumor cells, by measuring concentration and subcellular localization of  
PT adenomatous polyposis coli protein.

XX Claim 10; Page 13; 26pp; German.

CC This invention describes a novel method for determining the proliferative  
CC activity of cells, comprising detecting, in a sample, the concentration  
CC and/or subcellular localization of APC (adenomatous polyposis coli)  
CC protein (I). The invention also describes (i) determining function of (I)  
CC in a sample by detecting presence of the C-terminal, DNA-binding domain  
CC of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting  
CC the DNA-binding domain of (I); (3) purifying, enriching and/or detecting  
CC (I) or its fragments by reaction with a probe; (4) double-stranded DNA  
CC (II) that contains the sequence GCGCGA 2 3G (S1) and/or GATCCT 2 3GC  
CC (S2); (5) peptide fragment of (I) containing at least the DNA-binding  
CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340  
CC -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,  
CC one of which is Ab and the other directed against the N-terminal region  
CC (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or  
CC its fragments in a sample consisting of (I), Ab or the set of (7). The  
CC method is used to detect proliferative, especially tumor (precursor),  
CC cells, to detect function of (I) and mutations in (I), and to purify  
CC and/or enrich (I), or its fragments, from a sample. The method allows  
CC simple, rapid and reliable detection of proliferation, without the need  
CC for polymerase chain reaction or sequencing





PD 10-JAN-2002.  
 XX 02-JUL-2001; 2001WO-US020951.  
 PF 30-JUN-2000; 2000US-0215511P.  
 PR (GENA-) GENAISSANCE PHARM INC.  
 PA Anaestasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sauer EA,  
 PI Stephens CJ;  
 PT WPI; 2002-164539/21.  
 XX  
 PT Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene  
 PT polymorphic variants, useful e.g. in studying the expression and function  
 PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.  
 XX  
 PS Claim 17; Page 13; 104pp; English.  
 CC The invention relates to an isolated polypeptide comprising a sequence  
 CC which is a polymorphic variant of a reference sequence for the amyloid  
 CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its  
 CC fragment. The polymorphic variants are useful in studying the expression  
 CC and function of APPBP1, in expressing APPBP1 protein for use in screening  
 CC for candidate drugs to treat diseases related to APPBP1 activity, in  
 CC studying the effect of the variation on the biological activity of  
 CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for  
 CC the treatment of disorders such as Alzheimer's disease. The haplotyping  
 CC methods are useful in validating APPBP1 as a candidate target for  
 CC treating a specific condition or disease predicted to be associated with  
 CC APPBP1 activity, or in the design of clinical trials of candidate drugs  
 CC for treating a specific condition or disease associated with APPBP1  
 CC activity. The transgenic animals are useful for studying expression of  
 CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs  
 CC targeted against APPBP1 protein, and for testing the efficacy of  
 CC therapeutic agents and compounds for disorders related to platelet  
 CC aggregation in a biological system. ABK32771-ABK32327 represent human  
 CC APPBP1 gene allele-specific oligonucleotides used in the method of the  
 CC invention  
 CC  
 SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4470 TTTT TTTT TTTT TTTG 4484  
 Db 15 TTTT TTTT TTTT TTTG 1  
 RESULT 3211  
 AAT6167/C  
 ID AAT6167 standard; DNA; 20 BP.  
 XX  
 AC AAT6167;  
 XX  
 DT 15-JUL-1997 (first entry)  
 DE UDP-glucose:thiohydroximate S-glucosyltransferase primer g13.  
 XX  
 KW Glucosinolate: UDP-glucose:thiohydroximate S-glucosyltransferase; S-GT;  
 KW transgenic plant; rapeseed oil; oilseed rape; canola; Brassica napus;  
 KW polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 PS  
 PN EP71878-A1.  
 XX  
 PD 07-MAY-1997.  
 PF 31-OCT-1995; 95EP-00402425.  
 XX

PR 31-OCT-1995; 95EP-00402425.  
 XX  
 XX (PLBZ ) PLANT GENETIC SYSTEMS NV.  
 PA (CANADA ) NAT RES COUNCIL CANADA.  
 PI Van Audenhove K, Peferoen M, Grootwassink JWD, Underhill EW;  
 PI Hemmingen SM, Reed DW, Kolenovsky AD;  
 DR WPI; 1997-247418/23.  
 XX  
 PT Plants genetically transformed to interfere with UDP-  
 PT glucose:thiohydroximate S-glucosyltransferase gene expression - useful  
 PT for production or rapeseed oil with reduced glucosinolate content.  
 XX  
 PS Example 2; Page 17; 35pp; English.  
 CC  
 CC Degenerate primers based on 7 peptide sequences (AAW09826-32) of Brassica  
 CC oleracea UDP-glucose:thiohydroximate S-glucosyltransferase (S-GT) were  
 CC used in the PCR-RACE amplification of Brassica napus S-GT cDNA (see also  
 CC AAT66166). Primer g13 (AAT66167) was combined with the Anchor Primer of  
 CC the Clontech 3'RACE kit (AAT66170), and the product was used as template  
 CC in a second semi-nested PCR to yield S-GT partial clone pGL2-7 (AAT66173)  
 CC  
 SQ Sequence 20 BP; 6 A; 1 C; 1 G; 4 T; 0 U; 8 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 20;  
 Best Local Similarity 55.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
 QY 7110 AAAATGAATTACTTCTCTG 7129  
 Db 20 AATTTAAATTTNSWTCYTG 1  
 RESULT 3212  
 ABN83985  
 ID ABN83985 standard; DNA; 20 BP.  
 XX  
 AC ABN83985;  
 XX  
 DT 02-OCT-2002 (first entry)  
 DE Leishmania kinetoplast mini circle DNA PCR primer #1.  
 XX  
 KW Leishmania parasite; pharmaceutical; kinetoplast; PCR; primer; ss.  
 KM  
 OS Leishmania sp.  
 XX  
 OS  
 PN BR200004507-A.  
 XX  
 PD 30-APR-2002.  
 XX  
 PF 28-SEP-2000; 2000BR-00004507.  
 XX  
 PR 28-SEP-2000; 2000BR-00004507.  
 XX  
 PA (FIOC-) FIOCRUZ FUNDACAO CRUZ OSWALDO.  
 PA (UTMT-) UNIV FEDERAL MINAS GERAIS.  
 PI Romanha AJ, Volpini AC, De Azeredo Passos VM, Correa Oliveira G;  
 PI WPI; 2002-417703/45.  
 DR Molecular differentiation of Leishmaniosis parasites consists of  
 PT detection by PCR RFLP technique via initiators and nucleotides.  
 XX  
 PS Claim 2; Page 11; 38pp; Portuguese.  
 CC  
 CC The invention relates to the molecular differentiation of Leishmaniasis  
 CC parasites. The method of the invention comprises detection of parasites  
 CC of the Leishmania (Viannia) braziliensis, Leishmania (Viannia) guyanensis  
 CC and Leishmania amazonensis species. The method employs initiators  
 CC nucleotides and buffer solution in a polymerase chain reaction-

```
CC restriction length polymorphism (PCR-RFLP) technique. Methods of the
CC invention are useful in pharmaceuticals. The current sequence represents
CC a PCR primer for amplification of conserved regions of Kinetoplast mini
CC circle DNA
XX
SQ Sequence 20 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 2 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.1e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 5150 GGGAGAGGAGGAGTCTCC 5166
    |||:|||||:|||||:
Db 1 GGGAGAGGAGGAGTCTCSC 17

RESULT 3213
AAQ90391
ID AAQ90391 standard; DNA; 21 BP.
XX
AC AAQ90391;
XX
DT 08-JAN-1996 (first entry)
XX
DE CP-1 (synthetic DNA probe with 3'-ribonucleoside terminal #2).
XX
KW CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
KW SAED; hybridisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 21
FT /*tag= a
FT /note= "3'-ribonucleoside terminal"
XX
PN WO9512808-A1.
XX
PD 11-MAY-1995.
XX
PF 26-OCT-1994; 94WO-US012270.
XX
PR 01-NOV-1993; 93US-00146504.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ; Tu E;
XX
DR WPI; 1995-185870/24.
XX
FT New self-addressable electronic devices - used for multi-step and
FT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
FT and bio:polymer synthesis.
XX
PS Example 1; Page 40; 86pp; English.
XX
CC The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
CC are synthetic DNA probes with 5' amino termini. These sequences were
CC specific for the polymorphisms of HLA gene dQa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAED) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy 4020 AAAAAGAGAGAAACAAAT 4040
    |||||:|||||:|||||:
Db 1 AAAAAGAGAGAGAAACAAAU 21

RESULT 3214
AA110743
ID AA110743 standard; RNA; 21 BP.
XX
AC AA110743;
XX
DT 09-SEP-1996 (first entry)
XX
DE Oligonucleotide probe, CP-1.
XX
KW Electronically self-addressable device; ED; electrode; current source;
KW attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 21
FT /*tag= a
FT /note= "3'-ribonucleoside terminus"
XX
PN WO9601836-A1.
XX
PD 25-JAN-1996.
XX
PF 05-JUL-1995; 95WO-US008570.
XX
PR 07-JUL-1994; 94US-00271882.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
DR WPI; 1996-097582/10.
XX
FT Electronically self-addressable device - used for electronic control of,
FT e.g. nucleic acid hybridisation.
XX
PS Example 1; Page 60; 155pp; English.
XX
CC The sequences given in AA110742-67 are synthetic oligonucleotides which
CC are used in the construction of the electronically self-addressable
CC device (ED) of the invention. The ED comprises a substrate, an electrode
CC or opt. a number of electrodes supported by the substrate, a current
CC source operatively connected to the electrode and an attachment layer
CC adjacent to the electrode which is permeable to a counterion but not
CC permeable to the molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 4020 AAAAAGAGAGAAACAAAT 4040
    |||||:|||||:|||||:
Db 1 AAAAAGAGAGAGAAACAAAU 21

RESULT 3215
AAK81302
ID AAK81302 standard; DNA; 21 BP.
```

```

AC AAX81302;
XX
XX 20-AUG-1999 (first entry)
XX
XX 3' ribonucleoside oligonucleotide probe CP-1.
XX
XX Microelectronic device; multi-step reaction; microscopic format;
XX ion-permeable permeation layer; electrode; electrical control; transport;
XX attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX Synthetic.
XX
XX Key location/Qualifiers
XX mibc_RNA 21 /*tag= a
XX
XX MO9929711-A1.
XX
XX 17-JUN-1999.
XX
XX 01-DEC-1998; 98WO-US025475.
XX
XX 05-DEC-1997; 97US-00986065.
XX
XX (NANO-) NANOGEN INC.
XX
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MT, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
XX New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX
XX Example 1; Page 89; 179pp; English.
XX
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic format. A key aspect of this invention is played by the ion
XX -permeable permeation layer which overrules the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific micro-
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analyses or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analyses and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analyses. The
XX present sequence represents a probe used to exemplify the invention
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 76.2%; Pred. No. 2.3e+03;
XX Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4020 AAAAAAGAGAAAACAAAT 4040
XX ||||| ||||| |||||
XX 1 AAAAAAAAAAAAAAAAAAAAAU 21
XX
XX RESULT 3216
XX AAQ75780/c
XX ID AAQ75780 standard; DNA; 21 BP.
XX AC AAQ75780;
XX XX

```

```

DT 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ7547-Q7578)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4016 TGAGAAAAAGAGAAAACA 4036
XX ||||| ||||| |||||
XX 21 TGAGAAAAAGAGAAAACA 1
XX
XX RESULT 3217
XX AAQ75761/c
XX ID AAQ75761 standard; DNA; 21 BP.
XX AC AAQ75761;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX

```

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.  
PS Disclosure; Page 8, 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4014 AATGAGAAAAAGAGAGAAA 4034  
DB 21 AATGAGAAAAAGAGAGAAA 1  
XX  
RESULT 3218  
AAZ26485/C  
ID AAZ26485 standard; DNA; 21 BP.  
XX  
AC AAZ26485;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 674.  
XX  
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX cell viability; loss of heterozygosity; precancerous condition; AS1;  
XX allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
EN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
XX (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, ledley PD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7, 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor

CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AA225812-226825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 16 A; 0 C; 5 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4468 TTTTCTCTCTCTCTCTT 4488  
DB 21 TTTTCTCTCTCTCTCTT 1  
XX  
RESULT 3219  
AAQ13763/C  
ID AAQ13763 standard; DNA; 21 BP.  
XX  
AC AAQ13763;  
XX  
DT 18-DEC-1991 (first entry)  
XX  
DE Oligonucleotide for detection of Agrobacterium rhizogenes derived plasmid  
DE DNA in transformed plant.  
XX  
XX Agrobacterium rhizogenes A4 strain; ss.  
XX  
OS Synthetic.  
XX  
PN JP03198780-A.  
XX  
XX 29-AUG-1991.  
XX  
PF 27-DEC-1989; 89JP-00341678.  
XX  
PR 27-DEC-1989; 89JP-00341678.  
XX  
PA (SHMA) SHIMADZU CORP.  
XX  
DR WPI; 1991-299436/41.  
XX  
PT Oligonucleotide for detection of transformant of plant - uses polymerase  
PT chain reaction process to enable detection of specific extraneous gene  
PT with high sensitivity and selectivity.  
XX  
PS Claim 1; Page 1; 6pp; Japanese.  
XX  
CC The oligonucleotide sequence is used as a probe to selectively detect  
CC Agrobacterium rhizogenes-derived plasmid DNA, as inserted into a plant  
CC genome. It is chemically synthesised and is complementary to T-DNA coding  
CC for the R1 plasmid of A. rhizogenes. It can also be used as a PCR primer  
CC and can easily detect a particular extraneous gene from a transformant  
CC plant with high sensitivity and selectivity  
XX  
SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3007 CTCACCCCATCTTGTACATC 3027  
DB 21 CTCATCCGCTGCTGTACATC 1  
XX  
RESULT 3220

AAQ14885	standard; DNA; 21 BP.
AAQ14885	
20-FEB-1992	(first entry)
Oligo #10	hybridisable to synovial fluid phospholipase A2 cDS.
arachidonic acid; antisease oligonucleotide; rheumatoid arthritis;	
osteoarthritis; lupus; anaphylaxis; urticaria; asthma; psoriasis;	
hepatitis; cerebral oedema; contact dermatitis; ulcerative colitis;	
phosphorothioate linkage; SF-PLA2; ss.	
Synthetic.	
WO9116901-A.	
14-NOV-1991.	
30-APR-1990;	90US-00516969.
30-APR-1990;	90US-00516969.
(ISIS-) ISIS PHARM INC.	
Bennett CF, Ecker DJ, Crooke ST, Mirabelli CK;	
WPI, 1991-353508/48.	
Oligo-nucleotide analogues which modulate arachidonic acid metabolism -	
for treatment and diagnosis of conditions caused by lipoxygenase,	
phospholipase, leukotriene(s) etc.	
Claim 18; Page 54; 87pp; English.	
This oligonucleotide can hybridise to nucleic acids encoding	
phospholipase A2 typical of the synovial fluid of patients with	
rheumatoid arthritis. (SF-PLA2 is more closely related to group II PLA2	
enzymes such as those in rattlesnake venom than to pancreatic PLA2). The	
oligonucleotide (especially its phosphorothioate analogue) would be	
useful in inhibiting SF-PLA2 expression. SF-PLA2 secretion has been	
detected from a human epidermal carcinoma cell line and primary human	
epidermal keratinocytes. This suggests that the inhibitory	
oligonucleotide would be useful in the treatment of inflammatory	
disorders of the skin. See AAQ14859-Q14895	
Sequence 21 BP; 6 A; 2 C; 10 G; 3 T; 0 U; 0 Other;	
Query Match	0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity	81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
1631 GGAAGATTCCGAAGATCGCG 1651	
1 GGAAGCTTCCAGCGAAGNG 21	
RESULT 3221	
AAQ42900/C	
ID	AAQ42900 standard; DNA; 21 BP.
AAQ42900;	
07-OCT-1993	(first entry)
HLA type analysis method DRI & DR4 primer RRGb.	
Human leukocyte antigen; HLA classII gene; DNA polymerase method; ss.	
Synthetic.	
JP05111490-A.	

```

XX 07-MAY-1993.
PD
XX
XX 02-MAR-1992; 92JP-00044935.
PF
XX
XX 29-AUG-1991; 91JP-00244530.
PR
XX
XX (SUMQ ) SUMITOMO METAL IND LTD.
PA
XX
XX WPI; 1993-184838/23.
DR
XX
XX HLA type analysis method and its reagents - includes e.g. amplification
PT of HLA class II gene, digestion by restriction enzyme, electrophoresis
PR and detection.
PT
XX
XX Example; Page 16; 21pp; Japanese.
PS
XX
XX The sequence is that of DR1 & DR4 primer RRGb which was used as part of a
CC method of HLA type analysis involving amplification of a HLA class II
CC gene, or fragments of it, using 2 or more kinds of primers by the DNA
CC polymerase method and subsequent restriction enzyme digestion and
CC analysis. The method enables easier analysis of HLA type
CC
SQ Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1610 AGAAGCTTCACGACGACGTCG 1630
Db 21 AGAGCTTCACGACGACGCGC 1
RESULT 3222
AAQ42902/C
ID AAQ42902 standard; DNA; 21 BP.
XX
XX AAQ42902;
XX
XX 07-OCT-1993 (first entry)
XX
XX HLA type analysis method DR3, 5, 6, 8 primer RRGb.
DE
XX Human leukocyte antigen; HLA classII gene; DNA polymerase method; ss.
XX
XX Synthetic.
OS
XX
XX JP0511490-A.
PN
XX
XX 07-MAY-1993.
PD
XX
XX 02-MAR-1992; 92JP-00044935.
PF
XX
XX 29-AUG-1991; 91JP-00244530.
PR
XX
XX (SUMQ ) SUMITOMO METAL IND LTD.
PA
XX
XX WPI; 1993-184838/23.
DR
XX
XX HLA type analysis method and its reagents - includes e.g. amplification
PT of HLA class II gene, digestion by restriction enzyme, electrophoresis
PR and detection.
PT
XX
XX Example; Page 16; 21pp; Japanese.
PS
XX
XX The sequence is that of DR3, 5, 6, 8 primer RRGb which was used as part
CC of a method of HLA type analysis involving amplification of a HLA class
CC II gene, or fragments of it, using 2 or more kinds of primers by the DNA
CC polymerase method and subsequent restriction enzyme digestion and
CC analysis. The method enables easier analysis of HLA type
CC
SQ Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ

```

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1610 AGAAGCTTCACAGACCGCTGC 1630  
DB 21 AGAGCTTCACAGTGCAGCGGC 1

RESULT 3223  
AAQ35258/C  
ID AAQ35258 standard; DNA; 21 BP.

XX AAQ35258;  
AC  
XX 24-MAY-1993 (first entry)  
DT  
XX Agrobacterium rhizogenes dwarfism gene PCR primer.  
DE  
XX Polymerase chain reaction; detection; ss.  
KW  
XX

OS Synthetic.

XX JP04356189-A.

XX 09-DEC-1992.

XX 31-MAY-1991; 91JP-00128924.

XX 31-MAY-1991; 91JP-00128924.

XX (SHMA ) SHIMADZU CORP.

XX WPI; 1993-030366/04.

XX Oligo:nucleotide for detecting plant transforming principle - is gene  
PT coded to DNA of agrobacterium rhizogenes.

XX Claim 2; Page 2; 10pp; Japanese.

XX The sequence is that of a PCR primer which is used as part of a method  
CC for the detection of a gene relating to dwarfism of Agrobacterium  
CC rhizogenes. The method provides highly sensitive, easy and highly  
CC selective detection

XX Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3007 CTCACCCCATCTGTGCATC 3027  
DB 21 CTCATCGCTGCTGTGCATC 1

RESULT 3224  
AAQ35262/C  
ID AAQ35262 standard; DNA; 21 BP.

XX AAQ35262;  
AC  
XX 24-MAY-1993 (first entry)  
DT  
XX Agrobacterium rhizogenes dwarfism gene PCR primer.  
DE  
XX Polymerase chain reaction; detection; ss.  
KW  
XX

OS Synthetic.

XX JP04356189-A.

XX

PD 09-DEC-1992.

XX 31-MAY-1991; 91JP-00128924.

XX 31-MAY-1991; 91JP-00128924.

XX (SHMA ) SHIMADZU CORP.

XX WPI; 1993-030366/04.

XX Oligo:nucleotide for detecting plant transforming principle - is gene  
PT coded to DNA of agrobacterium rhizogenes.

XX Claim 2; Page 2; 10pp; Japanese.

XX The sequence is that of a PCR primer which is used as part of a method  
CC for the detection of a gene relating to dwarfism of Agrobacterium  
CC rhizogenes. The method provides highly sensitive, easy and highly  
CC selective detection

XX Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3007 CTCACCCCATCTGTGCATC 3027  
DB 21 CTCATCGCTGCTGTGCATC 1

RESULT 3225  
AAQ35268/C  
ID AAQ35268 standard; DNA; 21 BP.

XX AAQ35268;

XX 24-MAY-1993 (first entry)

XX Agrobacterium rhizogenes dwarfism gene PCR primer.

XX Polymerase chain reaction; detection; ss.

XX Synthetic.

XX JP04356189-A.

XX 09-DEC-1992.

XX 31-MAY-1991; 91JP-00128924.

XX 31-MAY-1991; 91JP-00128924.

XX (SHMA ) SHIMADZU CORP.

XX WPI; 1993-030366/04.

XX Oligo:nucleotide for detecting plant transforming principle - is gene  
PT coded to DNA of agrobacterium rhizogenes.

XX Claim 2; Page 2; 10pp; Japanese.

XX The sequence is that of a PCR primer which is used as part of a method  
CC for the detection of a gene relating to dwarfism of Agrobacterium  
CC rhizogenes. The method provides highly sensitive, easy and highly  
CC selective detection

XX Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      3007 CTCACCCCATCTGTCTACATC 3027
      ||||| ||||| ||||| |||||
Db      21 CTCATCGCTGCTGTCTACATC 1

RESULT 3226
AAQ70288/c
ID      AAQ70288 standard; DNA; 21 BP.
XX
AC      AAQ70288;
XX
DT      25-MAR-2003 (revised)
DT      13-APR-1995 (first entry)
XX
DE      Chlamydia trachomatis detection probe CT3.
XX
KM      Capture probe; detection probe; 16S ribosomal RNA; Chlamydia;
KM      nucleic acid hybridisation assay; ss.
XX
OS      Synthetic.
XX
PN      FR2701961-A1.
XX
PD      02-SEP-1994.
XX
PF      24-FEB-1993; 93FR-00002127.
XX
PR      24-FEB-1993; 93FR-00002127.
XX
PA      (INMR ) BIO MERIEUX.
XX
PI      Mabilat C, Christen R;
XX
DR      WPI; 1994-281768/35.
XX
PT      Solid-phase capture probes for nucleic acid hybridisation assays -
PT      comprising immobilised oligo:nucleotide capable of destabilisation of
PT      secondary structure formed in target nucleic acid.
XX
PS      Claim 18; Page 15; 21pp; French.
XX
CC      The detection probe CT3 (AAQ70288) is complementary to a region of the
CC      16S rRNA sequence of Chlamydia trachomatis which forms part of a hairpin
CC      loop. The probe is only able to hybridise to the target RNA in the
CC      presence of a capture probe (i.e. dCT4, AAQ70289) immobilised on a
CC      support. The capture probe destabilises the secondary structure of the
CC      hairpin loop. The oligonucleotide probes CT3 and dCT4 are useful for
CC      distinguishing Chlamydia trachomatis from other closely related Chlamydia
CC      species. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      6938 TGTTCGGCATCCAGAAAGG 6958
      ||||| ||||| ||||| |||||
Db      21 TATTTGGCATCCGAGTAAAG 1

RESULT 3227
AAQ61922
ID      AAQ61922 standard; DNA; 21 BP.
XX
AC      AAQ61922;
XX
DT      25-MAR-2003 (revised)
DT      04-NOV-1994 (first entry)
XX
DE      Human type II phospholipase A2 inhibiting oligomer, ISIS no 3192.
XX
KM      Inhibition; replication; herpes simplex virus; HSV; HIV; aging;
KM      inhibition; replication; herpes simplex virus; HSV; HIV; aging;
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```
KM      human cytomegalovirus; influenza virus; inflammation; telomere length;
KM      neurological disorders; phospholipase A2 activity; hyperproliferation;
KM      malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FH      FT      1..21
FH      misc_feature /tag= a
FH      FT      /note="Phosphorothioate intersugar linkages"

XX
XX      MO9408053-A1.
XX
XX      14-APR-1994.
XX
XX      29-SEP-1993; 93WO-US009297.
XX
XX      29-SEP-1992; 92US-00954185.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
XX      Ecker DU, Vickers TA, Wyatt JR, Imbach JL;
XX      WPI; 1994-135613/16.
XX
XX      New modified oligo-nucleotide contg guanine quartet - inhibits activity
XX      of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
XX      of chromosomes.
XX
XX      Disclosure; Page 26; 144pp; English.
XX
XX      The sequences given in AAQ61917-55 are oligonucleotides which contain a
XX      G4 stretch and which may be used for inhibiting phospholipase A2 enzyme
XX      activity. Oligonucleotides such as these may also be used for inhibiting
XX      activity of HSV, HIV, human cytomegalovirus or influenza virus, or for
XX      treating inflammatory and neurological disorders caused by phospholipase
XX      A2 activity in cases of hyperproliferation, malignancy, cardiovascular
XX      disease and snake bite. They may also be used for inhibiting division of
XX      malignant cells by modulating telomere length, which may also retard
XX      aging. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ      Sequence 21 BP; 6 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1631 GGAAGATTTCACAGATGCGG 1651
      ||||| ||||| ||||| |||||
Db      1 GGAAGTTTCCAGGAAAGAG 21

RESULT 3228
AAQ61989
ID      AAQ61989 standard; DNA; 21 BP.
XX
AC      AAQ61989;
XX
DT      25-MAR-2003 (revised)
DT      04-NOV-1994 (first entry)
XX
DE      HIV replication inhibiting oligomer, T1364T4.
XX
XX      Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
XX      human cytomegalovirus; influenza virus; inflammation; telomere length;
XX      neurological disorders; phospholipase A2 activity; hyperproliferation;
XX      malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
XX
OS      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      FT      modified_base 1
```



```

FT      /*tag= a
FT      /note= "labeled with 32P"
XX      WO9408053-A1.
XX      14-APR-1994.
XX      29-SEP-1993; 93WO-US009297.
XX      29-SEP-1992; 92US-00954185.
XX      (ISIS-) ISIS PHARM INC.
XX      Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL,
PI      Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX      WPI; 1994-135613/16.
XX      New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT      of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT      of chromosomes.
XX      Example 21; Page 60; 144pp; English.
XX      This sequence may be used for inhibiting replication of human immuno-
CC      deficiency virus (HIV). Oligonucleotides such as this may also be used
CC      for inhibiting activity of HSV, human cytomegalovirus or influenza virus,
CC      or for treating inflammatory and neurological disorders caused by
CC      phospholipase A2 activity in cases of hyper-proliferation, malignancy,
CC      cardiovascular disease and snake bite. They may also be used for
CC      inhibiting division of malignant cells by modulating telomere length,
CC      which may also retard aging. (Updated on 25-MAR-2003 to correct PN
CC      field.)
XX      Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      4468 TTTTGTGCTTGTGCTT 4468
DB      1 TTTTGTGCTTGTGCTT 21
RESULT 3229.
AAT11995/C
ID      AAT11995 standard; DNA; 21 BP.
XX      AAT11995;
AC      AAT11995;
XX      25-MAR-2003 (revised)
DT      13-MAR-1996 (first entry)
XX      CMV antisense oligonucleotide (ISIS 4847).
DE      antisense; cytomegalovirus; CMV; human; therapy; prophylaxis; diagnosis;
KM      intermediate early complex; IE1; IE2; DNA polymerase gene; ss.
XX      Synthetic.
OS      Synthetic.
XX      Key Location/Qualifiers
FT      modified_base 1..21 a
FT      /*tag= a
FT      /note= "phosphorothioate backbone"
XX      US5442049-A.
XX      15-AUG-1995.
XX      25-JAN-1993; 93US-00009263.
XX      19-NOV-1992; 92US-00927506.

```

```

XX      (ISIS-) ISIS PHARM INC.
PA      Baker B, Draper K, Anderson K;
XX      WPI; 1995-292538/38.
XX      New oligo-nucleotide inhibits cytomegalovirus replication - by binding to
PT      a portion of cytomegalovirus RNA, for the diagnosis, prophylaxis and
PT      treatment of CMV diseases.
XX      Example 12; Col 17-18; 66pp; English.
XX      A series of 21 phosphorothioate antisense oligonucleotides (ONs)
CC      (AAT11987-2007) were examined for anti-cytomegalovirus (CMV) activity.
CC      ISIS 4847 targets the DNA polymerase gene 5' untranslated region. It has
CC      an IC50 value of 0.9 microm. (ONs which inhibit CMV at one-third the
CC      dosage (or below) at which the negative control shows activity in this
CC      experiment (IC50 = 1 microm. or less) are preferred). Antisense ONs
CC      targeting CMV DNA or RNA coding for the IE1, IE2 or DNA polymerase
CC      proteins have been shown to be effective in therapy, prophylaxis and
CC      diagnosis of CMV infection. The ONs may be modified to reduce nuclease
CC      resistance and to increase their efficacy. Modifications include
CC      phosphorothioate backbones, alkyl and halogen-substituted sugar moieties
CC      at the 2' position. (Updated on 25-MAR-2003 to correct PF field.)
XX      Sequence 21 BP; 6 A; 6 C; 9 G; 0 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      3024 CATCTGCGCTGACCCCACTG 3044
DB      21 CTTCTGCGCTGCGCCGCTG 1
RESULT 3230
AAT01661/C
ID      AAT01661 standard; DNA; 21 BP.
XX      AAT01661;
AC      AAT01661;
XX      17-DEC-1995 (first entry)
DT      Peptide nucleic acid targeting CMV DNA pol 5'-UTR.
XX      peptide nucleic acid; PNA; cytomegalovirus; CMV; papillomavirus;
KM      antiviral; diagnostic; ss.
XX      Synthetic.
OS      Synthetic.
XX      Key Location/Qualifiers
FT      misc_feature 1..21 a
FT      /*tag= a
FT      /note= "at least one (and preferably all) of the backbone
FT      subunits are composed of amide units, so that the
FT      oligomer consists of the nucleobases attached covalently
FT      to a polyamide backbone"
XX      WO9504748-A1.
XX      16-FEB-1995.
XX      09-AUG-1994; 94WO-US009039.
XX      09-AUG-1993; 93US-00104438.
XX      (ISIS-) ISIS PHARM INC.
XX      Anderson KP, Crooke ST, Mirabelli CK, Ecker DJ, Cowsett LM,
PI      WPI; 1995-090841/12.

```

XX New peptide nucleic acid oligomers hybridisable to cytomegalovirus or  
PT papilloma-virus - are stable anti-sense molecules with high affinity for  
PT single stranded DNA, used for treating infections.  
XX  
PS Claim 2; Page 44; 65pp; English.  
XX  
CC New oligomers are claimed which (A) have at least one peptide nucleic  
CC acid (PNA) subunit and (B) have a sequence hybridisable to AUG region, 5'  
CC untranslated region, intron/exon junction or coding sequence of  
CC cytomegalovirus gene selected from DNA polymerase, IE1 and IE2, or  
CC hybridisable to the E, E2, E4, E5, E6, E7, I1 or I2 reading frames of a  
CC papillomavirus. The PNAs can be used to target RNA and single stranded  
CC DNA (ssDNA) to produce antisense-type gene regulation moieties. Hence  
CC they may be used therapeutically for modulating cytomegalovirus and  
CC papillomavirus processes and also as diagnostics (e.g., as probes for  
CC specific mRNAs). PNA oligomers have high affinity for complementary  
CC single stranded DNA. They are also able to form triple helices in which a  
CC first PNA strand binds with RNA or ssDNA and a second PNA strand binds  
CC with the resulting double helix or with the first PNA strand. The PNAs  
CC possess no significant charge and are water soluble, which facilitates  
CC cellular uptake. Further, since they contain amides of non-biological  
CC amino acids, they are biostable and resistant to enzymatic degradation by  
CC processes. The present sequence targets CMV DNA polymerase 5'  
CC untranslated region (5' UTR)  
XX  
SQ Sequence 21 BP; 6 A; 6 C; 9 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3024 CATGTGGCCTGACCCACTG 3044  
DB 21 CTTCTGGCCTGGCCCTG 1  
XX  
RESULT 3231  
AAT35317/c  
ID AAT35317 standard; cDNA; 21 BP.  
XX  
AC AAT35317;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-NOV-1996 (first entry)  
XX  
DE Human SH-PTP1 gene PCR primer; 400B.  
XX  
KM PRP; protein tyrosine phosphatase; SH2; Src homology region 2;  
KM chromosome 12p; abnormality; mutation; detection; probe; neoplasia;  
KM cancer; leukemia; diagnosis; megakaryocyte regulation;  
KM polymerase chain reaction; ds.  
XX  
OS Homo sapiens.  
XX  
PN US5536636-A.  
XX  
PD 16-JUL-1996.  
XX  
PF 28-FEB-1994; 94US-00202389.  
XX  
PR 26-JUN-1991; 91US-00721112.  
PR 31-JAN-1992; 92US-00829141.  
PR 01-DEC-1992; 92US-00983926.  
XX  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
XX  
PI Neel BG, Rosenberg RD, Freeman RM, Plutzky J;  
XX WPI; 1996-341506/34.  
XX  
PT Detecting 12p chromosomal abnormality associated with neoplastic disease

PT - using SH-PTP1 protein tyrosine phosphatase gene specific probe.  
XX  
XX Claim 1; Fig 9; 63pp; English.  
XX  
XX AAT35314-T35327 are a set of PCR primers used to amplify regions of the  
CC human cDNA sequence encoding SH-PTP1 (protein tyrosine phosphatase-1,  
CC with two SH2 domains). The primers are used in the analysis of the SH-  
CC PRP1 gene of patients with acute lymphoblastic leukaemia (ALL). A  
CC fragment complementary to the SHPRP-1 sequence from nucleotides 537-653 is  
CC used as a probe to detect a chromosome 12p13 abnormality associated with  
CC neoplastic disease, in partic. ALL. The probe hybridises to a part of the  
CC region coding for the two tandem SH2 domains (see AAR9312). If the probe  
CC will not hybridise DNA of chromosome 12p13 from a patient sample it is  
CC indicative of an abnormality, normally associated with neoplasia.  
CC Alternatively the wild-type SH-PTP1 or SH-PRP2 gene or protein may be  
CC used for comparison to sequenced PRP genes taken from a patient, where  
CC differences indicate an abnormality. The activity of SH-PTP1 may also be  
CC purposely altered by mutation to effect a change in megakaryocyte  
CC function and hence platelet production. (updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4436 CTAGGCGCATGTGGGTGGTGG 4456  
DB 21 CAAGGTCAATGTGGAGGCTGG 1  
XX  
RESULT 3232  
AAT35001  
ID AAT35001 standard; DNA; 21 BP.  
XX  
AC AAT35001;  
XX  
DT 25-MAR-2003 (revised)  
DT 03-DEC-1996 (first entry)  
XX  
DE HIV inhibitor #4.  
XX  
KM HTV; infection inhibitor; triplex forming; purine rich promoter; V3 loop;  
KM transfection inhibitor; gp120 protein; viral growth; enzyme inhibitor;  
KM PUA2; telomere length; glove coating; condom; ss.  
XX  
OS Synthetic.  
XX  
FT Key Location/Qualifiers  
FT misc\_feature 1..21  
FT /tag= a  
FT /note= "phosphorothioate nucleotides"  
XX  
PN US5523389-A.  
XX  
PD 04-JUN-1996.  
XX  
PF 28-SEP-1993; 93US-00128011.  
XX  
PR 29-SEP-1992; 92US-00954185.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Imbach JL, Ecker DJ, Wyatt JR;  
XX WPI; 1996-285782/29.  
XX  
PT New octa-nucleotide with guanosine quarter and phosphoro:chisto links -  
PT is inhibitor of HIV infection by binding to the V3 loop.  
XX  
XX Example 3; Col 8; 14pp; English..  
XX

CC AAT34998-PT5001 represent HIV inhibitors. Sequences containing only G and  
CC T residues (such as these sequences) are triplex forming  
CC oligonucleotides, and form putative rich promoter elements used to inhibit  
CC transcription. These sequences bind to the HIV gp120 protein at the V3  
CC loop via the internal guanine quartet. This binding prevents cell-to-  
CC cell and virus-to-cell infection. The sequences may also be used for  
CC inhibiting viral growth, and other viral genes, for inhibiting the enzyme  
CC PLAT, and to modulate telomere length. In some cases these sequences need  
CC to be chemically modified. The chemically modified oligonucleotides  
CC preferably include at least one phosphorothioate linkage. Other modified  
CC intersugar links, or 2'-modified sugar residues can also be used. These  
CC oligonucleotides can be used for coating gloves, condoms, etc, or for  
CC topical application. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4468 TTTTCTTTTCTTTTCTT 4468  
DB 1 TTTTCTTTTCTTTTCTT 21  
RESULT 3233  
AAT31784/c  
ID AAT31784 standard; DNA; 21 BP.  
XX  
AC AAT31784;  
XX  
DT 27-JAN-1997 (first entry)  
XX  
DE Cytokeratin 19 mRNA specific antisense PCR primer.  
XX  
KM Determination; tumour; metastasis; cytokeratin 19; CK19; detection;  
KM epithelial cell; colorectal; stomach; mucinous ovarian; gall bladder;  
KM adenocarcinoma; bladder; transitional cell; carcinoma; primer; PCR;  
KM polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN W09617080-A1.  
XX  
PD 06-JUN-1996.  
XX  
PF 24-NOV-1995; 95WO-GB002734.  
XX  
PR 26-NOV-1994; 94GB-00023912.  
XX  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
XX  
PI Selby PJ, Burchill SA;  
XX  
DR WPI; 1996-277793/28.  
XX  
PT Detection of human tumours or metastasis - by detecting a cyto-keratin 20  
PT gene prod. in a tissue sample which does not normally contain CK20.  
XX  
PS Example 1; Page 17; 36pp; English.  
XX  
CC Determining whether a human patient has a tumour or a metastasised  
CC tumour, comprises determining whether a cytokeratin 20 (CK20) gene prod.  
CC is present in a tissue sample that does not normally contain CK20. This  
CC method is partic. useful for the detection of epithelial cell tumours,  
CC e.g. colorectal, stomach, mucinous ovarian or gall bladder adenocarcinoma  
CC or bladder or transitional cell carcinoma. In an example RNA was  
CC extracted from normal human blood samples and samples spiked with  
CC adenocarcinoma HT29 cells, transitional cell carcinoma RT12 cells or  
CC breast adenocarcinoma MCF-7 cells and subjected to PCR amplification  
CC using the CK20, CK8 or CK19 mRNA specific primers AAT31769/70,  
CC AAT31781/82 and AAT31783/84, respectively. CK20, CK8 and CK19 mRNA was  
CC not detected in normal blood, but a respective 370, 244 or 214 bp prod.

CC was detected in the HT29, RT112 and MCF-7 spiked blood  
XX  
SQ Sequence 21 BP; 3 A; 7 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 985 AAGGAGTCAAGGCTGAAG 1005  
DB 21 ATGCAGATCGAAGGCTGAAG 1  
RESULT 3234  
AAX33889/c  
ID AAX33889 standard; DNA; 21 BP.  
XX  
AC AAX33889;  
XX  
DT 30-JUN-1999 (first entry)  
XX  
DE Initialising oligonucleotide for pUC19 fragment amplification.  
XX  
KM Primer; sequence determination; genomic analysis; genetic identification;  
KM forensic analysis; genetic counselling; medical diagnostics;  
KM Initialising oligonucleotide; amplification; ss.  
XX  
OS Synthetic.  
XX  
PN W09633205-A1.  
XX  
PD 24-OCT-1996.  
XX  
PF 16-APR-1996; 96WO-US005245.  
XX  
PR 17-APR-1995; 95US-00424663.  
XX  
PA (SPEC-) SPECTRAGEN INC.  
XX  
PI Macev1cz SC;  
XX  
DR WPI; 1996-485723/48.  
XX  
PT Sequencing DNA by parallel oligo:nucleotide extension - involving  
PT extending initialising oligonucleotide by ligating probe to form duplex,  
PT avoiding electrophoretic segms.  
XX  
PS Example 1; Page 20; 40pp; English.  
XX  
CC This sequence represents an initialising oligonucleotide for a fragment  
CC of pUC19. The invention relates to a method for the identification of a  
CC sequence of nucleotides in a polynucleotide (PNT), which involves: (a)  
CC extending an initialising oligonucleotide (ONT) along the PNT by ligating  
CC an ONT probe to form a duplex; (b) identifying one or more nucleotides of  
CC the PNT; and (c) repeating steps (a) and (b) until the nucleotide  
CC sequence is determined. The method is useful e.g. in gene function and  
CC control investigations, genomic analysis, genetic identification,  
CC forensic analysis, genetic counselling or medical diagnostics. The method  
CC avoids the need for electrophoretic separation of similarly sized DNA  
CC fragments, eliminates the difficulties associated with detection and  
CC analysis of spatially overlapping bands of DNA fragments in a gel or  
CC similar medium and avoids the need to generate DNA fragments from long  
CC single-stranded template with a DNA polymerase  
SQ Sequence 21 BP; 7 A; 0 C; 14 G; 0 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3441 CCCACCTTACTCTCTCTCC 3461  
DB 21 CCTCTCTTCTCTCTCTCTCC 1

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RESULT 3235
AAX3890/c
ID AAX3890 standard; DNA; 21 BP.
XX
AC AAX3890;
XX
DT 30-JUN-1999 (first entry)
XX
DE Initialising oligonucleotide for pUC19 fragment amplification.
XX
KM Primer: sequence determination; genomic analysis; genetic identification;
KM forensic analysis; genetic counselling; medical diagnostic;
KM initialising oligonucleotide; amplification; ss.
XX
OS Synthetic.
XX
PN WO9633205-A1.
XX
PD 24-OCT-1996.
XX
PF 16-APR-1996; 96WO-US005245.
XX
PR 17-APR-1995; 95US-00424663.
XX
PA (SPEC-) SPECTRAGEN INC.
XX
PI Macev1cz SC;
XX
DR WPI; 1996-485723/48.
XX
PT Sequencing DNA by parallel oligo:nucleotide extension - involving
PT extending initialising oligonucleotide by ligating probe to form duplex,
PT avoiding electrophoretic seps.
XX
PS Example 1; Page 20; 40pp; English.
XX
CC This sequence represents an initialising oligonucleotide for a fragment
CC of pUC19. The invention relates to a method for the identification of a
CC sequence of nucleotides in a polynucleotide (PNT), which involves: (a)
CC extending an initialising oligonucleotide (ONT) along the PNT by ligating
CC an ONT probe to form a duplex; (b) identifying one or more nucleotides of
CC the PNT; and (c) repeating steps (a) and (b) until the nucleotide
CC sequence is determined. The method is useful e.g. in gene function and
CC control investigations, genomic analysis, genetic identification,
CC forensic analysis, genetic counselling or medical diagnostics. The method
CC avoids the need for electrophoretic separation of similarly sized DNA
CC fragments, eliminates the difficulties associated with detection and
CC analysis of spatially overlapping bands of DNA fragments in a gel or
CC single-stranded template with a DNA polymerase
CC
XX
SQ Sequence 21 BP; 8 A; 0 C; 13 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3442 CCACCTTACTTCTCTCCCT 3462
DB 21 CTCCTCTCCCTCTCCCTCT 1
XX
RESULT 3236
AAT86582
ID AAT86582 standard; DNA; 21 BP.
XX
AC AAT86582;
XX
DT 25-MAR-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide #1.

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```

XX
KM Phosphorothioate oligonucleotide; dimeric phosphoramidite synthon;
KM thioester; DNA synthesis; antisense oligonucleotide; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..21
FT /tag= a
FT /note= "Phosphorothioate linkages between alternate
FT nucleotides (1 and 2, 3 and 4 etc.)."
XX
PN WO9729116-A1.
XX
PD 14-AUG-1997.
XX
PF 06-FEB-1997; 97WO-GB000327.
XX
PR 06-FEB-1996; 96GB-00002326.
XX
PA (CRUA-) CRUACHEM LTD.
XX
PI Reese CB, Rao MV;
XX
DR WPI; 1997-415290/38.
XX
PT Solid phase synthesis of phosphorothioate oligo:nucleotide(s) using new
PT dimeric synthon(s) - useful as anti:sense molecules for inhibiting gene
PT expression.
XX
PS Example 3; Page 20; 38pp; English.
XX
CC The present sequence represents a phosphorothioate oligonucleotide which
CC was prepared by solid phase synthesis. The method comprises adding at
CC least one dimeric phosphoramidite synthon, optionally having a protected
CC thioester group in its internucleotide link, during the synthesis cycle.
CC These novel dimeric phosphoramidite synthons are used as antisense
CC molecules for inhibition of gene expression. The method gives increased
CC yields of the phosphorothioate oligonucleotide (since fewer cycles are
CC needed) and facilitates separation of impurities (greater difference in
CC size compared with use of monomeric synthons)
CC
XX
SQ Sequence 21 BP; 0 A; 10 C; 0 G; 11 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 5327 TCTCTCTTGCCTCACTCTCT 5347
DB 1 TCTCTCTCTCTCTCTCTCT 21
XX
RESULT 3237
AAT77232
ID AAT77232 standard; DNA; 21 BP.
XX
AC AAT77232;
XX
DT 12-FEB-1998 (first entry)
XX
DE Rat fibroblast growth factor FGF-10 RACE primer B.
XX
KM Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KM wound healing; cartilage; RACE primer; ss.
XX
OS Synthetic.
XX
PN WO9720929-A1.
XX
PD 12-JUN-1997.
XX

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PF 06-DEC-1996; 96MO-JP003579.
XX
XX 07-DEC-1995; 95JP-00345689.
PR 28-MAR-1996; 96JP-00103240.
PR 24-JUL-1996; 96JP-00214378.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI Itoh N, Negoro T, Kateumata T, Tagashira S;
DR WPI; 1997-319776/29.
XX
PT Recombinant fibroblast growth factor FGF-10 and related DNA - useful for
PT the treatment of bone disease and for wound healing.
XX
PS Example 1; Page 35; 51pp; Japanese.
XX
CC The present sequence represents a RACE primer involved in the
CC amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,
CC vector, containing the DNA, and host cells, containing the vectors, are
CC useful for the recombinant production of FGF-10. The recombinant FGF-10
CC is useful for the treatment of diseases and injury of bone or cartilage,
CC and as a wound healing promoter
XX
SQ Sequence 21 BP; 2 A; 9 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5740 TCCCTTCTCTATTCACATC 5760
DB 1 TCCATTTCTCTATCTCTC 21

RESULT 3238
AAV30731
ID AAV30731 standard; DNA; 21 BP.
XX
AC AAV30731;
XX
DT 13-AUG-1998 (first entry)
XX
DE Telomerase reverse transcriptase primer 260-280.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; phosphorothioate;
KW primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key modified_base 1..21
FT /tag= a
FT /note= "phosphorothioate linkages"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00911312.
XX 14-AUG-1997; 97US-00912951.
XX 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.

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PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cheh TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
PI Andrews WH;
XX WPI; 1996-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Disclosure; Page 44; 387pp; English.
XX
CC The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
SQ Sequence 21 BP; 5 A; 4 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4735 GGCCAGCTGGAGGAAGGG 4755
DB 1 GGACACCTGGCGGAAGAGGG 21

RESULT 3239
AAV08273/c
ID AAV08273 standard; DNA; 21 BP.
XX
AC AAV08273;
XX
XX 27-JAN-1999 (first entry)
XX
DE PCR primer ABCR-EXON43:F for ABCR coding sequence.
XX
KW ATP binding cassette; ABC transporter; ABCR; Stargardt Disease; therapy;
KW Fundus Flavimaculatus; age-related macular degeneration; diagnosis;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W09837764-A1.
XX
XX 03-SEP-1998.
XX
XX 27-FEB-1998; 98MO-US003895.
XX
XX 27-FEB-1997; 97US-0039388P.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX (UYTO ) UNIV JOHNS HOPKINS.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (UTAH ) UNIV UTAH.

```

XX Allikmets R, Anderson KL, Dean M, Leppart M, Lewis RA, Li Y;  
PI Lupski JR, Nathans J, Rattner A, Shroyer NF, Singh N, Smallwood PM;  
PI Sun H;  
XX WPI; 1998-495375/42.  
XX  
PT Retina-specific ATP-binding cassette transporter and DNA - useful for,  
PT e.g. diagnosis and treatment of macular degeneration, such as in  
PT Stargardt Disease, Fundus Flavimaculatus and age-related degeneration.  
XX  
PS Claim 41; Page 31; 79pp; English.  
XX  
CC This sequence represents a PCR primer for DNA encoding the human retina  
CC specific ATP binding cassette transporter (ABCR) of the invention. ABCR  
CC may be used in compositions for screening agents that alters ABCR. The  
CC agent can inhibit Stargardt Disease, Fundus Flavimaculatus and age-  
CC related macular degeneration (MD). Primers (such as this sequence) and  
CC probes for the ABCR DNA can be used in a diagnostic kit for detecting MD  
XX  
SQ Sequence 21 BP; 4 A; 9 C; 1 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 3228 GAGGAGAGATTTTGTAGAG 3248  
DB 21 GAGCAAGAGATGTTTGGAG 1  
XX  
RESULT 3240  
AAV08280  
ID AAV08280 standard; DNA; 21 BP.  
XX  
AC AAV08280;  
XX  
DT 27-JAN-1999 (first entry)  
XX  
DE PCR primer ABCR. EXON46.R for ABCR coding sequence.  
XX  
XX ATP binding cassette; ABC transporter; ABCR; Stargardt Disease; therapy;  
XX Fundus Flavimaculatus; age-related macular degeneration; diagnosis;  
XX PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9837764-A1.  
XX  
PD 03-SEP-1998.  
XX  
XX 27-FEB-1998; 98WO-US003895.  
XX  
XX 27-FEB-1997; 97US-0039388P.  
XX  
XX 27-FEB-1997; 97US-0039388P.  
XX  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX (UTXO ) UNIV JOHNS HOPKINS.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX (UTAH ) UNIV UTAH.  
XX  
XX Allikmets R, Anderson KL, Dean M, Leppart M, Lewis RA, Li Y;  
PI Lupski JR, Nathans J, Rattner A, Shroyer NF, Singh N, Smallwood PM;  
PI Sun H;  
XX  
XX WPI; 1998-495375/42.  
XX  
PT Retina-specific ATP-binding cassette transporter and DNA - useful for,  
PT e.g. diagnosis and treatment of macular degeneration, such as in  
PT Stargardt Disease, Fundus Flavimaculatus and age-related degeneration.  
XX  
PS Claim 41; Page 32; 79pp; English.  
XX

CC This sequence represents a PCR primer for DNA encoding the human retina  
CC specific ATP binding cassette transporter (ABCR) of the invention. ABCR  
CC may be used in compositions for screening agents that alters ABCR. The  
CC agent can inhibit Stargardt Disease, Fundus Flavimaculatus and age-  
CC related macular degeneration (MD). Primers (such as this sequence) and  
CC probes for the ABCR DNA can be used in a diagnostic kit for detecting MD  
XX  
SQ Sequence 21 BP; 5 A; 10 C; 2 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 5907 ACCTGTTCCCAAGCCAGAG 5927  
DB 1 ACCTCTTCCCAAGCCAGAG 21  
XX  
RESULT 3241  
AAV37790/c  
ID AAV37790 standard; DNA; 21 BP.  
XX  
AC AAV37790;  
XX  
DT 09-SEP-1998 (first entry)  
XX  
DE Interleukin-15 gene inhibitor oligonucleotide 1.  
XX  
XX Interleukin gene; IL-15; inhibitor; oligomer; expression;  
XX transcription-inhibiting complex; polypurine-polypyrimidine region;  
XX inflammatory poly-arthritis; rheumatoid arthritis; asthma; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9818812-A1.  
XX  
PD 07-MAY-1998.  
XX  
XX 29-AUG-1997; 97WO-US015397.  
XX  
XX 25-OCT-1996; 96US-00740215.  
XX  
XX (HISM ) HISAMITSU PHARM CO LTD.  
XX  
XX Veerapanane D, Hamanaka S, Nozawa I;  
XX  
XX WPI; 1998-272129/24.  
XX  
XX  
PT Oligomer capable of inhibiting expression of an interleukin gene - is  
PT used to alleviate inflammatory poly-arthritis, especially rheumatoid  
PT arthritis.  
XX  
XX Claim 19; Page 7; 19pp; English.  
XX  
XX An oligomer has been developed which is capable of inhibiting expression  
XX of an interleukin gene. The interleukin gene is preferably an interleukin  
XX -15 (IL-15) gene. The oligomer can be an oligonucleotide or an  
XX oligonucleotide analogue. When it is an oligonucleotide analogue it is  
XX selected from protein nucleic acid, morpholino, methylene linkage,  
XX boronated, and pteridine oligonucleotide analogues. The analogue is  
XX linked at its 5' end or 3' end to an intercalator. The intercalator is a  
XX poralen or acridine derivative. The oligomer is preferably an  
XX oligonucleotide made of DNA. The oligonucleotide is a phosphodiester,  
XX phosphorothioate, methylphosphonate, or methylphosphonothioate  
XX oligonucleotide derivative, especially a phosphodiester oligonucleotide.  
XX The oligonucleotide is at least 5 (preferably 5-50) nucleotides, in  
XX length. The present sequence represents a specifically claimed  
XX oligonucleotide of the present invention. The oligomer can be used to  
XX alleviate inflammatory polyarthritis, especially that associated with  
XX rheumatoid arthritis. The oligomer can also be used to alleviate  
XX eosinophilic inflammation, especially that associated with chronic asthma  
XX

SQL Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5412 AAGAAATATAAGCAAGAGAA 5432

DB 21 AAGAAAAAGAAAGAAAGGAA 1

RESULT 3242

AAV37793  
 ID AAV37793 standard; DNA; 21 BP.

AC AAV37793;

DT 09-SEP-1998 (first entry)

DE Interleukin-15 gene inhibitor oligonucleotide 4.

XX Interleukin gene; IL-15; inhibitor; oligomer; expression;

KW transcription-inhibiting complex; polypurine-polypyrimidine region;

KW inflammatory poly-arthritis; rheumatoid arthritis; asthma; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9818812-A1.

PD 07-MAY-1998.

PF 29-AUG-1997; 97WO-US015397.

PR 25-OCT-1996; 96US-00740215.

PA (HISM ) HISAMITSU PHARM CO LTD.

PI Veerapanane D, Hamanaka S, Nozawa I;

XX WPI; 1998-272129/24.

DR Oligomer capable of inhibiting expression of an interleukin gene - is

PT used to alleviate inflammatory poly-arthritis, especially rheumatoid

XX arthritis.

PS Claim 20; Page 8; 19pp; English.

CC An oligomer has been developed which is capable of inhibiting expression

CC of an interleukin gene. The interleukin gene is preferably an interleukin

CC -15 (IL-15) gene. The oligomer can be an oligonucleotide or an

CC oligonucleotide analogue. When it is an oligonucleotide analogue it is

CC selected from protein nucleic acid, morpholino, methylene linkage,

CC boronated, and pteridine oligonucleotide analogues. The analogue is

CC linked at its 5' end or 3' end to an intercalator. The intercalator is a

CC psoralen or aridine derivative. The oligomer is preferably an

CC phosphorochiolate, methylphosphonate, or methylphosphonothioate

CC oligonucleotide derivative, especially a phosphodiester oligonucleotide.

CC length. The present sequence represents a specifically claimed, in

CC oligonucleotide of the present invention. The oligomer can be used to

CC alleviate inflammatory polyarthritis, especially that associated with

CC rheumatoid arthritis. The oligomer can also be used to alleviate

CC eosinophilic inflammation, especially that associated with chronic asthma

XX Sequence 21 BP; 15 A; 0 C; 6 G; 0 T; 0 U; 0 Other;

SQL Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5412 AAGAAATATAAGCAAGAGAA 5432

DB 1 AAGAAAAAGAAAGAAAGGAA 21

RESULT 3243

AAV10466/c  
 ID AAV10466 standard; DNA; 21 BP.

AC AAV10466;

DT 17-JUN-1998 (first entry)

DE Human osteosarcoma PCR primer #2.

XX Osteosarcoma; haematopoietic cell; osteoblast; human; immature; antibody;

KW immunoreactive; cell antigen; CD34; blood; bone marrow; treatment;

KW disorder; PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5733541-A.

PD 31-MAR-1998.

PF 21-APR-1995; 95US-00426792.

PR 21-APR-1995; 95US-00426792.

PA (UNMI ) UNIV MICHIGAN.

PI Emerson SG, Taichman RS;

XX WPI; 1998-229763/20.

DR Maintenance of haematopoietic cells in culture - by co-culturing with

PT osteoblast(s).

XX Example 4; Col 19; 38pp; English.

PS Primers AAV10465-V10492 are used to amplify regions of the human

CC osteosarcoma cell lines MC-63 and SAOS-2 which contain ligands and growth

CC factors and have been designed to cross intron/exon boundaries. The

CC products are used in a process for propagating and maintaining the

CC immature morphology of mammalian haematopoietic cells. The process

CC involves obtaining an enriched population of mammalian haematopoietic

CC cells having the immature morphology of CD34+, HLA-DR+, Thy-1+ and Lin-

CC and co-culturing this population in the presence of osteoblast cells for

CC between 2 weeks and 8 weeks. The immature cells can be detected by

CC exposing them to an anti-CD34 antibody immunoreactive with the

CC haematopoietic cell antigen CD34, and removing cells that do not immuno-

CC react with the antibody. Such haematopoietic cells can be infused into

CC the blood stream or bone-marrow cavity to treat blood disorders

XX Sequence 21 BP; 0 A; 11 C; 0 G; 10 T; 0 U; 0 Other;

SQL Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3638 AGGAGCTAGATGGGAGAGAA 3658

DB 21 AGGAGAGAAAGAGAGAGAGAA 1

RESULT 3244

AAZ26171  
 ID AAZ26171 standard; DNA; 21 BP.

AC AAZ26171;

DT 30-NOV-1999 (first entry)

DE	Human polymorphic region 360.
XX	
KW	polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KM	cell viability; loss of heterozygosity; precancerous condition; ASI;
KW	allele specific inhibitor; somatic cell; diagnosis; prevention;
KW	atherosclerotic plaque; premalignant metaplastic lesion; endometriosiis;
KW	dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW	graft versus host disease; malignant cell removal; bone marrow; ss.
XX	
OS	Homo sapiens.
XX	
PN	MO9641648-A2.
XX	
PD	24-SEP-1998.
XX	
PF	19-MAR-1998; 98WO-US005419.
XX	
PR	20-MAR-1997; 97US-0041057P.
XX	
PA	(VARI-) VARIAGENICS INC.
XX	
PI	Houman D, Ledley FD, Stanton VP;
XX	
DR	WPI, 1998-521232/44.
XX	
PT	Identifying target genes for allele-specific drugs - used for diagnosis,
PT	prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT	dysplastic lesions, endometriosis or graft versus host disease.
XX	
PS	Disclosure; Fig 7; 605pp; English.
XX	
CC	This invention describes a novel method for identifying an inhibitor
CC	potentially useful for growth of cancer, where the inhibitor is active
CC	on a gene vital for cell growth or viability, and where the gene is
CC	subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC	used for preventing the development of cancer in a patient having a
CC	precancerous condition, by administering to the patient a first allele
CC	specific inhibitor (ASI) targeted to an allele of a first essential gene
CC	present in cells of the precancerous condition, where the normal somatic
CC	cells of the patient are heterozygous for the first gene, the inhibitor
CC	is active on at least one but less than all allelic forms of the gene
CC	present in a population and targets only one allelic form present in the
CC	normal somatic cells, and the first gene. The products and methods can be
CC	used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC	cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC	lesions, benign tumors, endometriosis, polycystic kidney disease, and
CC	graft versus host disease. The method can also be used to remove
CC	malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC	human polymorphic sites described in the method of the invention
XX	
SQ	Sequence 21 BP; 6 A; 5 C; 10 G; 0 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity	81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	7414 AGCAGCAGCAGCAGCAGC 7434
Db	1 AGCAGCAGCGGGAAGAGCGGC 21
RESULT 3245	
AAZ26812/C	
ID	AAZ26812 standard; DNA; 21 BP.
XX	
AC	AAZ26812;
XX	
DT	30-NOV-1999 (first entry)
XX	
DE	Human polymorphic region 1001.
XX	
KW	Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW	cell viability; loss of heterozygosity; precancerous condition; ASI;

XX	allele specific inhibitor; somatic cell; diagnosis; prevention;
KW	atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW	dyplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW	graft versus host disease; malignant cell removal; bone marrow; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO9841648-A2.
XX	
PD	24-SEP-1998.
XX	
PF	19-MAR-1998; 98WO-US005419.
XX	
PR	20-MAR-1997; 97US-0041057P.
XX	
PA	(VARI-) VARIAGENICS INC.
XX	
PI	Housman D, Ledley FD, Stanton VP;
DR	WPI; 1998-521232/44.
XX	
PT	Identifying target genes for allele-specific drugs - used for diagnosis,
PT	prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT	dyplastic lesions, endometriosis or graft versus host disease.
XX	
PS	Disclosure; Fig 7; 605bp; English.
XX	
CC	This invention describes a novel method for identifying an inhibitor
CC	potentially useful for treatment of cancer, where the inhibitor is active
CC	on a gene vital for cell growth or viability, and where the gene is
CC	subject to loss of heterozyosity (LOH) in a cancer. The inhibitor is
CC	used for preventing the development of cancer in a patient having a
CC	precancerous condition, by administering to the patient a first allele
CC	specific inhibitor (ASI) targeted to an allele of a first essential gene
CC	present in cells of the precancerous condition, where the normal somatic
CC	cells of the patient are heterozygous for the first gene, the inhibitor
CC	is active on at least one but less than all allelic forms of the gene
CC	present in a population and targets only one allelic form present in the
CC	normal somatic cells, and the first gene. The products and methods can be
CC	used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC	cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC	lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC	graft versus host disease. The method can also be used to remove
CC	malignant cells from bone marrow transplants. AA25812-226825 represent
CC	human polymorphic sites described in the method of the invention
XX	
SO	Sequence 21 BP; 3 A; 14 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;	
Best Local Similarity 81.0%; Pred. No. 2.3e+03;	
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	2876 GGGAGCTGGGGTAGGAGGAG 2896
DB	21 GGGAGCTGGGGTAGGAGGAG 1
RESULT 3246	
AA226398	
ID AA226398 standard; DNA; 21 BP.	
XX	
AC AA226398;	
XX	
DT 30-NOV-1999 (first entry)	
XX	
DE Human polymorphic region 587.	
XX	
KW polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;	
KW cell viability; loss of heterozyosity; precancerous condition; ASI;	
KW allele specific inhibitor; somatic cell; diagnosis; prevention;	
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;	
KW dyplastic lesion; benign tumour; polycystic kidney disease; transplant;	
KW graft versus host disease; malignant cell removal; bone marrow; ss.	



XX Homo sapiens.  
OS  
XX  
XX WO9841648-A2.  
XX  
XX 24-SEP-1998.  
XX  
XX 19-MAR-1998; 98WO-US005419.  
XX  
XX 20-MAR-1997; 97US-0041057P.  
XX  
XX (VARI-) VARIAGENICS INC.  
XX  
XX Housman D, Ledley FD, Stanton VP;  
XX  
XX WPI; 1998-521232/44.  
XX  
XX Identifying target genes for allele-specific drugs - used for diagnosis,  
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
XX dysplastic lesions, endometriosis or graft versus host disease.  
XX  
XX Disclosure; Fig 7; 605pp; English.  
XX  
XX This invention describes a novel method for identifying an inhibitor  
XX potentially useful for treatment of cancer, where the inhibitor is active  
XX on a gene vital for cell growth or viability, and where the gene is  
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
XX used for preventing the development of cancer in a patient having a  
XX precancerous condition, by administering to the patient a first allele  
XX specific inhibitor (ASI) targeted to an allele of a first essential gene  
XX present in cells of the precancerous condition, where the normal somatic  
XX cells of the patient are heterozygous for the first gene, the inhibitor  
XX is active on at least one but less than all allelic forms of the gene  
XX present in a population and targets only one allelic form present in the  
XX normal somatic cells, and the first gene. The products and methods can be  
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and  
XX graft versus host disease. The method can also be used to remove  
XX malignant cells from bone marrow transplants. AA25812-226825 represent  
XX human polymorphic sites described in the method of the invention  
XX  
XX Sequence 21 BP; 9 A; 2 C; 1 G; 9 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;  
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
XX QY 5473 TTTTGTGTAAGATATT 5493  
XX Db 1 TTTTTCAGAAAACATAAT 21  
XX  
XX RESULT 3247  
XX AA226192/C  
XX ID AA226192 standard; DNA; 21 BP.  
XX  
XX AA226192;  
XX  
XX 30-NOV-1999 (first entry)  
XX  
XX Human polymorphic region 381.  
XX  
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX cell viability; loss of heterozygosity; precancerous condition; ASI;  
XX allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9841648-A2.  
XX

XX 24-SEP-1998.  
XX  
XX 19-MAR-1998; 98WO-US005419.  
XX  
XX 20-MAR-1997; 97US-0041057P.  
XX  
XX (VARI-) VARIAGENICS INC.  
XX  
XX Housman D, Ledley FD, Stanton VP;  
XX  
XX WPI; 1998-521232/44.  
XX  
XX Identifying target genes for allele-specific drugs - used for diagnosis,  
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
XX dysplastic lesions, endometriosis or graft versus host disease.  
XX  
XX Disclosure; Fig 7; 605pp; English.  
XX  
XX This invention describes a novel method for identifying an inhibitor  
XX potentially useful for treatment of cancer, where the inhibitor is active  
XX on a gene vital for cell growth or viability, and where the gene is  
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
XX used for preventing the development of cancer in a patient having a  
XX precancerous condition, by administering to the patient a first allele  
XX specific inhibitor (ASI) targeted to an allele of a first essential gene  
XX present in cells of the precancerous condition, where the normal somatic  
XX cells of the patient are heterozygous for the first gene, the inhibitor  
XX is active on at least one but less than all allelic forms of the gene  
XX present in a population and targets only one allelic form present in the  
XX normal somatic cells, and the first gene. The products and methods can be  
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and  
XX graft versus host disease. The method can also be used to remove  
XX malignant cells from bone marrow transplants. AA25812-226825 represent  
XX human polymorphic sites described in the method of the invention  
XX  
XX Sequence 21 BP; 2 A; 7 C; 7 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;  
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
XX QY 7415 GCAGCAGCAGCAGCAGCA 7435  
XX Db 21 GCAGCAGCAGCTGTGAGCA 1  
XX  
XX RESULT 3248  
XX AA226714/C  
XX ID AA226714 standard; DNA; 21 BP.  
XX  
XX AA226714;  
XX  
XX 30-NOV-1999 (first entry)  
XX  
XX Human polymorphic region 903.  
XX  
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
XX cell viability; loss of heterozygosity; precancerous condition; ASI;  
XX allele specific inhibitor; somatic cell; diagnosis; prevention;  
XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
XX graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9841648-A2.  
XX  
XX 24-SEP-1998.  
XX  
XX 19-MAR-1998; 98WO-US005419.  
XX

XX	20-MAR-1997;	97US-0041057P.
PR	(VARI-) VARIAGENICS INC.	
XX	Housman D, Ledley FD, Stanton VP;	
XX	WPI; 1998-521232/44.	
DR	Identifying target genes for allele-specific drugs - used for diagnosis,	
PT	prevention and treatment of, e.g. cancers, atherosclerotic plaque,	
PR	dysplastic lesions, endometriosis or graft versus host disease.	
XX	Disclosure; Fig 7; 605pp; English.	
PS	This invention describes a novel method for identifying an inhibitor	
XX	potentially useful for treatment of cancer, where the inhibitor is active	
CC	on a gene vital for cell growth or viability, and where the gene is	
CC	subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is	
CC	used for preventing the development of cancer in a patient having a	
CC	precancerous condition, by administering to the patient a first allele	
CC	specific inhibitor (ASI) targeted to an allele of a first essential gene	
CC	present in cells of the precancerous condition, where the normal somatic	
CC	cells of the patient are heterozygous for the first gene, the inhibitor	
CC	is active on at least one but less than all allelic forms of the gene	
CC	present in a population and targets only one allelic form present in the	
CC	normal somatic cells, and the first gene. The products and methods can be	
CC	used in the diagnosis, prevention and treatment of LOH disorders, e.g.	
CC	cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic	
CC	lesions, benign tumors, endometriosls, polycystic kidney disease, and	
CC	graft versus host disease. The method can also be used to remove	
CC	malignant cells from bone marrow transplants. AAZ25812-Z26825 represent	
CC	human polymorphic sites described in the method of the invention	
XX	Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;	
SQ		
Qy	Query Match	0.2%; Score 14.6; DB 1; Length 21;
	Best Local Similarity	81.0%; Pred. No. 2.3e+03;
	Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Dn	4466 TTTTGTGTC 4486	
	21 TTTTTTTTATTCTTAGGC 1	
RESULT 3249		
ID	AAZ26761/C	
AC	AAZ26761 standard; DNA; 21 BP.	
XX	AAZ26761;	
DT	30-NOV-1999 (first entry)	
DE	Human polymorphic region 950.	
XX	Polymorphism: human; inhibitor: cancer; treatment: cell growth; LOH:	
KM	cell viability; loss of heterozygosity; precancerous condition; ASI;	
KM	allele specific inhibitor; somatic cell; diagnosis; prevention;	
KM	atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;	
KM	dysplastic lesion; benign tumour; polycystic kidney disease; transplant;	
KM	graft versus host disease; malignant cell removal; bone marrow; ss.	
OS	Homo sapiens.	
PN	WO9841648-A2.	
PD	24-SEP-1998.	
PF	19-MAR-1998; 98WO-US005419.	
PR	20-MAR-1997; 97US-0041057P.	
PA	(VARI-) VARIAGENICS INC.	

XX	Houseman D, Ledley FD, Stanton VP;
PI	DR
XX	WP1; 1998-521232/44.
XX	
PT	Identifying target genes for allele-specific drugs - used for diagnosis,
PT	prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT	diaplastic lesions, endometriosis or graft versus host disease.
XX	
P8	Disclosure; Fig 7; 605pp; English.
XX	
CC	This invention describes a novel method for identifying an inhibitor
CC	potentially useful for treatment of cancer, where the inhibitor is active
CC	on a gene vital for cell growth or viability, and where the gene is
CC	subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC	used for preventing the development of cancer in a patient having a
CC	precancerous condition, by administering to the patient a first allele
CC	specific inhibitor (ASI) targeted to an allele of a first essential gene
CC	present in cells of the precancerous condition, where the normal somatic
CC	cells of the patient are heterozygous for the first gene, the inhibitor
CC	is active on at least one but less than all allelic forms of the gene
CC	present in a population and targets only one allelic form present in the
CC	normal somatic cells, and the first gene. The products and methods can be
CC	used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC	cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC	lesions, benign tumour, endometriosis, polycystic kidney disease, and
CC	graft versus host disease. The method can also be used to remove
CC	malignant cells from bone marrow transplants. AA25812-226825 represent
CC	human polymorphic sites described in the method of the invention
XX	
SQ	Sequence 21 BP; 3 A; 12 C; 2 G; 4 T; 0 U; 0 Other;
	Query Match 0.2%; Score 14.6; DB 1; Length 21;
	Best Local Similarity 81.0%; Pred. No. 2.3e+03;
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	2865 AGCAGAGGAGGAGGAGGCGG 2885
DB	21 AGCGAGGAGACGGGTGTGTG 1
RESULT 3250	
AAAX17913/C	
ID	AAAX17912 standard; DNA; 21 BP.
XX	
AC	AAAX17912;
XX	
DT	11-MAY-1999 (first entry)
XX	
DE	Anti-CMV oligonucleotide #4847.
XX	
KX	Antisense; oligonucleotide; immediate early; DNA polymerase; CMV;
KW	cytomegalovirus; inhibition; replication; sugar modification;
KW	phosphorochioate; infection; retinits; ss.
XX	
OS	Synthetic.
OS	Human herpesvirus 5.
XX	
FH	Key
FT	modified_base
FT	1. .21
FT	/*tag= a
FT	/note= "contains phosphorochioate internucleotide
FT	linkages"
XX	
XX	
PN	WO9845314-A1.
XX	
PD	15-OCT-1998.
XX	
PF	07-APR-1998; 98WO-US006895.
XX	
PR	09-APR-1997; 97US-00838715.
XX	
PA	(ISIS-) ISIS PHARM INC.

[illegible]

CC	and behaviour, such as somatic overgrowth and tumour formation. AA200581
CC	.200586 represent novel glypican sequence tags (STS's)
XX	..
SO	Sequence 21 BP; 3 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
QY	4305 TTTCCTTCCCTCGACTGTC 4325
DB	1 TCTCCTTCCCTGACTAACC 21
RESULT 3252	
AAV71751/c	
ID	AAV71751 standard; DNA; 21 BP.
XX	AAV71751;
AC	
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Human V3 loop HIV receptor P30/PHAPI sense PCR primer.
KW	HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
XX	P30 protein; PHAPI; infection; therapy; PCR; primer; ss.
XX	
OS	Synthetic.
XX	Homo sapiens.
XX	MO3840480-A1.
XX	
PN	17-SBP-1998.
XX	
PE	12-MAR-1998; 98MO-EP001409.
PR	
XX	12-MAR-1997; 97US-0040969P.
XX	
PA	(INSP ) INST PASTEUR.
PA	(CNRS ) CENT NAT RECH SCI.
PI	Hovanessian A, Callebaut C, Krust B, Jacotot E, Muller S;
XX	Briand J, Guichard G;
XX	
DR	WPI; 1999-034588/03.
XX	
PS	Disclosure; Page 48; 267pp; English.
XX	
CC	This oligonucleotide is complementary to a portion of DNA sequence (see
CC	AAV71743) coding for the P30/PHAPI (see AA84053) of the newly identified
CC	V3 loop HIV receptor. It is used as a sense primer, together with an
CC	antisense primer (see AAV71752) in a PCR amplification of P30/PHAPI
CC	reverse-transcribed mRNA. The V3 loop HIV receptor consists of an
CC	association of 3 proteins, named P95/nucleolin, P40/PHAPI and P30/PHAPI
CC	(see AA84052-54). A method for screening molecules that modulate the
CC	expression of the receptor comprises: cultivating cells transfected with
CC	a nucleotide sequence encoding P95/nucleolin, P30/PHAPI or P30/PHAPI,
CC	placed under the control of its own promoter; bringing the cells into
CC	contact with a test molecule; and quantifying expression of the
CC	P95/nucleolin, P30/PHAPI or P40/PHAPI e.g. by quantitative PCR using the
CC	primers provided (see AAV71749-54). Active molecules that have the
CC	ability to alter and/or prevent the binding of the HIV receptor to the
CC	HIV retrovirus can be used in pharmaceutical and diagnostic compositions
XX	of the invention
XX	
SO	Sequence 21 BP; 1 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
QY	
Query Match	0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity	81.0%; Pred. No. 2.3e+03;
	Mismatches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 60 CGAGGCTGCGGGCGCGG 80  
 |||||  
 Db 21 CAGAGGCTGCGCGCGCGG 1

RESULT 3253  
 AAX32391/c  
 ID AAX32391 standard; DNA; 21 BP.  
 XX  
 AC AAX32391;  
 XX  
 DT 17-JUN-1999 (first entry)  
 XX  
 DE Ab1 variable light (VL) chain CDR2 encoding DNA.  
 XX  
 KM Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;  
 KM megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;  
 KM bone marrow hypoplasia; disseminated intravascular coagulation; anemia;  
 KM myelodysplasia; myelotoxic chemotherapy; leukemia; tumour; MDS; CDR;  
 KM neuromuscular; muscular dystrophy; complementarity determining region;  
 KM variable heavy chain; variable light chain; VH; VL; ss.  
 OS Homo sapiens.  
 XX  
 PN WO9910494-A2.  
 PD 04-MAR-1999.  
 XX  
 PF 21-AUG-1998; 98WO-US017364.  
 XX  
 PR 25-AUG-1997; 97US-00918148.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Adams CW, Carter PJ, Fendly BM, Gurney AL;  
 DR WPI; 1999-204666/17.  
 DR P-PSDB; AAY06691.  
 XX  
 PT New thrombopoietin receptor agonist antibodies - useful for treating  
 PT immunological or hematological disorders.  
 XX  
 PS Claim 10; Page 75; 86pp; English.

CC The invention relates to an agonist antibody (Ab) which binds to a  
 CC thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can  
 CC be used in the same way and for the same indications as thrombopoietin  
 CC (TPO). They can stimulate proliferation, differentiation or growth of  
 CC megakaryocytes. They may also be able to stimulate megakaryocytes to  
 CC increase platelet production. They can be used for treating immunological  
 CC or hematopoietic disorders, especially thrombocytopenia. Thrombocytopenia  
 CC -associated bone marrow hypoplasia (e.g. aplastic anemia following  
 CC chemotherapy or bone marrow transplant) may be effectively treated with  
 CC the antibody compounds as well as disorders such as disseminated  
 CC intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and  
 CC non HIV-induced), chronic idiopathic thrombocytopenia, congenital  
 CC thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They  
 CC can also be used in e.g. myelotoxic chemotherapy for treatment of solid  
 CC tumours or leukaemia, myeloablative chemotherapy for autologous or  
 CC allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic  
 CC anemia, congenital thrombocytopenia, and immune thrombocytopenia. The  
 CC antibodies which bind to the TPO-R receptor can be used for improving  
 CC neuromuscular function in a patient, e.g. in muscular dystrophy. The  
 CC products can also be used for detection and diagnosis. The antibodies  
 CC have a longer half-life than the natural ligand for the TPO-R. Sequences  
 CC AAX32387-X32413 represent DNA fragments encoding the CDR1, CDR2, and CDR3  
 CC regions of variable heavy (VH) chains and variable light (VL) chains of  
 CC antibodies Ab1 to Ab6  
 XX  
 SQ Sequence 21 BP; 6 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2785 TGAAGGAGACGCTGTACC 2805  
 |||||  
 Db 21 TGAAGGCGGATGCTGTACC 1

RESULT 3254  
 AA206694/c  
 ID AA206694 standard; DNA; 21 BP.  
 XX  
 AC AA206694;  
 XX  
 DT 02-DEC-1999 (first entry)  
 XX  
 DE Reverse PCR primer DLX7R, for amplification of DLX7.  
 XX  
 KM PCR primer; DLX7; Distal-less homeobox gene 3; DLX3; dentition;  
 KM craniofacial development; Tricho-dento-osseous syndrome; TDO;  
 KM abnormal hair; teeth; bone; osseous structure repair; bone defect;  
 KM bone thickness; bone density; broken bone; periodontal disease;  
 KM osteoporosis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO943784-A2.  
 PD 02-SEP-1999.  
 XX  
 PF 26-FEB-1999; 99WO-US004237.  
 XX  
 PR 27-FEB-1998; 98US-00031962.  
 XX  
 PA (UYWA-) UNIV WAKE FOREST.  
 PI Hart TC, Price JA;  
 DR WPI; 1999-527612/44.  
 XX  
 PT New isolated DLX3 proteins and nucleic acids, used to develop products  
 PT for enhancing growth, development and repair of osseous structures,  
 PT particularly for treating bone defects.  
 XX  
 PS Example 1; Page 24; 54pp; English.

CC PCR primers AA206693-206694 are used to amplify the coding sequence of  
 CC DLX7. DLX7 is a member of the distal-less homeobox gene family. DLX7 is  
 CC used in the isolation of DLX3 (AA206690). The DLX3 gene consists of three  
 CC exons with the homeobox contained in exons 2 and 3. Exons 1 and 2 are  
 CC separated by a 1.1 kb intron, and exons 2 and 3 are separated by a 1.6 kb  
 CC intron. The DLX3 gene has been localised to chromosome 17q20-21. The DLX3  
 CC protein has a molecular weight of 32kD. The dlx genes are thought to  
 CC function in the normal craniofacial development and the development of  
 CC normal dentition. Tricho-Dento-Osseous syndrome (TDO) is an autosomal  
 CC dominant disorder characterised by abnormal hair, teeth and bone. Studies  
 CC on TDO patients show that they have a mutated form of DLX3 called  
 CC DLX3delta (AA206691). DLX3delta has a deletion of 4 guanine nucleotide  
 CC residues, this results in a frame shift causing the DLX3delta protein  
 CC (AAY92227) to be a truncated form of DLX3. The nucleotide and amino acid  
 CC sequences of both DLX3 and DLX3delta can be used in the development of  
 CC products for enhancing growth, development and repair of osseous  
 CC structures, particularly for treating bone defects especially in TDO  
 CC sufferers. Addition of DLX3delta proteins and DLX3delta-encoding nucleic  
 CC acids should serve to enhance bone thickness and increase bone density at  
 CC the sites of application. Exogenously added DLX3delta proteins and  
 CC DLX3delta-encoding nucleic acids should have utility in the treatment of  
 CC bone/osseous defects secondary to trauma, such as broken bones. Finally,  
 CC the DLX3delta proteins and nucleic acids should also have utility in the  
 CC treatment of defects secondary to certain pathologies, such as  
 CC periodontal disease defects or congenital/acquired defects such as

CC osteoporosis. The products can also be used for detection and diagnosis  
XX  
SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4570 CCCCCCTGCGCTTTTCTTG 4590  
DB 21 CCACCCAGCATTTTCTTG 1  
RESULT 3255  
AA17984  
ID AA17984 standard; DNA; 21 BP.  
XX  
AC AA17984;  
XX  
DT 11-MAY-1999 (first entry)  
XX  
DE Primer D399S to generate variant humanised anti-CD3 heavy chain.  
XX  
KW Variant; antibody; heavy chain; light chain; immunoadhesin; immunos assay;  
KM diagnosis; cancer; primer; PCR; amplification; ss.  
XX  
OS Synthetic.  
XX  
PN MO9850431-A2.  
XX  
PD 12-NOV-1998.  
XX  
PF 30-APR-1998; 98WO-US008762.  
XX  
PR 02-MAY-1997; 97US-00850058.  
PR 24-JUN-1997; 97US-0050661P.  
XX  
PA (GETH ) GENENTECH INC.  
PI Arathoon R, Carter PJ, Merchant AM, Presta LG;  
PI WPI; 1999-070091/06.  
XX  
DR WPI; 1999-070091/06.  
XX  
PT Selective preparation of multispecific antibodies - with heteromultimeric  
PT heavy chain and common light chain components, useful for, e.g. in vivo  
PT diagnosis of cancer.  
XX  
PS Example 1; Page 43; 69pp; English.  
XX  
CC This oligonucleotide was used to generate a variant anti-CD3 antibody  
CC (Ab) heavy chain in a new method for preparing a multispecific Ab  
CC comprising a first polypeptide (PP) and at least 1 extra PP, where: (1)  
CC the first PP comprises a multimerisation domain (MD) forming an interface  
CC positioned to interact with an interface of a MD of the extra PP; and  
CC (1i) the first and extra PPs each have a binding domain, which comprises  
CC a heavy chain and a light chain, where the variable light chains of the  
CC first and extra PPs comprise a common sequence. The method comprises: (a)  
CC culturing a host cell comprising nucleic acid encoding the first PP and  
CC extra PP, and the variable light chain, such that the nucleic acid is  
CC expressed; and (b) recovering the multispecific Ab from the culture. The  
CC method prepares heteromultimeric PPs, such as bispecific Abs, bispecific  
CC immunoadhesins and Ab-immunoadhesin chimeras. The method allows for the  
CC enhanced formation of the desired heteromultimer relative to the  
CC undesired heteromultimers and homomultimers. The Abs can be used in  
CC immunoassays and for the in vitro or in vivo diagnosis of various  
CC diseases, such as cancer  
XX  
SQ Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 185 GCCGCTGACCTCGACGAGG 205  
DB 1 GCCGCTCGAGCTCGACGAGG 21  
RESULT 3256  
AA184089/c  
ID AA184089 standard; DNA; 21 BP.  
XX  
AC AA184089;  
XX  
DT 27-AUG-1999 (first entry)  
XX  
DE PCR primer for TCV S1 protein coding sequence.  
XX  
KW TCV; S1 protein; turkey enteritis coronavirus; turkey coronavirus; SMT;  
KM spiking mortality of turkeys; vaccine; immunogenic composition;  
KM poult enteritis and mortality syndrome; diarrhoea; turkey poult;  
KM diagnosis; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
OS Turkey coronavirus.  
XX  
PN MO925838-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 13-NOV-1998; 98WO-US024313.  
XX  
PR 14-NOV-1997; 97US-0065556P.  
PR 10-NOV-1998; 98US-00188979.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (BROW/) BROWN T P.  
PA (VILL/) VILLEGAS P.  
XX  
PI Brown TP, Villegas P, Contreras A;  
PI WPI; 1999-347478/29.  
XX  
DR Turkey coronavirus isolates associated with spiking mortality of turkeys.  
XX  
PT  
PT  
XX  
PS Example 7; Page 7; 90pp; English.  
XX  
CC This sequence represents a PCR primer for DNA encoding a turkey  
CC coronavirus (TCV) S1 protein. The invention relates to an isolate of TCV  
CC obtained from a turkey having spiking mortality of turkeys (SMT) or  
CC obtained from an animal exposed to the turkey, which isolate is adapted  
CC to cell culture. The TCV and bovine coronavirus isolates are useful for  
CC forming vaccines or immunogenic compositions useful for preventing or  
CC inhibiting SMT. SMT is a form of poult enteritis and mortality syndrome  
CC and causes diarrhoea in turkey poults. The methods are useful in  
CC diagnosis and detection of turkey coronavirus associated with SMT. The  
CC oligonucleotides are useful as primers for amplification of the  
CC coronavirus, which is useful for detecting the replication or presence  
CC of a virus in a sample. N.B. The protein encoded by the amplified  
CC sequence is referred to in the specification, but is not given in the  
CC specification  
XX  
SQ Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 2679 TGGAGAGGAGGCACATATC 2699  
DB 21 TGGAGAGGAGGCACATATC 1  
RESULT 3257  
AA184710/c  
ID AA184710 standard; DNA; 21 BP.

XX AAX54710;  
AC 05-JUL-1999 (first entry)  
XX Human fibronectin antisense oligonucleotide fragment.  
XX  
XX Antisense oligonucleotide; multiple target; antisense treatment;  
XX impaired respiration; inflammation; lung disease;  
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
XX acute asthma; allergy; asthma; impeded respiration;  
XX respiratory distress syndrome; pain; cystic fibrosis;  
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
XX prostate cancer; ss.  
XX  
XX Synthetic.  
OS  
XX WO9913886-A1.  
XX  
XX 25-MAR-1999.  
XX  
XX 17-SEP-1998; 98WO-US019419.  
XX  
XX 17-SEP-1997; 97US-0059160P.  
XX  
XX 09-JUN-1998; 98US-00093972.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nyce JM;  
XX  
XX WPI; 1999-229400/19.  
XX  
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
XX vasoconstriction.  
XX  
XX PS Disclosure; Page 55; 120pp; English.  
XX  
XX The specification describes antisense oligonucleotides (AAX52869-X55271)  
XX directed against at least 2 mRNAs selected from target genes, coding and  
XX non-coding regions of RNAs corresponding to target genes, gene initiation  
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
XX end and the juxta-section between coding and non-coding regions and all  
XX segments of RNAs encoding proteins associated with one or more diseases,  
XX conditions or mixtures. The antisense oligonucleotides may be derived  
XX from sequences AAX55272-74. These multiple target oligonucleotides  
XX (specifically AAX55180-271) can be used for the antisense treatment of  
XX diseases and conditions. Typical diseases and conditions are those  
XX associated with impaired respiration and inflammation, including lung  
XX diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
XX acute asthma, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
XX pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
XX disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
XX colon cancer, breast cancer, lung cancer, pancreatic cancer,  
XX hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
XX well as all types of cancers which may metastasize or have metastasized  
XX to the lungs, including breast and prostate cancer  
XX  
XX Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3384 CCTCCCCAGCTGCACCCCG 3404  
DB 21 CCGCCACACGCGCCACCC 1

RESULT 3258

AAX83847/C  
ID AAX83847 standard; DNA; 21 BP.  
XX  
XX AAX83847;  
AC  
XX  
XX 09-SEP-1999 (first entry)  
DT  
XX  
XX Mouse ligand polypeptide PCR primer SEQ ID NO:9.  
DE  
XX  
XX G protein-coupled receptor protein; APJ; central nervous system;  
XX circulation; immune function; gastrointestinal function; reproduction;  
XX metabolic function; HIV; infection; AIDS; PCR primer; ss.  
XX  
XX Synthetic.  
OS  
XX Mus sp.  
XX  
XX WO9933976-A1.  
XX  
XX 08-JUL-1999.  
XX  
XX 22-DEC-1998; 98WO-JP005805.  
XX  
XX 24-DEC-1997; 97JP-00353955.  
XX  
XX 16-FEB-1998; 98JP-00032577.  
XX  
XX 04-AUG-1998; 98JP-00220853.  
XX  
XX 25-SEP-1998; 98JP-00271645.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Hinuma S, Tatemoto K, Hosoya M, Habata Y, Fujii R, Kitada C;  
XX  
XX WPI; 1999-405507/34.  
XX  
XX New ligand polypeptide for the G protein-coupled receptor, APJ, useful  
XX for modulating central nervous system.  
XX  
XX Example 11; Page 93; 169pp; English.  
XX  
XX The present invention describes a ligand polypeptide for the G protein-  
XX coupled receptor, APJ. The APJ ligand can modulate central nervous system  
XX function, circulatory function, immune function, gastrointestinal  
XX function, metabolic function and reproductive function. An antibody  
XX against the APJ ligand can be used in diagnosis. The APJ ligand can be  
XX used in an assay to screen for compounds that change its binding activity  
XX to its receptor. The ligand can also be used for treating HIV infection  
XX and AIDS. The present sequence represents a PCR primer used in an example  
XX from the present invention  
XX  
XX Sequence 21 BP; 6 A; 3 C; 11 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3866 TTCTCTTACTCTCCGCCCG 3886  
DB 21 TTCTCTTACTCTCCGCCG 1

RESULT 3259

AAX09053  
ID AAX09053 standard; DNA; 21 BP.  
XX  
XX AAX09053;  
AC  
XX  
XX 14-JUN-1999 (first entry)  
DT  
XX  
XX Tumour necrosis factor alpha antisense oligonucleotide.  
DE  
XX  
XX Tumour necrosis factor alpha; TNF-alpha; antisense oligonucleotide; ASO;  
XX inhibition; expression; treatment; disease; disorder; ss.  
XX  
XX Synthetic.  
OS

OS Rattus rattus.  
XX  
XX WO9901139-A1.  
XX  
XX 14-JAN-1999.  
XX  
XX  
XX 02-JUL-1998; 98WO-US013711.  
XX  
XX 03-JUL-1997; 97US-0051705P.  
XX  
XX (UYJC-) UNIV JEFFERSON THOMAS.  
XX  
XX Tu G, Israel Y;  
XX  
XX WPI, 1999-105767/09.  
XX  
XX  
XX Generation of antisense oligonucleotides - by specifically targeting a  
PT GGGA motif found in mRNA sequences.  
XX  
XX  
XX Example 1; Page 32; 55pp; English.  
XX  
XX Antisense oligonucleotides (ASO) for inhibiting a tumour necrosis factor-  
CC alpha (TNF-alpha) gene in an animal, preferably a human, comprise 12-50  
CC nucleotides, 90% of which are complementary to a region of mRNA  
CC containing a GGGA sequence motif. The ASO is used to inhibit expression  
CC of a gene in an animal and for treating the animal when afflicted with a  
CC disease or disorder characterised by the presence of an mRNA from a gene  
CC containing a GGGA motif. The ASO are specifically targeted to a GGGA  
CC sequence motif found in mRNA from a gene. A study of known ASO has shown  
CC that at least half of the most efficacious ASO's contain one or more TCCC  
CC motifs. This ASO was designated RU-2826 and corresponds to a region of  
CC the 3' untranslated region of the primary transcript of rat TNF-alpha  
XX  
XX  
SQ Sequence 21 BP; 8 A; 1 C; 11 G; 1 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 566 CTGGGGAAGGAGGATCGAA 586  
DB 1 CTGAGGAGGAGGAGGAGGAA 21  
RESULT 3260  
AAA3157/C  
ID AAA34157 standard; DNA; 21 BP.  
XX  
XX AAA34157;  
XX  
XX  
XX 28-JUL-2000 (first entry)  
XX  
XX Human adenosine receptor related polynucleotide SEQ ID NO:1846.  
XX  
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KM phosphorothioate; impaired respiration; inflammation; allergy;  
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KM antiallergic; antiaesthetic; cytostatic; analgesic; impaired airway;  
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KM cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX

PA (UYEC-) UNIV EAST CAROLINA.  
XX  
XX Nye JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX  
XX Disclosure; Page 496; 1343pp; English.  
XX  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiaesthetic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3384 CTTCCCCAGCTGCCACCCCC 3404  
DB 21 CCGCCGACAGCGGCACCCCC 1  
RESULT 3261  
AAZ88382/C  
ID AAZ88382 standard; DNA; 21 BP.  
XX  
XX AAZ88382;  
XX  
XX 04-MAY-2000 (first entry)  
XX  
XX Oligonucleotide PCR primer #10.  
XX  
XX PCR primer; polymerase chain reaction; amplification; probe; detection;  
KM Trachoma chlamydia; Mycobacterium tuberculosis; Hepatitis B virus;  
KM Hepatitis C virus; ss.  
XX  
XX Synthetic.  
XX  
XX CN1232182-A.  
XX  
XX 20-OCT-1999.  
XX  
XX 13-APR-1998; 98CN-00106616.  
XX  
XX 13-APR-1998; 98CN-00106616.  
XX  
XX

XX (FUXI-) FUXING HIGH SCI & TECH GROUP CO LTD SHAN.  
 XX Xia Y, Xie W, Ding Y;  
 XX WPI; 2000-098541/09.  
 XX Polymerase chain reaction test method and reagent box.  
 PT  
 PS Claim 16; Page 2; 19pp; Chinese.  
 XX  
 CC A method has been developed for detecting nucleic acid molecules. The  
 CC method includes using coating liquid to drop the specific probe onto a  
 CC detecting membrane (the salt concentration of coating liquid is higher  
 CC than 2M and the membrane is a high-molecular polymer with average pore  
 CC size of 1-10 microns); putting one end of the membrane in the liquid  
 CC containing amplified polymerase chain reaction (PCR) product, and  
 CC detecting if the amplified PCR product is hybridised with the probe. A  
 CC reagent box is also disclosed to efficiently and quickly detect Trachoma  
 CC chlamydia, Mycobacterium tuberculosis, Hepatitis B virus and Hepatitis C  
 CC virus. AA288369 to AA288383 represent specifically claimed  
 CC oligonucleotides used in the exemplification of the present invention  
 CC  
 SQ Sequence 21 BP; 3 A; 10 C; 1 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1023 TGGACAGATGAAGAGAGTA 1043  
 Db 21 TGGAAAGCTGAAGGCGCAGTA 1  
 XX  
 RESULT 3262  
 AAA40708/c  
 ID AAA40708 standard; DNA; 21 BP.  
 XX  
 AC AAA40708;  
 XX  
 DT 15-AUG-2000 (first entry)  
 XX  
 DE Rat Nos3 primer Nos3R SEQ ID NO:96.  
 XX  
 KM Human; rat; CD36; SHR; spontaneous hypertensive rat; diagnosis; therapy;  
 KM screening; polymorphism; variant; detection; mutant; blood; mutation;  
 KM insulin; glucose metabolism; fatty acid metabolism; catecholamine;  
 KM malaria; infection; parasite; antiparasitic; antidiabetic; primer; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200019883-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 07-OCT-1999; 99WO-US023418.  
 XX  
 PR 07-OCT-1998; 98US-00167750.  
 PR 28-DEC-1998; 98US-00221222.  
 PR 17-MAR-1999; 99US-00270542.  
 XX  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 PA (SCIO-) SCIOS INC.  
 PA (ATM/) ALTMAN T J.  
 PA (SCOT/) SCOTT J.  
 PA (STAN/) STANTON L W.  
 XX  
 PI Altman TJ, Scott J, Stanton LW;  
 XX  
 DR WPI; 2000-303596/26.  
 XX  
 PT Nucleic acid encoding mutant CD36 proteins useful for preventing,  
 PT diagnosing and treating parasitic infections, especially malaria.

XX Example 1; Page 111; 167pp; English.  
 PS  
 CC The present invention describes isolated nucleic acid molecules (A)  
 CC encoding mutant CD36 proteins (B). Parasites such as Plasmodium  
 CC falciparum (the major cause of malaria) are unable to utilise the mutated  
 CC proteins to gain entry to, and infect cells. The mutant CD36 proteins do  
 CC not function correctly preventing parasites utilising them to infect  
 CC cells. The nucleic acids may be used for the recombinant production of  
 CC mutant CD36 proteins according to standard methodologies. They may be  
 CC used in this way to prevent and treat parasitic infections that utilise  
 CC the CD36 protein to infect cells, such as P. falciparum, the major cause  
 CC of malaria. For example, the protein may be used to identify modulators  
 CC of CD36 expression and activity or a patient's CD36 DNA may be screened  
 CC to determine whether there are any mutations present that may confer  
 CC resistance to parasitic infections. The proteins and nucleic acids may  
 CC also be used to prevent, diagnose and treat diseases associated with  
 CC defects in insulin action and/or glucose metabolism and/or fatty acid  
 CC metabolism and/or catecholamine action in subjects possessing mutations  
 CC in the CD36 genes. AAA40606 to AAA40759, and AA802515 to AA802564,  
 CC represent nucleotide and amino acid sequences respectively which are used  
 CC in the exemplification of the present invention  
 CC  
 SQ Sequence 21 BP; 6 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1673 CTTGTTTCGCAAAATATGCAC 1693  
 Db 21 CATGTTTATGCACATGCAC 1  
 XX  
 RESULT 3263  
 AAZ73907/c  
 ID AAZ73907 standard; DNA; 21 BP.  
 XX  
 AC AAZ73907;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Human biallelic marker downstream amplification primer SEQ ID NO:8263.  
 XX  
 KM Human genome; biallelic marker; high density disequilibrium map;  
 KM genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KM haplotyping; hybridisation; identification; characterisation;  
 KM amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KM diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Cohen D, Blumenfeld M, Chumakov I;  
 XX  
 DR WPI; 2000-013267/01.  
 XX  
 PT Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX  
 PS Claim 8; Page 1992; 2745pp; English.  
 XX  
 CC AA265654 to AA269578 represent human biallelic markers from the present



CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AA269579 to AA277440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4138 GAACGTGTACTGATTGTT 4158  
Db 21 GAACGTGTGACAAAGATGTGT 1

RESULT 3264  
AA275773  
ID AA275773 standard; DNA; 21 BP.  
AC AA275773;  
XX  
DT 10-SEP-2001 (first entry)  
DE Human biallelic marker downstream amplification primer SEQ ID NO:10129.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
PA  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
XX WPI; 2000-013267/01.  
DR  
XX  
PT Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
PS Claim 9; Page 2390; 2745pp; English.  
XX  
XX AA26554 to AA269578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AA269579 to AA277440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6237 CTGTCTTGTGATTGTTATCC 6257  
Db 1 CTGCTCTTGTGATTGCTTCC 21

RESULT 3265  
AA272176/C  
ID AA272176 standard; DNA; 21 BP.  
AC AA272176;  
XX  
DT 10-SEP-2001 (first entry)  
DE Human biallelic marker upstream amplification primer SEQ ID NO:6532.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
PA  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
XX WPI; 2000-013267/01.  
DR  
XX  
PT Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
XX  
PS Claim 9; Page 1623; 2745pp; English.  
XX  
XX AA26554 to AA269578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AA269579 to AA277440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

Qy : Sequence 21 BP; 2 A; 9 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6177 GAAAAGAGTGATGAGAGAG 6197  
DB 21 GAAATAGAGAGATGAGAGAG 1

RESULT 3266

AAZ75738  
ID AAZ75738 standard; DNA; 21 BP.

AC AAZ75738;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:10094.

XX Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX Homo sapiens.

OS WO954500-A2.

PN 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (BEST ) GENSET.

PA Cohen D, Blumenfeld M, Chumakov I;

PI WPI; 2000-013267/01.

DR Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

PS Claim 8; Page 2382; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ6579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

CC Sequence 21 BP; 12 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3280 GAAGAAAATGTAACGAGCC 3300  
DB 1 GAAGAAAATGTAACGAGCC 21

RESULT 3267  
AAZ76866/c  
ID AAZ76866 standard; DNA; 21 BP.

XX AAZ76866;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:11222.

XX Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX Homo sapiens.

OS WO954500-A2.

PN 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (BEST ) GENSET.

PA Cohen D, Blumenfeld M, Chumakov I;

PI WPI; 2000-013267/01.

DR Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

PS Claim 9; Page 2623; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

CC Sequence 21 BP; 9 A; 1 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3851 CTCCTTTTCCTTATTCCTC 3871  
DB 21 CTCCTTTTCCTTATTCCTC 1

RESULT 3268  
AAZ76031  
ID AAZ76031 standard; DNA; 21 BP.

XX AAZ76031;

DT 10-SEP-2001 (first entry)  
 XX  
 DE Human biallelic marker downstream amplification primer SEQ ID NO:10387.  
 XX  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Cohen D, Blumenfeld M, Chumakov I;  
 XX  
 DR WPI: 2000-013267/01.  
 XX  
 PT Novel biallelic markers used to construct a high density disequilibrium  
 map of the human genome.  
 XX  
 PS Claim 9; Page 2445; 2745pp; English.  
 XX  
 CC AA265654 to AA269578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AA269579 to AA277440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 XX  
 SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 2388 TGGTACATCCAGCTGGGAC 2408  
 Db 1 TGGTACATCAACCTGGGAC 21  
 RESULT 3269  
 AAA97479/c  
 ID AAA97479 standard; DNA; 21 BP.  
 XX  
 AC AAA97479;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Phytolacca americana antifungal protein Pa-AFP XbaI 5' PCR primer.  
 XX  
 KW Phytolacca americana antifungal protein; Pa-AFP; Virginian pokeweed;  
 KW recombinant production; Escherichia coli; PCR primer; ss.  
 XX  
 OS Phytolacca americana.

OS Synthetic.  
 XX  
 PN CN1257918-A.  
 XX  
 PD 28-JUN-2000.  
 XX  
 PE 18-DEC-1998; 98CN-00125610.  
 XX  
 PR 18-DEC-1998; 98CN-00125610.  
 XX  
 PA (WUGG/) WU G.  
 XX  
 PI Wu G, Zhao J, Liu Y;  
 XX  
 DR WPI: 2000-544291/50.  
 XX  
 PT Recombination antifungal protein gene sequence, engineering bacterium and  
 process for preparing its products.  
 XX  
 PS Claim 2; Page 2; 12pp; Chinese.  
 XX  
 CC The invention to an antifungal protein (Pa-AFP; AAB23178) from the seeds  
 CC of Phytolacca americana (Virginian pokeweed), to cDNA encoding it  
 CC (AAA97476), to the processes and primers used to clone the AFP cDNA from  
 CC Virginian pokeweed seed total mRNA, and to its IPTG-inducible recombinant  
 CC production in Escherichia coli. Pa-AFP has activity against such fungi as  
 CC Rhizoctonia solani (black scurf of potato) and may therefore be useful in  
 CC agriculture. Sequences AAA97477-A97482 represent PCR primers used to  
 CC introduce restriction sites into cDNA encoding Pa-AFP in the cloning  
 CC process  
 XX  
 SQ Sequence 21 BP; 2 A; 2 C; 13 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 3878 CCCCCCCCCCCAGCTCTGA 3898  
 Db 21 CCCCCCCCCCCAGCTCTGA 1  
 RESULT 3270  
 AAF20279/c  
 ID AAF20279 standard; DNA; 21 BP.  
 XX  
 AC AAF20279;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human fibronectin polynucleotide fragment #1846.  
 XX  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; anticholinergic; hypotensive; cyclostatic;  
 KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200062736-A2.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US008020.  
 PF  
 PR 06-APR-1999; 99US-0127958P.  
 XX

PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 XX NYCE JW;  
 DR WPI; 2000-679539/66.  
 XX  
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX  
 PS Claim 14; Page 220; 1592pp; English.  
 XX  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antispasmodic, hypotensive and cytoskeletal activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensive, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasocostriction, inflammation,  
 CC allergies, asthma, impaired respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 CC  
 XX  
 SQ Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3384 CCGCCCGAGCTGCACCCCG 3404  
 DB 21 CCGCCCGAGCTGCACCCCG 1  
 RESULT 3271  
 AAC71664/c  
 ID AAC71664 standard; DNA; 21 BP.  
 XX  
 AC AAC71664;  
 XX  
 DT 09-FEB-2001 (first entry)  
 XX  
 DE Single nucleotide polymorphism PCR primer #996.  
 XX  
 KM Single nucleotide polymorphism; SNP; human; genetic disease;  
 KM disease susceptibility; cardiovascular system; endocrine system;  
 KM neurological system; forensic testing; paternity testing; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN W0200058519-A2.  
 PN  
 XX WPI; 2000-611722/58.  
 PD 05-OCT-2000.

XX  
 XX 30-MAR-2000; 2000MO-US008440.  
 PF  
 XX 31-MAR-1999; 99US-0127248P.  
 PR  
 XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Altschuler D, Cargill M, Daley GO, Ireland JS, Lander ES;  
 PI Lipshutz RJ, Patil N, Sklar P;  
 XX  
 DR WPI; 2000-611722/58.  
 XX  
 PT Nucleic acid selected from one of 106 genes comprising single nucleotide  
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful  
 PT for phenotypic correlations, forensics, paternity testing, medicine and  
 PT genetic analysis.  
 XX  
 PS Claim 8; Fig 5; 214pp; English.  
 XX  
 CC The present invention is concerned with a number of human single  
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human  
 CC genes. These SNPs can be used in disease diagnosis and prediction of an  
 CC individual's susceptibility to disease, in forensic and paternity testing  
 CC and in genetic mapping. In particular, the SNPs of the invention can be  
 CC used to diagnose susceptibility to diseases of the cardiovascular,  
 CC endocrine and neurological systems, such as coronary artery disease,  
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
 CC diseases  
 CC  
 XX  
 SQ Sequence 21 BP; 13 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4460 GGACTTTTCTTTTCTTTTCTTT 4480  
 DB 21 GGACTTTTCTTTTCTTTTCTTT 1  
 RESULT 3272  
 AAC71649/c  
 ID AAC71649 standard; DNA; 21 BP.  
 XX  
 AC AAC71649;  
 XX  
 DT 09-FEB-2001 (first entry)  
 XX  
 DE Single nucleotide polymorphism PCR primer #986.  
 XX  
 KM Single nucleotide polymorphism; SNP; human; genetic disease;  
 KM disease susceptibility; cardiovascular system; endocrine system;  
 KM neurological system; forensic testing; paternity testing; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN W0200058519-A2.  
 PN  
 XX WPI; 2000-611722/58.  
 PD 05-OCT-2000.  
 XX  
 PF 30-MAR-2000; 2000MO-US008440.  
 PR  
 XX 31-MAR-1999; 99US-0127248P.  
 XX  
 PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Altschuler D, Cargill M, Daley GO, Ireland JS, Lander ES;  
 PI Lipshutz RJ, Patil N, Sklar P;  
 XX  
 DR WPI; 2000-611722/58.

PT Nucleic acid selected from one of 106 genes comprising single nucleotide  
PT polymorphisms, allele-specific oligonucleotides to the genes are useful  
PT for phenotypic correlations, forensics, paternity testing, medicine and  
PT genetic analysis.  
PS Claim 8; Fig 5; 214pp; English.  
XX  
CC The present invention is concerned with a number of human single  
CC nucleotide polymorphisms (SNPs) which the inventors identified in human  
CC genes. These SNPs can be used in disease diagnosis and prediction of an  
CC individual's susceptibility to disease, in forensic and paternity testing  
CC and in genetic mapping. In particular, the SNPs of the invention can be  
CC used to diagnose susceptibility to diseases of the cardiovascular,  
CC endocrine and neurological systems, such as coronary artery disease,  
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
CC diseases  
XX  
SQ Sequence 21 BP; 13 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4460 GGACTTTTCTTTTCTTTTCTTTT 4480  
DB 21 GGACATGTTTCTTTCTTTCTTT 1  
RESULT 3273  
AAA10973  
ID AAA10973 standard; DNA; 21 BP.  
XX  
AC AAA10973;  
XX  
DT 14-JUN-2000 (first entry)  
XX  
DE Interleukin-6 (IL-6) microsphere genosensor target sequence.  
XX  
KW Microsphere genosensor; detect target analytes; library screening;  
KW potential drug; pollutant; solvent; therapeutic drug; illicit drug;  
KW hormone; cytokine; cancer; Alzheimer's disease; cystic fibrosis;  
KW toxic bacteria; forensic DNA fingerprinting; detect; infection; target;  
KW bioactive agent; optical signature; interleukin-6; IL-6; ss.  
XX  
OS Unidentified.  
XX  
PN WO200016101-A2.  
XX  
PD 23-MAR-2000.  
XX  
PF 10-SEP-1999; 99WO-US020914.  
XX  
PR 11-SEP-1998; 98US-00151877.  
XX  
PA (TUFT ) TUFTS COLLEGE.  
XX  
PI Walt DR, Michael KU;  
XX  
DR WPI; 2000-364508/31.  
XX  
PT Composition comprising microspheres with a bioactive agent and optical  
PT signature, at discrete sites on substrate, useful for detecting target  
PT analytes, e.g. nucleic acids.  
XX  
PS Disclosure; Page 29; 58pp; English.  
XX  
CC This sequence represents a target sequence for a microsphere genosensor  
CC created using the composition of the invention. The invention relates to  
CC a composition which comprises a substrate (other than a fibre optic  
CC bundle) with discrete sites on its surface, and microspheres distributed  
CC at these sites. The microspheres comprise at least two subpopulations,  
CC each with a bioactive agent and an optical signature that identifies the  
CC bioactive agent. Microsphere genosensors are made by attaching a probe

CC (examples include AAA10964-A10968) to the microsphere surface chemistry.  
CC A fluorescent dye molecule is attached to the target sequence (examples  
CC include AAA10965-A10973) which is in solution. The optically  
CC interrogatable signal change occurs with the binding of the target  
CC sequences to the microsphere. The composition of the invention is used to  
CC detect target analytes and screen large libraries of bioactive agents for  
CC those (potential drugs) that bind to the target analytes e.g. pollutants;  
CC solvents; therapeutic or illicit drugs; hormones; cytokines; nucleic  
CC acids (detecting genes associated with cancer, Alzheimer's disease or  
CC cystic fibrosis); antigens; whole cells; to screen foods and water for  
CC toxic bacteria; for forensic DNA fingerprinting; for sequencing and for  
CC detecting mutations; and detecting viral or bacterial infections  
XX  
SQ Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3653 AAGAAATACCCGAGCCCAAC 3673  
DB 1 AATACCAACCCCTGACCCAC 21  
RESULT 3274  
AAA94225  
ID AAA94225 standard; DNA; 21 BP.  
XX  
AC AAA94225;  
XX  
DT 12-JAN-2001 (first entry)  
XX  
DE Human testosterone-repressed prostate message-2 antisense oligo #1.  
XX  
KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200049937-A2.  
XX  
PD 31-AUG-2000.  
XX  
PF 25-FEB-2000; 2000WO-US004875.  
XX  
PR 26-FEB-1999; 99US-0121726P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Gleave M, Rennie PS, Miyake H, Nelson C;  
XX  
DR WPI; 2000-531132/48.  
XX  
PT Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
PS Example 5; Page 36; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
SQ Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      674 TGGAGTCTGTGCAAGCCCTGG 694
      |||||
DB      1 TGGAGTCTTTCAGCGCTCTCG 21

RESULT 3275
AAA97685/c
ID AAA97685 standard; DNA; 21 BP.
XX
XX      AAA97685;
AC
XX      15-FEB-2001 (first entry)
DT
XX
XX      Interleukin-6 (IL-6) array probe #5.
DE
XX
XX      Analyte detection; microsphere array; self-encoding sensor array;
KM      nucleic acid detection; biochip; disease-associated gene; probe; ss.
XX
XX      Unidentified.
OS
XX
XX      WO200060332-A2.
FN
XX      12-OCT-2000.
PD
XX
XX      06-APR-2000; 2000WO-US009183.
PF
XX      06-APR-1999; 99US-00287573.
PR
XX      (TUFT ) TUFTS COLLEGE.
PA
XX      Walt DR, Dickinson TA;
PI
XX      WPI; 2000-656240/63.
DR
XX
XX      Method for detecting target analyte in sample involves, providing array
PT      with several sub population of sensor elements, measuring optical
PT      response of each sensor element and statistically analyzing optical
PT      response.
XX
XX      Example 19; Fig 22; 99pp; English.
PS
XX
XX      The invention relates to a method for detecting a target analyte in a
CC      sample using a self-encoding sensor array comprising a population of
CC      microspheres on discrete locations on the surface of a substrate. The
CC      array has several subpopulations of microspheres, each of which provides
CC      a characteristic optical response signature when illuminated by
CC      excitation light energy in the presence of a reference analyte, which may
CC      in some cases be the target analyte. The method involves contacting the
CC      array with a sample, measuring the optical response of each microsphere
CC      sensor element, and performing statistical analysis on the measured
CC      optical response of the subpopulations. The method is used for detecting
CC      target analytes such as nucleic acids, proteins, hormones, lipids,
CC      carbohydrates, whole cells, environment pollutants and drugs. The method
CC      is inexpensive when compared to conventional methods. The array once
CC      loaded can be decoded or used after testing. The present sequence
CC      represents a probe used to detect the presence of a disease- associated
CC      gene fragment in an exemplification of the invention
CC
XX
SQ      Sequence 21 BP; 2 A; 1 C; 10 G; 8 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3653 AAGAAATATCCCGACGCCAAC 3673
      |||||
DB      21 AATTAACACCCCTGACCCAAC 1

RESULT 3276
AAA97679
ID AAA97679 standard; DNA; 21 BP.

```

```

XX      AAA97679;
AC
XX      15-FEB-2001 (first entry)
DT
XX
XX      Interleukin-6 (IL6) target sequence.
DE
XX
XX      Analyte detection; microsphere array; self-encoding sensor array;
KM      nucleic acid detection; biochip; target; ss.
XX
XX      Unidentified.
OS
XX
XX      WO200060332-A2.
FN
XX      12-OCT-2000.
PD
XX
XX      06-APR-2000; 2000WO-US009183.
PF
XX      06-APR-1999; 99US-00287573.
PR
XX      (TUFT ) TUFTS COLLEGE.
PA
XX      Walt DR, Dickinson TA;
PI
XX      WPI; 2000-656240/63.
DR
XX
XX      Method for detecting target analyte in sample involves, providing array
PT      with several sub population of sensor elements, measuring optical
PT      response of each sensor element and statistically analyzing optical
PT      response.
XX
XX      Disclosure; Page 39; 99pp; English.
PS
XX
XX      The invention relates to a method for detecting a target analyte in a
CC      sample using a self-encoding sensor array comprising a population of
CC      microspheres on discrete locations on the surface of a substrate. The
CC      array has several subpopulations of microspheres, each of which provides
CC      a characteristic optical response signature when illuminated by
CC      excitation light energy in the presence of a reference analyte, which may
CC      in some cases be the target analyte. The method involves contacting the
CC      array with a sample, measuring the optical response of each microsphere
CC      sensor element, and performing statistical analysis on the measured
CC      optical response of the subpopulations. The method is used for detecting
CC      target analytes such as nucleic acids, proteins, hormones, lipids,
CC      carbohydrates, whole cells, environment pollutants and drugs. The method
CC      is inexpensive when compared to conventional methods. The array once
CC      loaded can be decoded or used after testing. The present sequence
CC      represents a target sequence which can be detected using the method of
CC      the invention
CC
XX
SQ      Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3653 AAGAAATATCCCGACGCCAAC 3673
      |||||
DB      1 AATTAACACCCCTGACCCAAC 21

RESULT 3277
AAA97698
ID AAA97698 standard; DNA; 21 BP.
XX
XX      AAA97698;
AC
XX      15-FEB-2001 (first entry)
DT
XX
XX      Interleukin-6 (IL-6) array probe #18.
DE
XX
XX      Analyte detection; microsphere array; self-encoding sensor array;
KM      nucleic acid detection; biochip; disease-associated gene; probe; ss.

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```
XX Unidentified.
OS
XX WO200060332-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009183.
XX
XX 06-APR-1999; 99US-00287573.
XX
XX (TUFT ) TUFTS COLLEGE.
XX
XX Walt DR, Dickinson TA;
XX
XX WPI; 2000-656240/63.
XX
XX Method for detecting target analyte in sample involves, providing array
XX with several sub population of sensor elements, measuring optical
XX response of each sensor element and statistically analyzing optical
XX response.
XX
XX Example 19; Fig 22; 99pp; English.
XX
XX The invention relates to a method for detecting a target analyte in a
XX sample using a self-encoding sensor array comprising a population of
XX microspheres on discrete locations on the surface of a substrate. The
XX array has several subpopulations of microspheres, each of which provides
XX a characteristic optical response signature when illuminated by
XX excitation light energy in the presence of a reference analyte, which may
XX in some cases be the target analyte. The method involves contacting the
XX array with a sample, measuring the optical response of each microsphere
XX sensor element, and performing statistical analysis on the measured
XX optical response of the subpopulations. The method is used for detecting
XX target analytes such as nucleic acids, proteins, hormones, lipids,
XX carbohydrates, whole cells, environmental pollutants and drugs. The method
XX is inexpensive when compared to conventional methods. The array once
XX loaded can be decoded or used after testing. The present sequence
XX represents a probe used to detect the presence of a disease-associated
XX gene fragment in an exemplification of the invention
XX
XX Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3653 AAGAAATACCCGACGCCAAC 3673
XX |||||
XX 1 AATACCAACCCCTGACCCAAC 21
XX
XX RESULT 3278
XX ID AAA65238 standard; DNA; 21 BP.
XX
XX AAA65238;
XX
XX 12-DEC-2000 (first entry)
XX
XX Meloidogyne chitwoodi species-specific oligonucleotide #1.
XX
XX Species-specific oligonucleotide; crop parasite; crop damage;
XX root-knot nematode; PCR primer; ss.
XX
XX Meloidogyne chitwoodi.
XX
XX WO200040754-A1.
XX
XX 13-JUL-2000.
XX
XX 28-DEC-1999; 99WO-NL000812.
XX
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```
PR 30-DEC-1998; 98NL-01010917.
XX
XX (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
XX Zijlstra C;
XX
XX WPI; 2000-465998/40.
XX
XX Novel DNA oligonucleotide specific for Meloidogyne species, used to
XX detect specific Meloidogyne species in a sample.
XX
XX Claim 5; Page 20; 33pp; English.
XX
XX The present sequence is a species-specific oligonucleotide for the root-
XX knot nematode Meloidogyne chitwoodi. This is a crop parasite which can
XX cause damage to crops such as potatoes, beets, black salisifies and
XX carrots, the damage being so great that in Europe the organism has been
XX given a quarantine status. The oligonucleotide was identified using
XX random amplified polymorphic DNA and subjecting it to a series of
XX selection procedures until a species-specific fragment was found. The
XX sequence can be used in tests to determine both the presence and species
XX of Meloidogyne parasites, which is useful for seed export and also in the
XX search for resistance to the parasite
XX
XX Sequence 21 BP; 9 A; 2 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4731 TGGAGGCCAGCTGAGGAGA 4751
XX |||||
XX 1 TGGAGAGCAGCAGGAGAGA 21
XX
XX RESULT 3279
XX ID AAA76069 standard; DNA; 21 BP.
XX
XX AAA76069;
XX
XX 08-DEC-2000 (first entry)
XX
XX beta-actin PCR primer #2.
XX
XX PCR primer; prostate cancer cell line; androgen independent; C1-1; C1-2;
XX LNCaP cell line; beta-actin; Prostate-specific antigen;
XX Prostate specific membrane antigen; Basic fibroblast growth factor;
XX Vascular endothelial cell growth factor; Interleukin-6;
XX Transforming Growth Factor-beta1; Transforming Growth Factor-beta2;
XX AR; PSA; IL-8; VEGF; bFGF; IL-6; TGF-beta1; TGF-beta2; TGF-beta-R;
XX EGF-R; BCL-2; E-cadherin; p53; PTEN; Caveolin; c-myc; HER-2/neu; p27;
XX Androgen receptor; ss.
XX
XX Homo sapiens.
XX
XX WO200044879-A1.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US002223.
XX
XX 28-JAN-1999; 99US-0117562P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Belldegrun AS, Tso C;
XX
XX WPI; 2000-499329/44.
XX
XX Androgen independent, aggressively tumorigenic prostate cancer cell lines
XX designated C1-1 and C1-2, useful as tools for studying the cellular and
```

```
PT molecular mechanisms of prostate cancer progression.
XX
XX Example 2; Page 29; 90pp; English.
XX
CC The present invention relates to androgen independent, aggressively
CC tumorigenic prostate cancer cell lines, CL-1 and CL-2, which are
CC sublines of the LNCaP cell line. The present sequence is a PCR primer
CC used to amplify a coding sequence expressed by the cell lines. The coding
CC sequences which were amplified in the present invention by the primers in
CC AAA76068 to AAA76107 were: beta-actin, prostate-specific antigen (PSA),
CC Androgen receptor (AR), prostate specific membrane antigen (PSAM),
CC Interleukin-8 (IL-8), Vascular endothelial cell growth factor (VEGF),
CC Basic fibroblast growth factor (bFGF), Interleukin-6 (IL-6), Transforming
CC Growth Factor-beta1 (TGF-beta1), Transforming Growth Factor-beta2 (TGF-
CC beta2), Transforming Growth Factor-beta-R (TGF-beta-R), Epidermal growth
CC factor receptor (EGF-R), BCL-2, E-cadherin, p53, PTEN, Caveolin, c-myc,
CC HRR-2/nuu and p27. RT-PCR was used to monitor changes in coding sequence
CC expression, as the LNCaP parental lines progressed to the CL1 and CL2
CC sublines. The CL-1 and CL-2 sublines can be used as tools for studying
CC the cellular and molecular mechanisms of prostate cancer progression.
CC Such as the expression patterns of various transcripts and proteins that
CC are associated with the progression of the non-metastatic, androgen-
CC dependent state to the metastatic androgen-independent state
XX
SQ Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 712 CTGCGATCATGAGGTACACC 732
DB 1 CTGCGATCATGAGGTACACC 21
XX
RESULT 3280
AAF96869/c
ID AAF96869 standard; DNA; 21 BP.
XX
AC AAF96869;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1630.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Variation replace(11,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX PD 15-MAR-2001.
XX
XX PF 07-SEP-2000; 2000WO-US024503.
XX
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
```

```
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
XX Example; Page 158; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7384 TGTACAGTTCCTTCGACGA 7404
DB 21 TGTACAGTTCCTTCGACGA 1
XX
RESULT 3281
AAF97449/c
ID AAF97449 standard; DNA; 21 BP.
XX
AC AAF97449;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #2210.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Variation replace(11,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200118250-A2.
XX
XX PD 15-MAR-2001.
XX
XX PF 07-SEP-2000; 2000WO-US024503.
XX
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
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PT atherosclerosis.
XX
XX Example; Page 199; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 1 A; 5 C; 11 G; 4 T; 0 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2721 CCCCCAGGCGCTGCCAAGC 2741
DB 21 CCCCCAGGCTCCGGGCAAGC 1

RESULT 3282
AAF97249
ID AAF97249 standard; DNA; 21 BP.
XX
AC AAF97249;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #2010.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (MHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 185; 242pp; English.
XX
```

```
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match          0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 987 GGAGATCAAGGCGCTGMAAGT 1007
DB 1 GGAGTCAAGGCTCCTGTTGT 21

RESULT 3283
AAF96294
ID AAF96294 standard; DNA; 21 BP.
XX
AC AAF96294;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1055.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (MHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 124; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX
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```
CC      in the specification. In particular, the method can be used in the
CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
CC
SQ      Sequence 21 BP, 6 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
      Query Match          0.2%; Score 14.6; DB 1; Length 21;
      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
      Db      2938 TGGGGAACAGGGCCGACGAGA 2958
      1 TGGAGTTCATGCGCCAGCAGGA 21
      RESULT 3284
      AAF96296/c
      ID      AAF96296 standard; DNA; 21 BP.
      XX
      AC      AAF96296;
      XX
      DT      06-JUN-2001 (first entry)
      XX
      DE      Human gene single nucleotide polymorphism #1057.
      XX
      KW      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
      KW      polymorphism; vascular disease; coronary artery disease; forensics;
      KW      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
      KW      pulmonary embolism; paternity test; ds.
      XX
      OS      Homo sapiens.
      XX
      FH      Key          Location/Qualifiers
      FT      Variation    replace(11,T)
      FT      /*tag= a
      FT      /standard_name= "single nucleotide polymorphism"
      FT
      PN      WO200118250-A2.
      XX
      PD      15-MAR-2001.
      XX
      PF      07-SEP-2000; 2000WO-US024503.
      XX
      PR      10-SEP-1999; 99US-0153357P.
      PR      26-JUL-2000; 2000US-0220947P.
      PR      16-AUG-2000; 2000US-0225724P.
      XX
      PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
      PA      (MILL-) MILLENNIUM PHARM INC.
      XX
      PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JF;
      XX      WPI; 2001-226749/23.
      DR
      XX
      PT      Nucleic acids comprising single nucleotide polymorphisms, useful in
      PT      applications such as forensics, paternity testing, medicine, genetic
      PT      analysis and phenotype correlations to diseases such as diabetes and
      PT      atherosclerosis.
      XX
      PS      Example; Page 124; 242pp; English.
      XX
      CC      The present invention provides a method of diagnosing a vascular disease
      CC      in an individual, involving determining the sequence at various
      CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
      CC      genes. The sequences at a number of polymorphic sites are also provided
      CC      in the specification. In particular, the method can be used in the
      CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
      CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
      CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
```

```
CC      useful in forensics, paternity testing, genetic analysis and phenotype
CC      correlations to diseases. The present sequence is an example of one of
CC      the human gene SNPs shown in the specification
CC
SQ      Sequence 21 BP, 6 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
      Query Match          0.2%; Score 14.6; DB 1; Length 21;
      Best Local Similarity 81.0%; Pred. No. 2.3e+03;
      Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
      Db      4306 TTCCTTCCCTGACTGTCTT 4326
      21 TCCTTCCCGGAACGTGCT 1
      RESULT 3285
      AAF96817/c
      ID      AAF96817 standard; DNA; 21 BP.
      XX
      AC      AAF96817;
      XX
      DT      06-JUN-2001 (first entry)
      XX
      DE      Human gene single nucleotide polymorphism #1578.
      XX
      KW      Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
      KW      polymorphism; vascular disease; coronary artery disease; forensics;
      KW      myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
      KW      pulmonary embolism; paternity test; ds.
      XX
      OS      Homo sapiens.
      XX
      FH      Key          Location/Qualifiers
      FT      Variation    replace(11,G)
      FT      /*tag= a
      FT      /standard_name= "single nucleotide polymorphism"
      FT
      PN      WO200118250-A2.
      XX
      PD      15-MAR-2001.
      XX
      PF      07-SEP-2000; 2000WO-US024503.
      XX
      PR      10-SEP-1999; 99US-0153357P.
      PR      26-JUL-2000; 2000US-0220947P.
      PR      16-AUG-2000; 2000US-0225724P.
      XX
      PA      (WHED ) WHITEHEAD INST BIOMEDICAL RES.
      PA      (MILL-) MILLENNIUM PHARM INC.
      XX
      PI      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JF;
      XX      WPI; 2001-226749/23.
      DR
      XX
      PT      Nucleic acids comprising single nucleotide polymorphisms, useful in
      PT      applications such as forensics, paternity testing, medicine, genetic
      PT      analysis and phenotype correlations to diseases such as diabetes and
      PT      atherosclerosis.
      XX
      PS      Example; Page 154; 242pp; English.
      XX
      CC      The present invention provides a method of diagnosing a vascular disease
      CC      in an individual, involving determining the sequence at various
      CC      polymorphic sites within the human thrombospondin 1 and thrombospondin 4
      CC      genes. The sequences at a number of polymorphic sites are also provided
      CC      in the specification. In particular, the method can be used in the
      CC      diagnosis of atherosclerosis, myocardial infarction, coronary heart
      CC      disease, stroke, peripheral vascular diseases, venous thromboembolism and
      CC      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
      CC      useful in forensics, paternity testing, genetic analysis and phenotype
      CC      correlations to diseases. The present sequence is an example of one of
      CC      the human gene SNPs shown in the specification
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Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2713 GGGCGGAGCCCGAGCCCTG 2713  
21 GGGTGTGACGACGAGCCCTG 1

RESULT 3286  
AA96350/c  
ID AAF96350 standard; DNA; 21 BP.

AA96350;  
06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1111.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
polymorphism; vascular disease; coronary artery disease; forensics;  
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
pulmonary embolism; paternity test; ds.

Homo sapiens.

Key Location/Qualifiers  
replace(11,G)  
/\*tag= a  
/standard\_name= "single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.

26-JUL-2000; 2000US-0220947P.

16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolik S, Daley GQ, McCarthy JJ;  
WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in  
applications such as forensics, paternity testing, medicine, genetic  
analysis and phenotype correlations to diseases such as diabetes and  
atherosclerosis.

Example; Page 128; 242pp; English.

The present invention provides a method of diagnosing a vascular disease  
in an individual, involving determining the sequence at various  
polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
in the specification. In particular, the method can be used in the  
diagnosis of atherosclerosis, myocardial infarction, coronary heart  
disease, stroke, peripheral vascular diseases, venous thromboembolism and  
pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
useful in forensics, paternity testing, genetic analysis and phenotype  
correlations to diseases. The present sequence is an example of one of  
the human gene SNPs shown in the specification

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

900 TGACATTGATGTGAGTGCT 920  
21 TCAGTTCCTCTGTGAGTGCT 1

RESULT 3287  
AA97158  
ID AAF97158 standard; DNA; 21 BP.

AA97158;  
06-JUN-2001 (first entry)

Human gene single nucleotide polymorphism #1919.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
polymorphism; vascular disease; coronary artery disease; forensics;  
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
pulmonary embolism; paternity test; ds.

Homo sapiens.

Key Location/Qualifiers  
replace(11,G)  
/\*tag= a  
/standard\_name= "single nucleotide polymorphism"

WO200118250-A2.

15-MAR-2001.

07-SEP-2000; 2000WO-US024503.

10-SEP-1999; 99US-0153357P.

26-JUL-2000; 2000US-0220947P.

16-AUG-2000; 2000US-0225724P.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

(MILL-) MILLENNIUM PHARM INC.

Lander ES, Gargill M, Ireland JS, Bolik S, Daley GQ, McCarthy JJ;  
WPI; 2001-226749/23.

Nucleic acids comprising single nucleotide polymorphisms, useful in  
applications such as forensics, paternity testing, medicine, genetic  
analysis and phenotype correlations to diseases such as diabetes and  
atherosclerosis.

Example; Page 179; 242pp; English.

The present invention provides a method of diagnosing a vascular disease  
in an individual, involving determining the sequence at various  
polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
in the specification. In particular, the method can be used in the  
diagnosis of atherosclerosis, myocardial infarction, coronary heart  
disease, stroke, peripheral vascular diseases, venous thromboembolism and  
pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
useful in forensics, paternity testing, genetic analysis and phenotype  
correlations to diseases. The present sequence is an example of one of  
the human gene SNPs shown in the specification

Sequence 21 BP; 7 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3777 TGACATTGACCTTCAACA 3797  
||| ||||| |||||

Db 1 TTACTATTGCATTGCAACA 21

RESULT 3288

AAAF95280/c

ID AAAF95280 standard; DNA; 21 BP.

XX AAAF95280;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #41.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

XX polymorphism; vascular disease; coronary artery disease; forensics;

XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Variation replace(11,A)

XX FT /tag= a

XX /standard\_name= "single nucleotide polymorphism"

XX NO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000MO-US024503.

XX 10-SEP-1999; 99US-0153357P.

XX 26-JUL-2000; 2000US-0220947P.

XX 16-AUG-2000; 2000US-0225724P.

XX (MHED ) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis.

XX Example; Page 49; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism and

XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

XX the human gene SNPs shown in the specification

XX Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 719 CCATGAGGTACACCCCTGTGG 739

Db 21 CCTTACGAGTACACCACTGGGG 1

RESULT 3289

AAAF95372  
ID AAAF95372 standard; DNA; 21 BP.

XX AAAF95372;

XX 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #133.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

XX polymorphism; vascular disease; coronary artery disease; forensics;

XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

XX pulmonary embolism; paternity test; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Variation replace(11,C)

XX FT /tag= a

XX /standard\_name= "single nucleotide polymorphism"

XX NO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000MO-US024503.

XX 10-SEP-1999; 99US-0153357P.

XX 26-JUL-2000; 2000US-0220947P.

XX 16-AUG-2000; 2000US-0225724P.

XX (MHED ) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis.

XX Example; Page 57; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism and

XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

XX the human gene SNPs shown in the specification

XX Sequence 21 BP; 4 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 14.6; DB 1; Length 21;

XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;

XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 603 CAAAGTGGCTGCGCATTTGTGG 623

Db 1 CAAAGTGGCTGCGCATTTGTGGAG 21

RESULT 3290

AAAF62434

ID AAAF62434 standard; DNA; 21 BP.

XX AAAF62434;

```
XX 12-SEP-2001 (first entry)
XX DT
XX CHolinergic receptor polymorphism containing DNA fragment #335.
XX DE
XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX KW heart disease; paternity testing; forensic science; ds.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX FT Variation /tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX PN WO200138576-A2.
XX PD
XX 31-MAY-2001.
XX PF
XX 17-NOV-2000; 2000WO-US031639.
XX PR
XX 24-NOV-1999; 99US-0167334P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Cargill M, Ireland JS, Lander ES;
XX DR WPI; 2001-367705/38.
XX PT New nucleic acid segments of the human genome, particularly from genes
XX PT including polymorphic sites, for phenotype correlation, forensics,
XX PT paternity testing, medicine and genetic analysis.
XX PS
XX Claim 1; Page 57; 80pp; English.
XX PS
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
XX CC contain single nucleotide polymorphisms (SNPs). A method is included in
XX CC the invention for analysing a nucleic acid sample, which consists of
XX CC determining the base occupying any one of the polymorphic sites given in
XX CC the SNP containing sequences. The nucleotide sequences can be used in the
XX CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX CC diseases, diseases of the cardiovascular system, and infection by
XX CC microorganisms. The oligonucleotides are also useful in the manufacture
XX CC of a medicament for the treatment or prophylaxis of the diseases, and as
XX CC a pharmaceutical. SNP containing oligonucleotides are useful in
XX CC applications such as phenotype correlation, forensics, paternity testing,
XX CC medicine and genetic analysis
XX SQ
XX Sequence 21 BP; 2 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5161 TTCTCCTGGGACAGTGGGCTC 5181
XX DB 1 TGCCTATGGGCCACTGGGCTC 21
XX
XX RESULT 3291
XX AAH62275
XX ID AAH62275 standard; DNA; 21 BP.
XX AC
XX AAH62275;
XX DT
XX 12-SEP-2001 (first entry)
XX DE
XX SMRT polymorphism containing DNA fragment #176.
XX KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX KW heart disease; paternity testing; forensic science; ds.
XX OS
XX Homo sapiens.
```

```
XX FH
XX Key Location/Qualifiers
XX FT Variation /tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX PN WO200138576-A2.
XX PD
XX 31-MAY-2001.
XX PF
XX 17-NOV-2000; 2000WO-US031639.
XX PR
XX 24-NOV-1999; 99US-0167334P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Cargill M, Ireland JS, Lander ES;
XX DR WPI; 2001-367705/38.
XX PT New nucleic acid segments of the human genome, particularly from genes
XX PT including polymorphic sites, for phenotype correlation, forensics,
XX PT paternity testing, medicine and genetic analysis.
XX PS
XX Claim 1; Page 43; 80pp; English.
XX PS
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
XX CC contain single nucleotide polymorphisms (SNPs). A method is included in
XX CC the invention for analysing a nucleic acid sample, which consists of
XX CC determining the base occupying any one of the polymorphic sites given in
XX CC the SNP containing sequences. The nucleotide sequences can be used in the
XX CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX CC diseases, diseases of the cardiovascular system, and infection by
XX CC microorganisms. The oligonucleotides are also useful in the manufacture
XX CC of a medicament for the treatment or prophylaxis of the diseases, and as
XX CC a pharmaceutical. SNP containing oligonucleotides are useful in
XX CC applications such as phenotype correlation, forensics, paternity testing,
XX CC medicine and genetic analysis
XX SQ
XX Sequence 21 BP; 1 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 30 GAGCTGCTGCAGGCTCCGCG 50
XX DB 1 GAGCTGCCCTGGGCCCGCG 21
XX
XX RESULT 3292
XX AAH62422
XX ID AAH62422 standard; DNA; 21 BP.
XX AC
XX AAH62422;
XX DT
XX 12-SEP-2001 (first entry)
XX DE
XX SLC18A3 polymorphism containing DNA fragment #323.
XX KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX KW heart disease; paternity testing; forensic science; ds.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX FT Variation /tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX FT
XX PN WO200138576-A2.
XX PD
XX 31-MAY-2001.
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XX 17-NOV-2000; 2000MO-US031639.
XX
XX 24-NOV-1999; 99US-0167334P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Cargill M, Ireland JS, Lander ES;
XX
XX WPI; 2001-367705/38.
XX
XX New nucleic acid segments of the human genome, particularly from genes
XX including polymorphic sites, for phenotype correlation, forensics,
XX paternity testing, medicine and genetic analysis.
XX
XX Claim 1; Page 55; 80pp; English.
XX
XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
XX contain single nucleotide polymorphisms (SNPs). A method is included in
XX the invention for analysing a nucleic acid sample, which consists of
XX determining the base occupying any one of the polymorphic sites given in
XX the SNP containing sequences. The nucleotide sequences can be used in the
XX diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX diseases, diseases of the cardiovascular system, and infection by
XX microorganisms. The oligonucleotides are also useful in the manufacture
XX of a medicament for the treatment or prophylaxis of the diseases, and as
XX a pharmaceutical. SNP containing oligonucleotides are useful in
XX applications such as phenotype correlation, forensics, paternity testing,
XX medicine and genetic analysis
XX
XX Sequence 21 BP; 0 A; 8 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5778 GCCTGCTGCTGCTGCTGCTG 5798
XX 1 GCCTGCTGCTGCTGCTGCTG 21
XX
XX RESULT 3293
XX ID AAA91034/c
XX ID AAA91034 standard; DNA; 21 BP.
XX
XX AAA91034;
XX
XX 05-APR-2001 (first entry)
XX
XX PCR primer for Human secreted protein PRO7476 coding sequence.
XX
XX Secreted protein; human; PRO protein; neoplastic cell growth; tumour;
XX proliferation; leukaemia; lymphoid malignancy; inflammatory disorder;
XX angiogenic disorder; immunologic disorder; PRO7476; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX W0200075317-A2.
XX
XX 14-DEC-2000.
XX
XX 15-MAY-2000; 2000MO-US013358.
XX
XX 09-JUN-1999; 99US-0138365P.
XX 20-JUL-1999; 99US-0144790P.
XX 03-AUG-1999; 99US-0146843P.
XX 10-AUG-1999; 99US-0148188P.
XX 17-AUG-1999; 99US-0149320P.
XX 17-AUG-1999; 99US-0149327P.
XX 17-AUG-1999; 99US-0149366P.
XX 20-AUG-1999; 99US-0150114P.
XX 31-AUG-1999; 99US-0151700P.
XX 31-AUG-1999; 99US-0151734P.

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XX (GETH ) GENENTECH INC.
XX
XX Botstein DA, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI; 2001-071075/08.
XX
XX Antibodies against PRO polypeptides, useful for diagnosing and treating
XX tumors are associated with gene amplification, neoplastic cell growth and
XX proliferation in mammals.
XX
XX Example 10; Page 92; 143pp; English.
XX
XX This sequence represents a PCR primer used to isolate DNA encoding human
XX PRO7476 protein of the invention. The PRO proteins are secreted proteins.
XX Antagonists or antibodies of PRO polypeptides are useful for diagnosing
XX and treating tumours are associated with gene amplification, neoplastic
XX cell growth and proliferation in mammals, and those conditions
XX characterised by overexpression and/or activation of the amplified genes.
XX Such conditions include benign or malignant tumours (e.g. renal, liver,
XX kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
XX pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
XX glioblastomas and various head and neck tumours); leukaemias and lymphoid
XX malignancies; neuronal, glial, astrocytal, hypothalamic, and other
XX glandular, macrophageal, epithelial, stromal and blastocoele disorders;
XX and inflammatory, angiogenic and immunologic disorders. These may further
XX be used to qualitatively or quantitatively detect the expression of
XX proteins encoded by the amplified genes, and in tumour diagnostics or
XX prognostics. The PRO polypeptide or its antagonist may be used for the
XX preparation of a medicament in the treatment of a condition, which is
XX responsive to the PRO polypeptide, its antagonist or anti-PRO antibody
XX
XX Sequence 21 BP; 3 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 2.3e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5166 CTGGACAGTGGGCTGTCAT 5186
XX 21 CAGGCGCAGTGGGAGCTGCAT 1
XX
XX RESULT 3294
XX ID AAF76187/c
XX ID AAF76187 standard; DNA; 21 BP.
XX
XX AAF76187;
XX
XX 05-JUN-2001 (first entry)
XX
XX Human interleukin-6 (IL-6) PCR primer, SEQ ID NO:53.
XX
XX Transgenic mouse; immunodeficient; tissue recipient;
XX lymphocyte deficient; human cytokine; interleukin; IL-7; IL-6; SCF; LIF;
XX stem cell factor; leukaemia inhibitory factor; GM-CSF; M-CSF;
XX granulocyte macrophage-colony stimulating factor;
XX macrophage-colony stimulating factor; human MHC class II; DR3;
XX major histocompatibility complex; allelic specificity determination;
XX human monoclonal antibody generation; haematopoietic cell development;
XX human immune system animal model; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX W0200115521-A1.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000MO-US023971.
XX
XX 31-AUG-1999; 99US-0151688P.
XX
XX (GENV ) GENENCOR INT INC.

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XX
PI Huang MA, Harding FA;
XX
DR WPI: 2001-169001/17.
XX
PT New transgenic mice, useful as non-human mammalian models of human
PT disease, comprise recombination activation gene mutations and donor
PT specific transgenes encoding cytokines.
XX
PS Example 2; Page 38; 68pp; English.
XX
CC The invention relates to a transgenic immunodeficient recipient mouse
CC which is capable of supporting the growth of donor cells. In the mouse,
CC both alleles of a gene activated in early lymphocyte development are
CC disrupted, causing it to lack mature B and T cells. In particular, both
CC alleles of the recombination activation gene-2 (RAG-2) gene are
CC disrupted, which in turn prevents VDJ recombination. The mouse also
CC comprises donor (e.g., human) specific transgenes encoding the cytokines
CC interleukin-7 (IL-7), stem cell factor (SCF), leukemia inhibitory factor
CC (LIF), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC macrophage-colony stimulating factor (M-CSF), and IL-6, which enable it
CC to support the growth of transplanted donor cells. In another embodiment
CC of the invention, the mouse comprises DNA encoding the human major
CC histocompatibility complex (MHC) class II DR3 molecule, where the
CC transgene has naturally linked DRab and DQab alleles. The transgenic
CC mouse may be used as a model for determining the allergenicity of non-
CC donor, e.g., non-human, macromolecules; to determine the effect compounds
CC have on a human immune system; to generate fully human polyclonal or
CC monoclonal antibodies to specific antigens; to determine whether
CC humanised or other monoclonal antibodies will raise a response in a human
CC immune system; to investigate the human cell mediated response to
CC pathogens and other immunomodulatory compounds; and to determine the
CC factors involved in regulating the development and function of human
CC haematopoietic cells. The transgenic mouse supports the functional
CC properties of human haematopoietic cells, unlike previous animal models
CC which produce functionally impaired haematopoietic cells or are
CC immunologically dysfunctional. In addition the transgenic mouse provides
CC a unique model system which supports T cell development in a manner which
CC more closely resembles normal ontogeny, as they possess CD4+ T cells in
CC the periphery that exhibit MHC-restricted antigen- specific responses.
CC Sequences AAH6133-AAH6192 represent human cytokine PCR primers used in
CC the development of human cytokine-expressing transgenic mice
XX
SQ Sequence 21 BP; 0 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 7406 GCAACATGACGAGCAGCAGCA 7426
DB 21 GCAACACGAGGAGCAGGCCCA 1
XX
RESULT 3295
AAH23038/C
ID AAH23038 standard; DNA, 21 BP.
XX
AC AAH23038;
XX
DT 17-SEP-2001 (first entry)
XX
DE PlGF gene fragment.
XX
KW Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
KW antisense therapy; PlGF; da.
XX
OS Homo sapiens.
XX
PN WO200152904-A2.
XX
PD 26-JUL-2001.
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XX
PF 19-JAN-2001; 2001WO-US000019.
XX
PR 19-JAN-2000; 2000US-00487023.
XX
PA (GILL/) GILL P S.
XX
PI Gill PS, Masood R;
XX
DR WPI: 2001-451898/48.
XX
PT Novel antisense oligonucleotides useful for inhibiting vascular
PT endothelial growth factor expression, angiogenesis and for treating
PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostate cancer.
XX
PS Example; Fig 17b; 105pp; English.
XX
CC The invention provides a composition comprising one or more antisense
CC oligonucleotides directed against vascular endothelial growth factor
CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
CC cells exhibiting autocrine VEGF activity at an IC50 concentration of
CC between 0.5-2.5 micro Ma. The antisense oligonucleotides may be directed
CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
CC Preferably the oligonucleotide AAH23032 (a modified version of AAH23984)
CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
CC prostate cancer, pancreatic cancer or melanoma. The present sequence
CC represents a PlGF gene fragment
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 5175 TGCGCTCGCATGTTCTCCAC 5195
DB 21 TGCGCTGACATGCTCCAC 1
XX
RESULT 3296
AAH62077/C
ID AAH62077 standard; DNA, 21 BP.
XX
AC AAH62077;
XX
DT 10-SEP-2001 (first entry)
XX
DE PDGF B hairpin/hammerhead ribozyme recognition site SEQ ID NO:4501.
XX
KW Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiproliferative; dermatological; antiseborrheic; antidiabetic; vitinude;
KW anti-aging; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
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PI Robbins JM, Tritz R;  
XX  
XX WPI; 2001-300427/31.  
XX  
XX  
XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 25; 408pp; English.  
XX  
XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
CC dermatological, cytostatic, antileborrheic, antidiabetic, antickling,  
CC ophthalmological, vulnary, keratolytic and virucide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seboreic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing of  
CC scarring such as keloid, adhesion and hypertrophic or hyperrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 21 BP; 0 A; 9 C; 3 G; 9 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1321 GCTCCAGACAGACAGAGAG 1341  
Db 21 GCAGCAGAGACAGACAGAGAG 1  
RESULT 3297  
AAH24644/C  
ID AAH24644 standard; DNA; 21 BP.  
XX  
AC AAH24644;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE Rainbow trout galectin cDNA primer #2.  
XX  
KM Rainbow trout; galectin; cytostatic; antiinflammatory; immunity;  
KM fish disease; cell adhesion inhibition; inflammation; cancer;  
KM T cell movement; apoptosis; PCR primer; ss.  
XX  
OS Oncorhynchus mykiss.  
XX  
FN JP2001069976-A.  
XX  
PD 21-MAR-2001.  
XX  
PF 01-SEP-1999; 99JP-00247204.  
XX  
PR 01-SEP-1999; 99JP-00247204.  
XX  
PA (MORO ) NORINSUISANSO YOSHOKU KENKYU.  
XX  
DR WPI; 2001-321173/34.  
XX  
XX Novel recombinant Rainbow trout galectin protein and gene encoding the  
PT protein, useful for studying fish immunity mechanism, and diagnosis of  
PT fish diseases.  
XX

PS Example 1; Page 7; 17pp; Japanese.  
XX  
XX The invention relates to a recombinant protein having a 341 amino acid  
CC sequence fully defined in the specification, or its mutant in which at  
CC least one amino acid is deleted, substituted or added, but which retains  
CC the galectin activity. The protein is useful for studying mechanisms of  
CC fish immunity and for diagnosing fish diseases. The galectin proteins are  
CC involved in inhibition of cell adhesion, inflammation, metastasis of  
CC tumour cells, T cell movement, and apoptosis. The present sequence is a  
CC primer which was used in the production of a probe used to analyse  
CC expression of the rainbow trout galectin gene  
XX  
SQ Sequence 21 BP; 4 A; 10 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 5552 GCAGATGAGAAAGTGTGTTG 5572  
Db 21 GCCGATGGAAAGTGGAGTTG 1  
RESULT 3298  
AAF82667  
ID AAF82667 standard; DNA; 21 BP.  
XX  
AC AAF82667;  
XX  
DT 18-JUN-2001 (first entry)  
XX  
DE Human beta-actin PCR primer #2.  
XX  
KM Human; androgen response element; ARE; cytostatic; gene therapy;  
KM prostate-specific chimeric enhancer; transcriptional regulation;  
KM targeted gene expression; prostate cancer; prostate disorder;  
KM prostate-specific antigen; PSA; beta-actin; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200127256-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028444.  
XX  
PR 14-OCT-1999; 99US-0159691P.  
XX  
PR 15-OCT-1999; 99US-0159730P.  
XX  
PA (REGC ) UNIV CALIFORNIA SYSTEM.  
XX  
PI Wu L, Carey MF, Belldegrun AS;  
XX  
DR WPI; 2001-273768/28.  
XX  
XX New polynucleotide, useful for treating prostatic cancer, comprises  
PT prostate specific chimeric enhancer and proximal promoter sequence  
PT operably linked to nucleic acid encoding heterologous polypeptide.  
XX  
PS Example 5; Page 73; 131pp; English.  
XX  
XX The present sequence was used in reverse transcriptase polymerase chain  
CC reaction (RT-PCR) analysis of human prostate cancer cells. The invention  
CC relates to an isolated polynucleotide comprising a prostate-specific  
CC chimeric enhancer (PSE) sequence and a proximal promoter sequence  
CC operably linked to a nucleic acid segment that encodes a heterologous  
CC polypeptide. The PSE contains an ARE and specifically activates  
CC transcription of the nucleic acid segment in a mammalian prostate cell.  
CC The construct is useful for the treatment of a prostate disorder or a  
CC metastasised prostate cancer, such as hyperplasia or hyperproliferation  
CC of prostate cells. It is also useful for directing the tissue-specific  
CC expression of a heterologous polypeptide in a human prostate cell. The  
CC construct may be administered by injection, infection, transformation,



CC liposome-mediated transfection, polybrene-mediated transfection, receptor  
 CC -mediated uptake or Ca-PO4-mediated transformation  
 CC  
 SQ Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 712 CTGGCATCATGAGGTACACC 732  
 |||||  
 1 CTCGGCTCATGAGGCACACC 21

RESULT 3299  
 AAS22024/c  
 ID AAS22024 standard; DNA; 21 BP.  
 XX  
 AC AAS22024;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human COL1A1 PCR primer for Exon 19 #2.  
 XX  
 KW Human; collagen; COL1A1; COL1A2; COL9A1; COL9A2; COL9A3; ss;  
 KW osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;  
 KW shortness of stature; low bone density; gene therapy; PCR primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6265157-B1.  
 XX  
 PD 24-JUL-2001.  
 XX  
 PF 03-OCT-1997; 97US-00943731.  
 XX  
 PR 03-DEC-1991; 91US-00803628.  
 PR 13-MAR-1994; 94US-00212322.  
 XX  
 PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 PA (UYOU-) UNIV OULU.  
 XX  
 PI Prockop DJ, Spotila LD, Deltas CD, Sereida L.  
 PI Westenhansen Larson A, Pack M, Collige A, Early J, Koerkhoe J;  
 PI Ala-Kokko L, Annunen S, Pihlajamaa T, Vuorio M, Paasilta P;  
 XX  
 DR WPI; 2001-432201/46.  
 XX  
 PT Detecting collagen gene alteration, useful for diagnosing osteoporosis,  
 PT multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of  
 PT stature and low bone density in humans.  
 XX  
 PS Example 4; Fig 21; 617pp; English.  
 XX  
 CC The invention relates to Detecting a collagen gene alteration associated  
 CC with a pathological condition in a human subject by obtaining from the  
 CC subject a sample nucleic acid containing a portion of at least 15  
 CC consecutive nucleotides of the segment of the COL1A1 gene extending in  
 CC the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent  
 CC exon 28 through the 3' end of intron 51, where the portion contains an  
 CC intronic nucleotide and a first and second site, determining the sequence  
 CC of the portion and comparing the sequence of the portion with the  
 CC corresponding consensus sequence of the COL1A1 gene where a difference  
 CC between the sequence of the portion and the consensus sequence indicates  
 CC the presence of the collagen alteration in the subject. The method is  
 CC used for detecting abnormalities in a COL1 or COL3 gene is useful for  
 CC determining whether a subject is afflicted with pathological conditions  
 CC associated with an altered collagen gene such as osteoporosis, multiple  
 CC epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and  
 CC low bone density. Identification of an abnormality in a collagen gene is  
 CC also useful for designing a therapeutic nucleotide or gene therapy agent  
 CC which can be administered to the subject to correct or alleviate the

CC abnormality. The method is useful for detecting mutations in both the  
 CC coding and non-coding sequences of any of the COL1 or COL3 genes.  
 CC Therefore the method can be used to detect collagen gene alterations  
 CC which affect either the primary sequence of a collagen protein chain,  
 CC or the genes encoding such chains or regulation of expression of  
 CC the genes encoding such chains. The present sequence is a PCR primer  
 CC which amplifies a nucleic acid from a collagen gene of the invention  
 XX  
 SQ Sequence 21 BP; 7 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 961 GACTCTCAGCGCTTCCTTC 981  
 |||||  
 21 GACTCTCAGCTCATCTCTTC 1

RESULT 3300  
 ABR13278  
 ID ABR13278 standard; DNA; 21 BP.  
 XX  
 AC ABR13278;  
 XX  
 DT 30-JAN-2003 (first entry)  
 XX  
 DE Fanconi anaemia FANCD exon amplifying PCR primer SEQ ID No 181.  
 XX  
 KW Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;  
 KW Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;  
 KW cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;  
 KW Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;  
 KW Xeroderma pigmentosum; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200236761-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 02-NOV-2001; 2001WO-US045561.  
 XX  
 PR 03-NOV-2000; 2000US-0245756P.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA  
 PI D'andrea AD, Taniguchi T, Timmers C, Grome M;  
 XX  
 DR WPI; 2002-519251/55.  
 XX  
 PT Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,  
 PT useful for treating Fanconi anemia pathway defect in cell target or for  
 PT treating patient with defective FANCD2 gene.  
 XX  
 PS Claim 8; Page 56; 103pp; English.  
 XX  
 CC The invention relates to an isolated Fanconi anaemia protein complex  
 CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472  
 CC amino acids fully defined in the specification, its 904 identical  
 CC sequence, a sequence encoded by a polynucleotide that is at least 904  
 CC identical to sequences given in specification such as a 5127 base pair  
 CC sequence, or a fragment which is at least 50 amino acids in length. The  
 CC FANCD2 protein is useful for treating an FA pathway defect in a cell  
 CC target or for treating a patient with a defective FANCD2 gene. The FANCD2  
 CC gene is useful for making a recombinant expression vector. The FANCD2  
 CC protein and its gene are useful as a novel target for therapeutic  
 CC development, and in diagnostic test and screening assays for diseases  
 CC associated with DNA repair and cell cycle abnormalities such as Fanconi  
 CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis  
 CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2  
 CC gene is useful in producing probes and primers for screening patients in  
 CC genetic based test, for diagnosing Fanconi anaemia and cancer, for

CC preparing an experimental mouse model for use in screening new  
CC therapeutics for treating conditions involving defective DNA repair, and  
CC in gene therapy methods. A recombinant vector containing the FANCD2 gene  
CC of the invention is useful in gene therapy. This polynucleotide sequence  
CC represents a PCR primer for amplifying a FANCD2 exon relating to the  
CC invention  
XX  
SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
DY 2742 CGTGCAGTTCACGAGATAC 2762  
DB 1 CATTCAGTTCACGAGATAC 21  
RESULT 3301  
ABS60160/c  
ID ABS60160 standard; DNA; 21 BP.  
XX  
AC ABS60160;  
XX  
DT 05-NOV-2002 (first entry)  
DE Human polymorphism associated DNA sequence #54.  
XX  
XX Amino acid sequence P; XPNEP2; bradykinin receptor B1; ds; BDKRB1;  
KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
KM KXK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
KM myocardial infarction; ventricular hypertrophy; vascular disease;  
KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
KM autoimmune disease; inflammatory arthritis; cancer; wound;  
KM viral infection; bacterial infection; fungal infection; COPD;  
KM Chronic obstructive pulmonary disease; enterocolitis.  
XX  
OS Homo sapiens.  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 03-DEC-2001; 2001WO-US047235.  
XX  
XX 04-DEC-2000; 2000US-0251015P.  
PR 23-JAN-2001; 2001US-0253678P.  
PR 02-MAR-2001; 2001US-0273037P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUI/L) HUI L.  
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
PI Swanson BN, Powell JR;  
PI  
XX  
XX WPI; 2002-619265/66.  
XX  
XX New isolated nucleic acid with at least one polymorphic position, useful  
PT for detecting, diagnosing and treating disorders such as angiodaema,  
PT cancer, viral, bacterial or fungal infection, cardiovascular and  
PT autoimmune diseases.  
XX  
XX  
XX Disclosure; Page 707; 977pp; English.  
XX  
XX The invention relates to an isolated nucleic acid from a human gene  
CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),  
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein  
CC 1 (KXK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one  
CC polymorphic position. Also included are (1) a probe that hybridises to a  
CC polymorphic position as provided in the detailed summary of single  
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising  
CC obtaining the sample from one or more individuals and determining the  
CC nucleic acid sequence at one or more polymorphic positions in a gene  
CC encoding a protein selected from the group above; (3) constructing (M2)  
CC haplotypes using the genes comprising grouping at least two nucleic acids  
CC; (4) identifying (M3) an individual at risk of developing a disorder  
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
CC using the polymorphic data; (5) a library of nucleic acids, each of which  
CC comprises one or more polymorphic positions within a gene encoding a  
CC human protein selected from the group above; and (6) genotyping (M4) an  
CC individual comprising obtaining a nucleic acid sample, determining the  
CC nucleotide present in at least one polymorphic position, and comparing at  
CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
CC and compositions are useful for detecting, diagnosing, treating,  
CC preventing various disorders such as angiodaema and diseases which  
CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
CC hypertension, heart failure, myocardial infarction, ventricular  
CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
CC artery disease, arteriosclerosis and/or atherosclerosis, and  
CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic  
CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
CC diseases and disorders are listed in the specification). The  
CC polynucleotides are also useful for chromosome identification. Antinodes  
CC against the proteins may be utilised for immunophenotyping of cell lines  
CC and biological samples. The present sequence is included in the sequence  
CC listing but is not referred to anywhere else in the specification  
XX  
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
DY 2395 ATCCAGCTGGGACACAGTG 2415  
DB 21 ATACCACTGGGACACAGTG 1  
RESULT 3302  
ABS60171  
ID ABS60171 standard; DNA; 21 BP.  
XX  
XX  
XX ABS60171;  
XX  
XX 05-NOV-2002 (first entry)  
DE Human polymorphism associated DNA sequence #55.  
XX  
XX  
XX Amino acid sequence P; XPNEP2; bradykinin receptor B1; ds; BDKRB1;  
KM tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1;  
KM KXK1; bradykinin receptor B2; BDKRB2; gene therapy;  
KM angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;  
KM polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;  
KM cardiovascular disease; angina pectoris; hypertension; heart failure;  
KM myocardial infarction; ventricular hypertrophy; vascular disease;  
KM aneurysm; embolism; thrombosis; coronary artery disease; angiodaema;  
KM arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;  
KM autoimmune disease; inflammatory arthritis; cancer; wound;  
KM viral infection; bacterial infection; fungal infection; COPD;  
KM Chronic obstructive pulmonary disease; enterocolitis.  
XX  
XX  
XX Homo sapiens.  
XX  
XX  
XX WO200261131-A2.  
XX  
XX 08-AUG-2002.  
XX

PF 03-DEC-2001; 2001WO-US047235.  
 XX  
 XX 04-DEC-2000; 2000US-0251015P.  
 PR 23-JAN-2001; 2001US-0263678P.  
 PR 02-MAR-2001; 2001US-0273037P.  
 XX  
 PA (BRIM /) BRISTOL-MYERS SQUIBB CO.  
 PA (TSUC /) TSUCHIHASHI Z.  
 PA (HUI /) HUI L.  
 XX  
 PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;  
 PI Swanson BN, Powell JR;  
 PI  
 XX WPI: 2002-619265/66.  
 DR  
 XX  
 XX New isolated nucleic acid with at least one polymorphic position, useful  
 PT for detecting, diagnosing and treating disorders such as angioedema,  
 PT cancer, viral, bacterial or fungal infection, cardiovascular and  
 PT autoimmune diseases.  
 XX  
 XX Disclosure; Page 709; 977pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid from a human gene  
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDRB1),  
 CC tachykinin receptor B1 (TACR1), CI esterase inhibitor (CINH), kallikrein  
 CC 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme  
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one  
 CC polymorphic position. Also included are (1) a probe that hybridizes to a  
 CC polymorphic position as provided in the detailed summary of single  
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic  
 CC sequence; (2) analyzing (M1) at least one nucleic acid sample comprising  
 CC obtaining the sample from one or more individuals and determining the  
 CC nucleic acid sequence at one or more polymorphic positions in a gene  
 CC encoding a protein selected from the group above; (3) constructing (M2)  
 CC haplotypes using the genes comprising grouping at least two nucleic acids  
 CC ; (4) identifying (M3) an individual at risk of developing a disorder  
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor  
 CC using the polymorphic data; (5) a library of nucleic acids, each of which  
 CC comprises one or more polymorphic positions within a gene encoding a  
 CC human protein selected from the group above; and (6) genotyping (M4) an  
 CC individual comprising obtaining a nucleic acid sample, determining the  
 CC nucleotide present in at least one polymorphic position, and comparing at  
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)  
 CC and compositions are useful for detecting, diagnosing, treating,  
 CC preventing various disorders such as angioedema and diseases which  
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's  
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,  
 CC hypertension, heart failure, myocardial infarction, ventricular  
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary  
 CC artery disease, arteriosclerosis and/or atherosclerosis, and  
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory  
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection. Chronic  
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other  
 CC diseases and disorders are listed in the specification). The  
 CC polymorphisms are also useful for chromosome identification. Antibodies  
 CC against the proteins may be utilised for immunophenotyping of cell lines  
 CC and biological samples. The present sequence is included in the sequence  
 CC listing but is not referred to anywhere else in the specification  
 XX  
 SQ Sequence 21 BP; 1 A; 10 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5317 TCTGCTTCTCTGCTTGC 5337  
 |||||  
 1 TCTTACTCTCCTCCTTGC 21

RESULT 3303  
 ABS68528/c  
 ID ABS68528 standard; DNA; 21 BP.

XX  
 AC ABS68528;  
 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Clock gene Bmal2 (brain-muscle-Arnt-like protein 2)-related primer #17.  
 XX  
 KW Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia;  
 KW sleeping disorder; non-24-hour sleep; sleep-phase forward; primer;  
 KW retreat syndrome; time-zone variation syndrome; PCR; ss.  
 XX  
 OS Unidentified.  
 OS  
 XX W0200264785-A1.  
 XX  
 XX 22-AUG-2002.  
 XX  
 XX 23-AUG-2001; 2001WO-JP007197.  
 XX  
 XX 13-FEB-2001; 2001JP-00035743.  
 XX  
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 XX Fukada Y, Okano T;  
 XX  
 XX WPI: 2002-667007/71.  
 XX  
 XX  
 XX Clock gene Bmal2 and expressed clock protein BMAL2 important in clock  
 PT oscillation mechanism and relating to circadian rhythm, used in diagnosis  
 PT of and developing drugs for insomnia and other sleeping disorders.  
 XX  
 XX Example 4; Page 35; 187pp; Japanese.  
 XX  
 XX The invention relates to a DNA sequence encoding clock protein BMAL2  
 CC (brain-muscle-Arnt-like protein 2). The gene and protein are applicable  
 CC in diagnosis of and development of drugs for insomnia and other sleeping  
 CC disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome  
 CC and time-zone variation syndrome. ABS68501-ABS68552 represent BMAL2  
 CC coding sequences and PCR primers of the invention  
 XX  
 SQ Sequence 21 BP; 4 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 4996 CCAGCTGAGACGAATGGA 5016  
 |||||  
 21 CCAGCTGAGACGAATGCTGGA 1

RESULT 3304  
 ABK70498  
 ID ABK70498 standard; DNA; 21 BP.

AC ABK70498;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX

DE In-situ analysis synthetic probe #63.

XX Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;  
 KW Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;  
 KW kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;  
 KW Epstein-Barr early RNA; probe; ss.

OS Synthetic.

XX W0200222874-A2.

XX 21-MAR-2002.

XX 06-SEP-2001; 2001WO-US028014.

XX 15-SEP-2000; 2000US-0233177P.  
PR (VENT-) VENTANA MEDICAL SYSTEMS INC.  
XX  
PA Utermohlen JG, Connaughton J;  
PI  
XX WPI; 2002-371972/40.  
DR  
XX Novel oligonucleotide label-domain for incorporation into oligonucleotide  
PT probes useful for detecting or localizing nucleic acid target genes  
PT within a cell or tissue sample.  
XX  
PS Example 4; Page 19; 71pp; English.  
XX  
XX The present invention relates to a new oligonucleotide label-domain  
CC comprising the sequence (CTATT)n and its complement (AAATAG)n, where  
CC n is 1. The probe sets of the invention are useful for detecting kappa or  
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear  
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)  
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic  
CC sequences. The invention is a useful genetic sequence for incorporation  
CC into oligonucleotide probes for detecting gene-specific sequences within  
CC cells or tissue samples in situ hybridization analysis and for  
CC attaching a label to immunoglobulin or other proteins for detecting  
CC haptens and antigens in immunohistochemical analyses. The present nucleic  
CC acid sequence represents one of a collection (ABK70376-ABK70501) of  
CC oligonucleotide probes that were used in the invention for detecting or  
CC localizing a plurality nucleic acid target gene or antigen within a cell  
CC or tissue sample  
XX  
SQ Sequence 21 BP; 2 A; 3 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4463 CTTTCTTTCTTTCTTTCTTTT 4483  
DB 1 CTAATTTCTAATTTCTTTT 21  
RESULT 3305  
ABK87131/c  
ID ABK87131 standard; DNA; 21 BP.  
XX  
AC ABK87131;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human connective tissue growth factor, RT-PCR primer #1.  
XX  
XX Human; endothelial cell-specific molecule 4; EC5M4; neovascularization;  
KM imaging vascular endothelium; proliferative disease; cancer; psoriasis;  
KM diabetic retinopathy; atherosclerosis; endometriosis; endothelial damage;  
KM tumour neovascularization; cardiac disease; endometriosis; hypoxic condition;  
KM angiogenesis; cytoskeletal; RT-PCR; connective tissue growth factor;  
KM reverse transcription-PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200236771-A2.  
PN  
XX 10-MAY-2002.  
PD  
XX 06-NOV-2001; 2001WO-GB004906.  
PF  
XX 06-NOV-2000; 2000US-0245566P.  
PR  
XX 07-MAR-2001; 2001US-0273662P.  
PS  
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
PA  
XX Bicknell R, Humnicki L;  
PI

XX WPI; 2002-508120/54.  
DR  
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.  
XX  
XX Example 1; Page 165; 248pp; English.  
XX  
XX The present invention relates to endothelial cell-specific molecule 4  
CC (EC5M4), and the polynucleotide sequences encoding it. The EC5M4 proteins  
CC are useful for imaging vascular endothelium in the body of an individual,  
CC and for diagnosing and treating a proliferative disease or condition  
CC involving the vascular endothelium (preferably, neovascularization) such as  
CC cancer, psoriasis, diabetic retinopathy, atherosclerosis or endometriosis.  
CC The EC5M4 proteins are also useful in the manufacture of diagnostic or  
CC prognostic agent for such conditions. The proteins are also useful for  
CC detecting endothelial damage or activation, detecting a tumour or tumour  
CC neovascularization, cardiac disease, or endometriosis by detecting the amount  
CC of EC5M4 present in a sample. The polynucleotide sequences encoding EC5M4  
CC are useful in gene therapy for treating a hypoxic condition such as  
CC cancer, cardiac disease, endometriosis or atherosclerosis and in the  
CC manufacture of medicaments for treating the above disease. The sequences  
CC are useful for modulating angiogenesis in an individual. The present  
CC sequence represents a RT-PCR primer for RNA encoding human connective  
CC tissue growth factor  
XX  
SQ Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 6568 TTTTGACCTCGAATCATGTG 6588  
DB 21 TTTTCACTCGAAGCATTTG 1  
RESULT 3306  
AAD22642  
ID AAD22642 standard; DNA; 21 BP.  
XX  
AC AAD22642;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Antisense PCR primer #3, used as diagnostic marker for MAGE subtypes 1-6.  
XX  
XX PCR primer; melanoma antigen gene; MAGE; GAGE; cancer; RT-PCR;  
KM reverse transcription polymerase chain reaction; ss.  
XX  
XX Unidentified.  
OS  
XX WO200181575-A1.  
PN  
XX 01-NOV-2001.  
PD  
XX 24-APR-2001; 2001WO-KR000681.  
PF  
XX 25-APR-2000; 2000KR-00021837.  
PR  
XX (ICGI-) IC & G CO LTD.  
PA  
XX Park J, Jeon C;  
PI  
XX WPI; 2002-026166/03.  
DR  
XX Novel common primer useful for diagnosing cancer, is made from highly  
PT homologous areas of twelve melanoma antigen gene subtypes and eight GAGE  
PT subtypes.  
XX  
XX Claim 1; Page 4; 38pp; English.  
PS  
XX

CC The present invention relates to primers useful for diagnosis of one or  
CC more kinds of cancer and a diagnostic kit comprising the primers of the  
CC invention. The primers are derived from highly homologous areas of twelve  
CC melanoma antigen gene (MAGE) subtypes or eight GAGE subtypes. The primers  
CC of the invention are useful for diagnosing cancer by performing  
CC polymerase chain reaction (PCR), reverse transcription (RT)-PCR, and  
CC nested PCR. The kit of the invention is used to detect six MAGE subtypes  
CC and eight GAGE subtypes. The present DNA sequence is an antisense PCR  
CC primer which is used as a diagnostic marker for MAGE subtypes 1-6  
XX  
SQ Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 5803 CCTGCTGTCTGCTATGTGA 5823  
DB 1 CCAGCATTTCTGCTTGTGA 21  
RESULT 3307  
AAD33020/c  
ID AAD33020 standard; DNA; 21 BP.  
XX  
AC AAD33020;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE HCV-S1 overlapping cDNA region amplifying antisense PCR primer. H15.  
XX  
DE Nucleic acid construct; expression cassette; non-coding region; NCR;  
KM untranslated region; UTR; anti-viral drug; drug resistance; primer; PCR;  
KM HCV-S1; Hepatitis C virus; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200208447-A2.  
PD 31-JAN-2002.  
XX  
PF 20-JUL-2001; 2001WO-IL000669.  
XX  
PR 24-JUL-2000; 2000US-0220248P.  
XX  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
PA (EHRLL/) EHRLICH G.  
XX  
PI Tan YH, Lim SP, Lim SG, Hong WJ;  
XX WPI; 2002-280605/32.  
DR  
XX  
PT Novel nucleic acid construct useful for detecting the presence of RNA  
PT virus, comprises an expression cassette and a promoter operably linked to  
PT expression cassette for minus strand RNA transcription of the cassette.  
XX  
PS Example 1; Page 24; 81pp; English.  
XX  
CC The invention relates to nucleic acid construct which comprises an  
CC expression cassette including a first polynucleotide region including a  
CC 5' non-coding region (NCR) sequence of an RNA virus and at least an N-  
CC terminal portion of a coding sequence of RNA virus, a second  
CC polynucleotide region including a 3' untranslated region (UTR) sequence  
CC of the RNA virus and at least a C-terminal portion of a coding sequence  
CC of the virus and a third polynucleotide region encoding a reporter  
CC molecule, flanked by first and second polynucleotide regions; and a  
CC promoter sequence being operatively linked to expression cassette in a  
CC manner so as to enable a transcription of a minus strand RNA molecule  
CC from the expression cassette. Nucleic acid construct of the invention is  
CC useful for detecting the presence of an RNA virus in a cell. It is also  
CC useful for screening anti-viral drugs and determining drug resistance of  
CC an RNA virus. The present sequence is a PCR primer used to amplify the  
CC overlapping cDNA regions of the genome of Hepatitis C virus (HCV) isolate

CC HCV-S1  
XX  
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3094 TGACTCAGTGTAAAGACT 3114  
DB 21 TGTCTCACAGCGCTAAAGCCT 1  
RESULT 3308  
AAL46645/c  
ID AAL46645 standard; DNA; 21 BP.  
XX  
AC AAL46645;  
XX  
DT 05-AUG-2002 (first entry)  
XX  
DE A thaliana AKIN11 coding sequence PCR primer #3.  
XX  
DE AKIN11; pathogen resistance; transgenic; plant; antibacterial; virucide;  
KM fungicide; nematocide; PCR; primer; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200238780-A2.  
PD 16-MAY-2002.  
XX  
XX 07-NOV-2001; 2001WO-FR003457.  
PF 08-NOV-2000; 2000FR-00014354.  
PR  
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
PA (CNRS ) CENT NAT RECH SCI.  
XX  
PI Roby D, Balague C, Godard F, Lumerzhelm M;  
XX WPI; 2002-426954/45.  
DR  
XX  
PT Inducing or increasing resistance to pathogens in plants e.g. industrial  
PT scale flowers and vegetables, by introducing a nucleic acid that encodes  
PT the AKIN11 peptide.  
XX  
PS Example 2; Page 74; 76pp; French.  
XX  
CC The present invention relates to the use of a nucleic acid that causes  
CC the synthesis of the AKIN11 protein, to induce or increase the resistance  
CC to pathogen attack in plants. The nucleic acid and its encoded protein  
CC can be used to impart resistance to bacteria, viruses, fungi and  
CC nematodes, especially necrotrophic pathogens such as Xanthomonas  
CC campestris, in large-scale crops, vegetables and flowers. Probes and  
CC primers that hybridise with the AKIN11 gene can be used to detect  
CC resistance against pathogens, and antisense sequences can be used to  
CC modulate resistance. The present sequence is a PCR primer used to isolate  
CC the AKIN11 coding sequence of the invention  
XX  
SQ Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 26 GTGGAGCTCTGCAAGCTTC 46  
DB 21 GTGGAGCTCTCCCAAGTTC 1  
RESULT 3309  
ABK52977

```
ID ABK52977 standard; DNA; 21 BP.
XX
XX ABK52977;
AC
XX
XX
XX 22-AUG-2002 (first entry)
DT
XX
XX Human interleukin 6 target sequence #2.
DE
XX Human; interleukin 6; microsphere; genosensor; target; ss; microarray;
KW optical signature.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "A is covalently linked to a fluorescein moiety"
XX
XX
XX MO200228530-A2.
XX
XX 11-APR-2002.
XX
XX 09-OCT-2001; 2001WO-US031581.
XX
XX 06-OCT-2000; 2000US-0238866P.
XX
XX (TUFT ) TUFTS COLLEGE.
XX
XX Walt DR;
XX
XX WPI; 2002-463219/49.
XX
XX Detecting target analyte comprises providing a first classifier of a
PT first population of sensors, distributing a second population of sensors
PT and determining the response of the second population of sensors.
XX
XX
XX Example 19; Fig 22; 104pp; English.
XX
XX The invention relates to detecting a target analyte (TA) comprising: (a)
XX providing first classifier (I) for the response of a first population of
XX sensors (II) from a first pool of sensors (III) to a first TA; (b)
XX distributing a second population of sensors (IV) from (III) on an array;
XX and (c) determining response of (IV) to the sample, where response
XX resembles (I) for a first TA, indicating the presence of the first TA in
XX the sample. Also included is making an array comprising: (a) providing a
XX population of microspheres comprising an optical signature; (b)
XX connecting the response of the microspheres to the target analyte; (c)
XX recording the response of the microspheres to the target analyte; (d)
XX generating a classifier for the response of the microspheres to the
XX target analyte; and (e) distributing the microspheres on a substrate with
XX a surface comprising discrete sites. The new method detects a target
XX analyte in a sample by contacting the sample with a sensor array. The
XX method allows the synthesis of the bioactive agents i.e., nucleic acids
XX and antibodies, to be separated from their placement on an array. The
XX bioactive agents may be synthesised on the beads which are then randomly
XX distributed on a patterned surface. The beads are self-encoded with dyes
XX allowing a correlation of the location of an individual site on the
XX array. The self-encoding feature eliminates the need for a more complex,
XX multi-step encoding system. The identities of the individual sensors in
XX the array are self-encoded by exposing the array to a reference analyte
XX while illuminating the array with excitation light energy. The light
XX sensor array may carry thousands of discrete sensing elements whose
XX combined signal provides for substantial improvements in sensor detection
XX limits, response times and signal-to-noise ratios. The present sequence
XX is a target sequence which is detected by a probe attached to a
XX microsphere genosensor and used to illustrate the method of the invention
XX
XX Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred.No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3653 AAGAAATACCGAGACCCGAC 3673
DB |||||
1 AATTACCGACCCCTGACCCGAC 21
RESULT 3310
ABK52958
ID ABK52958 standard; DNA; 21 BP.
XX
XX ABK52958;
AC
XX
XX 22-AUG-2002 (first entry)
DT
XX
XX Human interleukin 6 target sequence, IL6-CF.
DE
XX Human; interleukin 6; IL6-CF; microsphere; genosensor; target; ss;
KW microarray; optical signature.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "A is covalently linked to a fluorescein moiety"
XX
XX
XX MO200228530-A2.
XX
XX 11-APR-2002.
XX
XX 09-OCT-2001; 2001WO-US031581.
XX
XX 06-OCT-2000; 2000US-0238866P.
XX
XX (TUFT ) TUFTS COLLEGE.
XX
XX Walt DR;
XX
XX WPI; 2002-463219/49.
XX
XX Detecting target analyte comprises providing a first classifier of a
PT first population of sensors, distributing a second population of sensors
PT and determining the response of the second population of sensors.
XX
XX
XX Disclosure, Page 38; 104pp; English.
XX
XX The invention relates to detecting a target analyte (TA) comprising: (a)
XX providing first classifier (I) for the response of a first population of
XX sensors (II) from a first pool of sensors (III) to a first TA; (b)
XX distributing a second population of sensors (IV) from (III) on an array;
XX and (c) determining response of (IV) to the sample, where response
XX resembles (I) for a first TA, indicating the presence of the first TA in
XX the sample. Also included is making an array comprising: (a) providing a
XX population of microspheres comprising an optical signature; (b)
XX connecting the response of the microspheres with a sample of the target analyte; (c)
XX recording the response of the microspheres to the target analyte; (d)
XX generating a classifier for the response of the microspheres to the
XX target analyte; and (e) distributing the microspheres on a substrate with
XX a surface comprising discrete sites. The new method detects a target
XX analyte in a sample by contacting the sample with a sensor array. The
XX method allows the synthesis of the bioactive agents i.e., nucleic acids
XX and antibodies, to be separated from their placement on an array. The
XX bioactive agents may be synthesised on the beads which are then randomly
XX distributed on a patterned surface. The beads are self-encoded with dyes
XX allowing a correlation of the location of an individual site on the
XX array. The self-encoding feature eliminates the need for a more complex,
XX multi-step encoding system. The identities of the individual sensors in
XX the array are self-encoded by exposing the array to a reference analyte
XX while illuminating the array with excitation light energy. The light
XX sensor array may carry thousands of discrete sensing elements whose
XX combined signal provides for substantial improvements in sensor detection
XX limits, response times and signal-to-noise ratios. The present sequence
```

```
CC is a target sequence which is detected by a probe attached to a
CC microsphere genosensor and used to illustrate the method of the invention
XX
SQ Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3653 AAGAAATATCCCGAGACCCCAAC 3673
DB 1 AATAACGACCCCTGACCCCAAC 21
RESULT 3311
ABK52964/c
ID ABK52964 standard; DNA; 21 BP.
XX
AC ABK52964;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human interleukin 6, IL6, probe sequence #2.
XX
KW Human; interleukin 6; IL6; microsphere; genosensor; probe; ss;
KW microarray; optical signature.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "G is covalently linked to an NH2-(CH2)8 moiety"
XX
PN WO200228530-A2.
XX
PD 11-APR-2002.
XX
PF 09-OCT-2001; 2001WO-US031581.
XX
PR 06-OCT-2000; 2000US-0238866P.
XX
PA (TUFT ) TUFTS COLLEGE.
XX
PI Walt DR;
XX
DR WPI; 2002-463219/49.
XX
PT Detecting target analyte comprises providing a first classifier of a
PT first population of sensors, distributing a second population of sensors
PT and determining the response of the second population of sensors.
XX
PS Example 19; Fig 22; 104pp; English.
XX
CC The invention relates to detecting a target analyte (TA) comprising: (a)
CC providing first classifier (I) for the response of a first population of
CC sensors (II) from a first pool of sensors (III) to a first TA; (b)
CC distributing a second population of sensors (IV) from (III) on an array;
CC and (c) determining response of (IV) to the sample, where response
CC resembles (I) for a first TA, indicating the presence of the first TA in
CC the sample. Also included is making an array comprising: (a) providing a
CC population of microspheres comprising an optical signature; (b)
CC contacting the microspheres with a sample of the target analyte; (c)
CC recording the response of the microspheres to the target analyte; (d)
CC generating a classifier for the response of the microspheres to the
CC target analyte; and (e) distributing the microspheres on a substrate with
CC a surface comprising discrete sites. The new method detects a target
CC analyte in a sample by contacting the sample with a sensor array. The
CC method allows the synthesis of the bioactive agents i.e., nucleic acids
CC and antibodies, to be separated from their placement on an array. The
CC bioactive agents may be synthesised on the beads which are then randomly
CC distributed on a patterned surface. The beads are self-encoded with dyes
```

```
CC allowing a correlation of the location of an individual site on the
CC array. The self-encoding feature eliminates the need for a more complex,
CC multi-step encoding system. The identities of the individual sensors in
CC the array are self-encoded by exposing the array to a reference analyte
CC while illuminating the array with excitation light energy. The light
CC sensor array may carry thousands of discrete sensing elements whose
CC combined signal provides for substantial improvements in sensor detection
CC limits, response times and signal-to-noise ratios. The present sequence
CC is a probe which is attached to a microsphere genosensor and used to
CC illustrate the method of the invention
XX
SQ Sequence 21 BP; 2 A; 1 C; 10 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3653 AAGAAATATCCCGAGACCCCAAC 3673
DB 21 AATAACGACCCCTGACCCCAAC 1
RESULT 3312
ABS97563
ID ABS97563 standard; DNA; 21 BP.
XX
AC ABS97563;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human epoxide hydrolase 2 polymorphic sequence #54.
XX
KW Human; de; cytochrome P450 A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; URA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCT LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 10; Page 119; 714pp; English.
XX
```

CC This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02B1 (CYP45002B1), adrennergic receptor beta1 (ADRB1), aryl hydrocarbon receptor (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), uridine kinase receptor (UPK), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. CC The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

XX Sequence 21 BP; 8 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2858 CAGGCAAGCAAGGAGGCG 2878  
DB 1 CAGGCAAGCAATGAGTGAG 21

RESULT 3313  
ABS98273 standard; DNA; 21 BP.

XX ABS98273;  
AC  
XX 23-DEC-2002 (first entry)  
DT  
XX  
DE Human lactoferrin (LTF) gene polymorphic sequence #36.

XX Human; db; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF;  
KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MR3; NR1I2;  
KM aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS;  
KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
KM NADPH quinone oxidoreductase 2; NQO2; sulfoxtransferase thermolabile; STM;  
KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPK;  
KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KM altered drug metabolism; cardiovascular function; colorectal tumour;  
KM central nervous system; pulmonary; immunological; SNP;  
KM single nucleotide polymorphism.

OS Homo sapiens.  
XX MO000257410-A2.  
XX 25-JUL-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044838.  
XX  
XX 28-NOV-2000; 2000US-00724389.  
XX  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
XX  
XX WPI; 2002-698522/75.  
XX  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes e.g., cytochrome p450 and catepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

PS Example 23; Page 148; 714pp; English.

XX  
XX  
XX This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02B1 (CYP45002B1), adrennergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxtransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), uridine kinase receptor (UPK), multidrug resistance 1 transferase (UGT2B15), uridine kinase receptor (UPK), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. CC The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

XX Sequence 21 BP; 2 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 337 TACTTGGAGTGAGATCCCT 357  
||||||| ||||| |||







Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

4573 CCTGCCCCCTTTCTTCTGACT 4593  
21 CTTGCCCCCTTTCTTCTGACT 1

RESULT 3317  
ABS97961/c  
ID ABS97961 standard; DNA; 21 BP.  
AC ABS97961;  
XX 23-DEC-2002 (first entry)  
XX Human UDP-glucuronosyl transferase 2B15 polymorphic sequence #5.  
XX  
XX Human; de; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP4502E1; LTP;  
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
KW aryl hydrocarbon receptor nuclear translocator; AHRNT; cathepsin S; CTSS;  
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
KW glutathione-S-transferase 12; GSTT2; histamine-N-methyl transferase;  
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;  
KW UGT2B7; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPA;  
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
KW altered drug metabolism; cardiovascular function; colorectal tumour;  
KW central nervous system; pulmonary; immunological; SNP;  
KW single nucleotide polymorphism.  
XX  
XX Homo sapiens.  
XX  
XX WO200257410-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044838.  
XX  
XX 28-NOV-2000; 2000US-00724389.  
XX  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
XX  
XX WPI; 2002-698522/75.  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes  
XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
XX for locating, identifying and characterizing the genes responsible for  
XX disorder-related traits.  
XX  
XX Example 20; Page 137; 714P; English.

This invention relates to the sequence of an isolated nucleic acid  
molecule comprising at least one base variation from that of a known  
human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),  
aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
(AHRNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating  
protein (FLAP), glutathione-S-transferase 12 (GSTT2), histamine-N-methyl  
transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl  
transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
(UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1.

(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
(MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
The polymorphisms in the human genes cited in the invention are useful as  
genetic linkage markers for locating and characterizing the genes that  
are responsible for specific traits within the genome and eventually  
identifying the genes responsible for a variety of disorder-related  
traits as a result of their e.g., overexpression, constitutive  
expression, mutation or underexpression, which may be used in diagnosing  
and/or treating the disorders. The nucleic acid molecules comprising the  
polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
AHRNT, EPHX2, GSTT2, NNMT, NQO2, NR112, STM, UGT2B7, UGT2B15, AHR,  
MDR1 and/or MDR3 are useful for screening individuals for altered drug  
metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
used to screen for altered cardiovascular function, in COX2 for altered  
susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
nervous system function, in FLAP and HNMT for altered pulmonary,  
immunological or haematological function, in KLK2 for altered serine  
protease activity in the prostate, in LTF for altered immunological or  
haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
peripheral nervous system function. The present sequence represents a  
polymorphic DNA sequence of the invention

Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

749 TCTTCTACCGCCTGAGGCT 769  
21 TCTTCTACCGCCTGAGGCT 1

RESULT 3318  
ABK94085/c  
ID ABK94085 standard; DNA; 21 BP.  
XX  
XX ABK94085;  
XX  
XX 27-AUG-2002 (first entry)  
XX  
XX Endothelin-1 (EDN-1) SNP detection PCR primer #29.  
XX  
XX Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;  
KW EDNR; signaling system; cardiovascular disease; coronary heart disease;  
KW hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;  
KW diabetes; familial hypercholesterolaemia; forensic marker;  
KW transgenic animal; solid support; cardiovascular regulator; SNP;  
KW single nucleotide polymorphism; PCR; primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO200224747-A2.  
XX  
XX 28-MAR-2002.  
XX  
XX 31-AUG-2001; 2001WO-EP010087.  
XX  
XX 19-SEP-2000; 2000EP-00120123.  
XX  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX  
XX Brinkmann U, Hoffmeyer S;  
XX  
XX WPI; 2002-435060/46.  
XX  
XX Novel polymorphisms of the endothelin/endothelin converting  
XX enzyme/receptor of endothelin and endothelin converting enzyme signaling  
XX system associated with cardiovascular disease, useful for treating the  
XX disease.

XX Claim 1, Page 55, 190pp; English.

PS The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolaemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

XX

SQ Sequence 21 BP; 12 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3722 TCCTCATTCATTGAGCTTTT 3742

DB 21 TCCTGATTAGTAGTCTTTT 1

RESULT 3319

ABK94086

ID ABK94086 standard; DNA; 21 BP.

XX

AC ABK94086;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #30.

XX

KM Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM hyperextension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolaemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Brinkmann U, Hoffmeyer S;

XX

DR WPI; 2002-435060/46.

XX

PT Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

PS Claim 1, Page 55, 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolaemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

XX

SQ Sequence 21 BP; 3 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3722 TCCTCATTCATTGAGCTTTT 3742

DB 1 TCCTGATTAGTAGTCTTTT 21

RESULT 3320

ABK94081/c

ID ABK94081 standard; DNA; 21 BP.

XX

AC ABK94081;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #25.

XX

KM Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;

KM hyperextension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolaemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Brinkmann U, Hoffmeyer S;

XX

DR WPI; 2002-435060/46.

XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

XX Example 6; Page 55; 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC polynucleotide variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

CC

XX Sequence 21 BP; 12 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

SO

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3722 TCCTCATTCATTGAGCTTTT 3742

Db 21 TCCGATTATGATCTTTT 1

RESULT 3321

ABK94242

ID ABK94242 standard; DNA; 21 BP.

XX

AC ABK94242;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin converting enzyme 1 (ECE-1) SNP detection primer #30.

XX

KM Endothelin; EDN, endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX Brinkmann U, Hoffmeyer S;

PI

XX WPI; 2002-435060/46.

DR

XX Novel polynucleotide of the endothelin/endothelin converting

PT enzyme/receptors of endothelin and endothelin converting enzyme signaling

PT system associated with cardiovascular disease, useful for treating the

PT disease.

XX Claim 1; Page 62; 190pp; English.

XX The invention describes a polynucleotide (I) of the endothelin

CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)

CC signaling system which is associated with a cardiovascular disease. (I),

CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)

CC or (II) is useful for producing cells capable of expressing a molecular

CC variant polypeptide which is associated with a cardiovascular disease.

CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a

CC molecular variant gene comprising (I) is useful for identifying and

CC obtaining a pro-drug or drug capable of modulating the activity of a

CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system

CC or its gene product, or for identifying and obtaining an inhibitor of the

CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE

CC signaling system or its gene product. The isolated proteins and

CC polynucleotides encoding them are useful for preparation of a

CC pharmaceutical composition for treating a cardiovascular disease such as

CC coronary heart disease, hypertension, atherosclerosis, or related to

CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial

CC hypercholesterolemia. The gene or a polynucleotide fragment of the

CC EDN/ECE/EDNR signaling system are useful as forensic markers, for

CC creating a transgenic animal and in creation of a solid support

CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or

CC host cells of the invention. This sequence represents a PCR primer used

CC to identify single nucleotide polymorphisms in DNA encoding

CC cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway

CC

XX Sequence 21 BP; 5 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

SO

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5355 GTTTGAGCTGGGGCTTGA 5375

Db 1 GATTTCATCTGTCCTTGA 21

RESULT 3322

ABK94082

ID ABK94082 standard; DNA; 21 BP.

XX

AC ABK94082;

XX

DT 27-AUG-2002 (first entry)

XX

DE Endothelin-1 (EDN-1) SNP detection PCR primer #26.

XX

KM Endothelin; EDN, endothelin converting enzyme; ECE; endothelin receptor;

KM EDNR; signaling system; cardiovascular disease; coronary heart disease;

KM hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;

KM diabetes; familial hypercholesterolemia; forensic marker;

KM transgenic animal; solid support; cardiovascular regulator; SNP;

KM single nucleotide polymorphism; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

```

PR 19-SEP-2000; 2000EP-00120123.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Brinkmann U, Hoffmeyer S;
XX
XX WPI; 2002-435060/46.
XX
PT Novel polynucleotide of the endothelin/endothelin converting
PT enzyme/receptors of endothelin and endothelin converting enzyme signalling
PT system associated with cardiovascular disease, useful for treating the
PT disease.
XX
XX
XX Example 6; Page 55; 190pp; English.
XX
XX The invention describes a polynucleotide (I) of the endothelin
XX (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
XX signalling system which is associated with a cardiovascular disease. (I),
XX the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
XX or (II) is useful for producing cells capable of expressing a molecular
XX variant polypeptide which is associated with a cardiovascular disease.
XX (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a
XX molecular variant gene comprising (I) is useful for identifying and
XX obtaining a pro-drug or drug capable of modulating the activity of a
XX molecular variant of a polypeptide of the EDN/EDNR/ECE signalling system
XX or its gene product, or for identifying and obtaining an inhibitor of the
XX activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
XX signalling system or its gene product. The isolated proteins and
XX polynucleotides encoding them are useful for preparation of a
XX pharmaceutical composition for treating a cardiovascular disease such as
XX coronary heart disease, hypertension, atherosclerosis, or related to
XX abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
XX hypercholesterolaemia. The gene or a polynucleotide fragment of the
XX EDN/ECE/EDNR signalling system are useful as forensic markers, for
XX creating a transgenic animal and in creation of a solid support
XX comprising polynucleotides, genes, vectors, polypeptides, antibodies or
XX host cells of the invention. This sequence represents a PCR primer used
XX to identify single nucleotide polymorphisms in DNA encoding
XX cardiovascular regulator proteins of the EDN/ECE/EDNR signalling pathway
XX
SQ Sequence 21 BP; 4 A; 3 C; 2 G; 12 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3722 TCCTCATTGATGAGCTTTT 3742
Db 1 TCCTGATTATGATCTTTT 21
RESULT 3323
ABN86025
ID ABN86025 standard; DNA; 21 BP.
XX
XX ABN86025;
XX
XX 06-SEP-2002 (first entry)
XX
XX Mutagenic primer D399S.
XX
XX Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
XX antiviral; vaccine; tumour; PCR primer; ss.
XX
XX Synthetic.
XX
XX US2002062010-A1.
XX
XX 23-MAY-2002.
XX
XX 23-MAY-2001; 2001US-00863693.
XX
XX 02-MAY-1997; 97US-0046816P.
XX

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PR 30-APR-1998; 98US-00070166.
XX
XX (GETH ) GENENTECH INC.
XX
XX Arachoon WR, Carter PU, Merchant AM, Presta LG;
XX
XX WPI; 2002-499676/53.
XX
XX
XX New multispecific antibodies having heteromultimeric and common
XX components are useful to direct treatment to a target site such as a
XX tumor cell, cell surface receptor or clot, as a vaccine adjuvant and to
XX treat infectious disease.
XX
XX
XX Example 2; Page 23; 36pp; English.
XX
XX The invention relates to a new multispecific antibody, comprising at
XX least two polypeptides (Pp1 and Pp2) which meet at a multiface, where Pp1
XX has a multimerisation domain forming an interface positioned to interact
XX with an interface of a multimerisation domain of Pp2, and both
XX polypeptides each comprise a binding domain consisting a heavy chain and
XX a variable light chain, where the light chain has a sequence common to
XX both polypeptides. Heteromultimers of the inventions include bispecific
XX antibodies, bispecific immunoadhesins and antibody-immunoadhesin
XX chimeras. The activity of antibodies of the invention may be described
XX as, cytostatic, antibacterial and antiviral. The heteromultimer can be
XX used for redirected cytotoxicity, for example to kill tumour cells, as a
XX vaccine adjuvant, for delivering thrombolytic agents to clots, for
XX converting enzyme activated prodrugs at a target site such as a tumour,
XX for treating infectious diseases, for targeting immune complexes to cell
XX surface receptors or for delivering immunotoxins to tumour cells. The
XX current sequence represents the mutagenic primer D399S for introducing a
XX mutation into the CH3 domain of a humanised anti-CD3 heavy chain or CD4-
XX IgG by site directed mutagenesis
XX
SQ Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 185 GCCGCTGACCTCCGACGGG 205
Db 1 GCCGTCGAGACTGACGACGG 21
RESULT 3324
AAL49183/C
ID AAL49183 standard; DNA; 21 BP.
XX
XX AAL49183;
XX
XX 30-OCT-2002 (first entry)
XX
XX Porcine CD 151 coding sequence PCR primer #7.
XX
XX CD 151; porcine reproductive and respiratory syndrome virus; PRRSV; pig;
XX selective breeding; xenotransplant; anti-RNA entry protein; anti-REP;
XX anti-viral; vaccine; PCR; primer; ss.
XX
XX Sus scrofa.
XX
XX WO200260924-A2.
XX
XX 08-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-US002868.
XX
XX 29-JAN-2001; 2001US-00772044.
XX
XX 28-JAN-2002; 2002US-00772044.
XX
XX (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
XX Kapil S, Shanmukhapra K;
XX

```

XX DR WPI: 2002-619225/66.  
XX  
PT Determining susceptibility and resistance to porcine reproductive and  
PT respiratory syndrome virus (PRRSV), useful for improving swine breeding,  
PT by assaying for CD 151 in a sample of cellular material of known origin  
PT from the animal.  
XX  
PS Example 17; Page 35; 77pp + Sequence Listing; English.  
XX  
CC The present invention relates to a method of determining the  
CC susceptibility or resistance of an animal to porcine reproductive and  
CC respiratory syndrome virus (PRRSV). This involves assaying for CD 151 in  
CC a sample of cellular material of known origin from the animal. In  
CC addition, coding sequences of CD 151 are described, and anti-viral  
CC compounds designated anti-RNA entry proteins (anti-RSPs). The method is  
CC useful for determining susceptibility and resistance to PRRSV in an  
CC animal. This is particularly useful for improving swine breeding or for  
CC screening different pig breeding lines. The method is also useful for  
CC developing non-simian recombinant cell lines for propagating the virus,  
CC for producing anti-viral compounds or vaccines for inducing immunity  
CC against PRRSV, and for diagnosing PRRSV infection in a swine. The present  
CC sequence is a PCR primer used to isolate the porcine CD 151 coding  
CC sequence. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 21 BP; 1 A; 8 C; 3 G; 9 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 7406 GCAACATCAGCAGCAGCAGCA 7426  
DB 21 GAAAGATGAGCAGCAGCAGCA 1  
RESULT 3325  
ABZ95973/C  
ID ABZ95973 standard; DNA; 21 BP.  
XX  
AC ABZ95973;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human fibronectin antisense fragment no.1833.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquitinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PP 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
PI Miller S, Tang L, Shahabuddin S,  
XX  
DR WPI: 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 11215; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 14 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3384 CTTCCCCCAGCTGCACCCCC 3404  
DB 21 CCGCCCAACAGCGCACCCCC 1  
RESULT 3326  
ABX94380  
ID ABX94380 standard; DNA; 21 BP.  
XX  
AC ABX94380;  
XX  
DT 18-JUN-2003 (first entry)  
XX  
DE Human endothelial cell differentiation gene-4, Edg-4 PCR primer #1.  
XX  
KW Human; ss; PCR; primer; Edg-4; prostatic disease; Edg-7 receptor;  
KW benign prostatic hyperplasia; intracellular signal transduction;  
KW endothelial cell differentiation gene; prostate cancer; LPA;  
KW lysophosphatidic acid.  
XX  
OS Homo sapiens.  
XX  
PN WO2003013605-A1.  
XX  
PD 20-FEB-2003.  
XX  
PP 06-AUG-2002; 2002WO-JP008016.  
XX  
PR 07-AUG-2001; 2001JP-00239306.  
XX  
PR 31-JUL-2002; 2002JP-00224215.  
XX  
PA (NISB ) JAPAN TOBACCO INC.  
XX  
PI Furuno M, Naito T, Yamamoto Y, Noki J, Arai H, Kakehi Y;  
XX  
DR WPI: 2003-248240/24.  
XX  
PT Composition for preventing or treating prostatic diseases e.g. benign  
PT prostatic hyperplasia and prostate cancer containing inhibitors of  
PT interaction between lysophosphatidic acid (LPA) and its receptor to

```

PF prevent cell proliferation.
XX
PS Example 2; Page 53; 59pp; Japanese.
XX
CC The invention relates to drug compositions for preventing, treating and/
CC or inhibiting progression of prostatic diseases, e.g. benign prostatic
CC hyperplasia or their accompanying diseases, comprises substances with an
CC activity of inhibiting intracellular signal transduction induced by a
CC stimulus mediated by Edg-7 (endothelial cell differentiation gene-7)
CC receptor (interacting with LPA, lysophosphatidic acid), and
CC pharmaceutically-acceptable carriers. The remedies are for prostatic
CC diseases e.g. benign prostatic hyperplasia and prostate cancer. The
CC present sequence is a PCR primer for human Edg-4 used in the
CC exemplification of the invention
CC
SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 818 AGCTGTGCGCCCTGCATGT 838
   ||||| ||||| |||||
Db 1 AGGCTGTGAGTCTCTGCATGT 21

RESULT 3327
ABX90522/C
ID ABX90522 standard; DNA; 21 BP.
XX
XX ABX90522;
XX
XX 01-MAY-2003 (first entry)
XX
XX Human PLGF A antisense target region.
XX
XX Antisense; ss; human; VEGF; vascular endothelial growth factor; cancer;
XX angiogenesis; neoplastic proliferation; cellular proliferation.
XX
XX Homo sapiens.
XX
XX US2002165174-A1.
XX
XX 07-NOV-2002.
XX
XX 13-MAR-2001; 2001US-00805761.
XX
XX 31-JAN-1997; 97US-0037004P.
XX 30-JAN-1998; 98US-00016541.
XX 19-JAN-2000; 2000US-00487023.
XX 19-JAN-2001; 2001WO-US000019.
XX
XX (GILL/) GILL P S.
XX (MASC/) MASOOD R.
XX
XX Gill PS, Masood R;
XX
XX WPI; 2003-255224/25.
XX
XX New composition comprising an antisense oligonucleotide directed against
XX PT vascular endothelial growth factor, useful for preparing a composition
XX PT for treating cancer.
XX
XX PS Example 13; Fig 17B; 54pp; English.
XX
XX The invention relates to a composition comprising an antisense
XX CC oligonucleotide directed against vascular endothelial growth factor
XX CC (VEGF). The antisense oligonucleotide is useful for preparing a
XX CC composition treating cancer, neoplastic proliferation, abnormal cellular
XX CC proliferation and preventing angiogenesis. The present sequence is a VEGF
XX CC cDNA target region for the antisense oligonucleotides of the invention
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

```

Query Match	0.2%;	Score 14.6;	DB 1;	Length 21;
Best Local Similarity	81.0%;	Pred. No. 2.3e+03;		
Matches 17;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Oy	5175	TTGGCTCTGCATGTTCTCCAC	5195	
Db	21	TGGGCTGAACTGTGCTCCAC	1	
RESULT 3328				
ACC49738/c				
ID	ACC49738	standard; DNA; 21 BP.		
XX	ACC49738;			
XX				
XX	03-JUL-2003	(first entry)		
XX				
DE	Mouse CRH-R1 PCR primer P163	SEQ ID NO:30.		
XX				
XX	Mouse; corticotropin releasing hormone receptor type 1; CRH-R1;			
XX	antiproliferic; anti-allergic; immunosuppressive; anti-inflammatory;			
KW	dermatological; pathological state; neuroendocrine disorder;			
KW	hyperproliferative epidermal disorder; allergic contact dermatitis;			
KW	autoimmune disorder; epidermal carcinogenesis; malignant transformation;			
KW	epidermal melanocyte; dermal melanocyte; chromosome 11; PCR primer; ss.			
XX				
XX	Mus musculus.			
OS	Synthetic.			
OS				
PN	WO2003024590-A2.			
XX				
PD	27-MAR-2003.			
XX				
PF	13-SEP-2002; 2002WO-US029117.			
XX				
XX	14-SEP-2001; 2001US-0322195P.			
XX				
PA	(UYTE-) UNIV TENNESSEE RES CORP.			
XX				
PI	Pisarchik A, Slominski A;			
XX				
DR	WPI, 2003-313342/30.			
XX				
PT	Novel DNA encoding corticotropin releasing hormone receptor type 1 which			
PT	is useful for treating pathophysiological state such as inflammatory skin			
PT	disease e.g. psoriasis and allergic contact dermatitis.			
XX				
XX	Example 3; Page 26; 110pp; English.			
XX				
XX	The present invention describes DNA (I) encoding a corticotropin			
CC	releasing hormone receptor type 1 (CRH-R1) protein comprising an amino			
CC	acid sequence given in ABR43055 to ABR43071. Also describe: (1) a vector			
CC	(II) capable of expressing (I) or its degenerate variant, and comprising			
CC	(1) or its degenerate variant, and regulatory elements necessary for			
CC	expression of the DNA in a cell; (2) a host cell (III) transfected with			
CC	(II); (3) an isolated CRH-R1 protein (IV) encoded by (I); (4) an antibody			
CC	(V) directed against (IV); (5) a pharmaceutical composition (VI)			
CC	comprising (IV), and a carrier; and (6) protecting (M) skin cells against			
CC	damage induced by an environmental factor, by inducing the expression of			
CC	CRH-R type 1g in the skin cells, where the expression of the receptor			
CC	protects the skin cells against the damage. CRH-R1 has antiproliferic,			
CC	anti-allergic, immunosuppressive, anti-inflammatory and dermatological			
CC	activities. (VI) can be used for treating a pathophysiological state such			
CC	as hyperproliferative epidermal disorder, neuroendocrine disorder,			
CC	allergic contact dermatitis, autoimmune disorder, epidermal			
CC	carcinogenesis, malignant transformation of epidermal or dermal			
CC	melanocytes. (M) is useful for protecting (M) skin cells against damage			
CC	induced by an environmental factor such as solar radiation. Human CRH-R1			
CC	is located on chromosome 17, and mouse CRH-R1 is located to chromosome			
CC	11. The present sequence represents a PCR primer for mouse CRH-R1, which			
XX	is used in an example from the present invention			
XX				



SQ Sequence 21 BP; 4 A; 6 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 823 GTGGCCCTGCGCATGTGAG 843  
 Db 21 GTCCGCTGTGCGCATGCGGAG 1  
 RESULT 3329  
 ABR34056  
 ID ABR34056 standard; DNA; 21 BP.  
 AC ABR34056;  
 XX 29-MAY-2003 (first entry)  
 DT  
 XX Human pigmentation trait-related PCR primer - SEQ ID No 155.  
 DE  
 XX Human; single nucleotide polymorphism; SNP; ss; melanocortin-1 receptor;  
 KM genetic pigmentation trait; MC1R; agouti signaling protein; ASIP; race;  
 KM hair colour; eye colour; forensic tool; PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200297047-A2.  
 XX  
 PD 05-DEC-2002.  
 PF 28-MAY-2002; 2002WO-US016789.  
 XX  
 PR 25-MAY-2001; 2001US-0293560P.  
 PR 21-JUN-2001; 2001US-0300187P.  
 PR 07-AUG-2001; 2001US-0310781P.  
 PR 17-SEP-2001; 2001US-0323662P.  
 PR 26-OCT-2001; 2001US-0344418P.  
 PR 15-NOV-2001; 2001US-0334674P.  
 PR 02-JAN-2002; 2002US-0346303P.  
 XX  
 PA (DNAP-) DNAPRINT GENOMICS INC.  
 XX  
 PI Frudakis T;  
 DR WPI; 2003-239091/23.  
 XX  
 PT Inferring genetic pigmentation trait such as hair/eye color or shade from  
 PT nucleic acid sample of human subject, by identifying a pigmentation-  
 PT related haplotype allele of a pigmentation gene in the sample.  
 PS  
 XX Example 17; Page 246; 396pp; English.  
 CC The invention comprises a method for inferring a genetic pigmentation  
 CC trait of a human. The method involves identifying a single nucleotide  
 CC polymorphism (SNP) in a pigmentation gene - where the pigmentation gene  
 CC is not melanocortin-1 receptor (MC1R) and agouti signaling protein  
 CC (ASIP). The method of the invention is useful for inferring the race of a  
 CC human subject. The method is useful for inferring a genetic pigmentation  
 CC trait such as hair shade or colour, or eye shade or colour of a human  
 CC subject. The method may be used as a forensic tool for obtaining  
 CC information relating to physical characteristics of a potential crime  
 CC victim or a perpetrator of a crime from a nucleic acid sample present at  
 CC a crime scene. The present PCR primer is used in the exemplification of  
 CC the invention  
 XX  
 SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1851 GGTGAAGACGTGTGTAAGAC 1871  
 Db 1 GATGAAGACGTGTGTAAGAC 21  
 RESULT 3330  
 ABR10723/c  
 ID ABR10723 standard; DNA; 21 BP.  
 AC ABR10723;  
 XX 15-APR-2003 (first entry)  
 DT  
 XX Human glycoprotein hormone Zluth1 PCR primer #11.  
 DE  
 XX Human; ss; PCR; Zluth1; glycoprotein hormone; hyperthyroidism;  
 KM antithyroid; chromosome 14q23.3; primer.  
 KM  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2002160953-A1.  
 XX  
 PD 31-OCT-2002.  
 PF 30-AUG-2001; 2001US-00943388.  
 XX  
 PR 25-APR-2000; 2000US-0199498P.  
 PR 20-APR-2001; 2001US-00839706.  
 XX  
 PA (HOLL/) HOLLOWAY J L.  
 PA (WEBSTER) WEBSTER P J.  
 PA (THAYER) THAYER E C.  
 XX  
 PI Holloway JL, Webster PJ, Thayer EC;  
 DR WPI; 2003-209228/20.  
 XX  
 PT New Zluth1 polypeptides and polynucleotides, useful for manufacturing a  
 PT medicament for treating hyperthyroidism.  
 PS  
 XX Example 8; Page 48; 51pp; English.  
 CC The invention relates to an isolated glycoprotein hormone Zluth1 sequence,  
 CC the mature protein or antigenic peptides derived from Zluth1. Also  
 CC included are an isolated polynucleotide encoding Zluth1, an isolated  
 CC antibody that specifically binds to Zluth1, treating hyperthyroidism in  
 CC female mammals by administering Zluth1 and a pharmaceutical composition  
 CC comprising Zluth1. Zluth1 is useful for manufacturing a medicament for  
 CC treating hyperthyroidism. Anti-Zluth1 antibodies can be used to detect  
 CC Zluth1 in tissue sections from a biopsy specimen or to screen biological  
 CC samples in vitro for the presence of Zluth1. Zluth1 is useful for treating  
 CC women with hyperthyroidism. The nucleic acid molecules are useful for  
 CC detecting the expression of a Zluth1 gene in a biological sample. The  
 CC present sequence is a PCR primer used to detect expression of Zluth1 in  
 CC pituitary cells, amplifying part of the 3' untranslated region  
 XX  
 SQ Sequence 21 BP; 12 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 4476 TTTTCTTGTGCTGAGCATG 4496  
 Db 21 TTTTCTTGTGCTGAGCATG 1  
 RESULT 3331  
 ACF64056/c  
 ID ACF64056 standard; DNA; 21 BP.  
 AC ACF64056;  
 XX

DT	13-OCT-2003	(first entry)
XX	IFNARI reverse PCR primer #32.	
XX	Human; detection; computer-readable storage medium; polymorphic site;	
KW	signal carrying data; data processing system; multiple sclerosis;	
KM	PCR primer; ss.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	MO2003014319-A2.	
XX	20-FEB-2003.	
PD	07-AUG-2002; 2002WO-US025268.	
XX	07-AUG-2001; 2001US-0310741P.	
PR	24-SEP-2001; 2001US-0324790P.	
XX	(DNAS-) DNA SCI INC.	
PA	Jones HB, Xu H, White R, Rienhoff HY, Jin W, Naresouls G;	
PI	WPI, 2003-269196/26.	
DR	New polynucleotide, useful for detecting loci associated with multiple	
PT	sclerosis.	
PT	Diocloure; Page 10; 93pp; English.	
XX	The present invention describes an isolated polynucleotide (PN)	
CC	comprising: (a) a sequence comprising at least 15 contiguous nucleotides	
CC	of a sequence comprising variant sequences (A) from Table 4 given in the	
CC	specification; or (b) a sequence that is complementary to (A). Also	
CC	described: (1) an array of (PN)s comprising two or more of the isolated	
CC	(PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable	
CC	storage medium, where each record has a field identifying a base	
CC	occupying a (PN) site and a location of the polymorphic site; and (4) a	
CC	signal carrying data for access by an application program having executed	
CC	on a data processing system. The (PN) can be used for detecting loci	
CC	associated with multiple sclerosis. ACF64025 to ACF64424 represent	
CC	sequences used in the exemplification of the present invention	
XX	Sequence 21 BP; 10 A; 7 C; 2 G; 2 T; 0 U; 0 Other;	
SQ		
Query Match	0.2%; Score 14.6; DB 1; Length 21;	
Match Local Similarity	81.0%; Pred.No. 2.3e+03;	
Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
OY	6449 CAGTGTGTTGGATCTTTT 6469	
DB	21 CGGTGTGTTGGATCTTTAT 1	
RESULT 3332		
ACF64052/C		
ID	ACF64052 standard; DNA; 21 BP.	
XX	ACF64052;	
AC		
XX	13-OCT-2003 (first entry)	
DT		
XX	ESR1 reverse PCR primer #28.	
DE		
XX	Human; detection; computer-readable storage medium; polymorphic site;	
KW	signal carrying data; data processing system; multiple sclerosis;	
KM	PCR primer; ss.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	WO2003014319-A2.	

```
XX PI Walt DR, Michael KL;
XX DR WPI: 2003-092858/08.
XX PT Detecting a target analyte or an enzymatic reaction useful for forensic
XX PT DNA fingerprinting or detecting environmental pollutants, comprises
XX PT providing an array comprising an array substrate, first and second sites,
XX PT and microphones.
XX PS Disclosure; Page 28; 61pp; English.
XX CC The invention relates to a novel method for detecting a target analyte in
XX CC the sample. The novel method comprises providing an array comprising an
XX CC array substrate, at least first and second sites, and a population of
XX CC microphones, where first and second reaction components are attached
XX CC with a non-cleavable linker to the first and second microphones that are
XX CC randomly distributed on the sites. The methods are useful for detecting
XX CC the presence of a particular target analyte, or for detecting an
XX CC enzymatic reaction, such as the presence or absence of, or mutations on a
XX CC particular nucleotide sequence or protein, e.g. an enzyme, antibody or
XX CC antigen. They are also useful in forensic DNA fingerprinting, detecting
XX CC environmental pollutants such as pesticides or herbicides, and in
XX CC bacterial, fungal, protozoal, Mycoplasma, Rickettsial diagnostic tests,
XX CC as well as in pregnancy tests. This polynucleotide represents a target
XX CC sequence of the microsphere genosensors of the invention
SQ Sequence 21 BP; 8 A; 10 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3653 AAGAAATACCCGACGCCAAC 3673
DB 1 AATAACACACCCCTGACCCCAAC 21

RESULT 3334
ACCA2623/c
ID ACCA2623 standard; DNA; 21 BP.
XX AC ACCA2623;
XX DT 26-AUG-2003 (first entry)
XX DE Human interleukin-6, IL-6, PCR primer hIL6-F2.
XX KW Human; PCR; primer; transgenic mouse; lymphocyte maturation; IL-3; IL-7;
XX KW cytokine; interleukin-3; interleukin-6; IL-6; interleukin-7; M-CSF; SCF;
XX KW macrophage-colony stimulating factor; stem cell factor; oncostatin M; OM;
XX KW granulocyte-colony stimulating factor; GM-CSF; LIF;
XX KW leukaemia inhibitory factor; ss.
XX OS Homo sapiens.
XX EN WO2003018744-A2.
XX PD 06-MAR-2003.
XX PF 05-AUG-2002; 2002WO-US024807.
XX PR 23-AUG-2001; 2001US-00938689.
XX PA (GENV ) GENENCOR INT INC.
XX PI Harding PA, Huang M;
XX DR WPI: 2003-278650/27.
XX PT New recipient mammal, preferably a mouse, useful as a model of human
XX PT disease to assess efficacy of therapeutic or prophylactic treatments, or
XX PT for facilitating production of donor-specific functional immunity.
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XX PS Example; Page 36; 70pp; English.
XX CC The present invention relates to a new transgenic mouse, which comprises
XX CC a disruption in both alleles of a gene such that lymphocyte maturation
XX CC does not occur and exogenous cytokines. The cytokines are selected from:
XX CC interleukin-3 (IL-3), interleukin-6 (IL-6), interleukin-7 (IL-7),
XX CC macrophage-colony stimulating factor (M-CSF), granulocyte-colony
XX CC stimulating factor (GM-CSF), stem cell factor (SCF), leukaemia inhibitory
XX CC factor (LIF) and oncostatin M (OM). The gene disruption is in a gene that
XX CC modulated V $\beta$ D $\beta$  recombination e.g. a  $\beta$ AG gene. The gene is disrupted by
XX CC insertion of a transgene comprising major histocompatibility complex
XX CC (MHC) Class II DR3 and DQ2 genes. The transgenic mouse is useful as a
XX CC model of human disease to assess efficacy of therapeutic or prophylactic
XX CC treatments, or to assess the antigenic potential of compounds. The
XX CC transgenic mouse is also useful for supporting donor haematopoietic stem
XX CC cells or facilitating production of donor-specific functional immunity.
XX CC PCR primers ACCA2571-ACCA2639 were used to generate the transgenic mouse
SQ Sequence 21 BP; 0 A; 5 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7406 GCACATCAGCAGCAGCAGCA 7426
DB 21 GCACACACGAGAGCAGCCCA 1

RESULT 3335
ABT3411
ID ABT3411 standard; DNA; 21 BP.
XX AC ABT3411;
XX DT 22-MAY-2003 (first entry)
XX DE NOVA PCR primer SEQ ID No 266.
XX KW Hepatotropic; immunosuppressive; cardiac; hypertensive; tranquilizer;
XX KW vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
XX KW antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
XX KW anticonvulsant; antidiabetic; analgesic; dermatological; keratolytic;
XX KW antiseborrheic; antineumatic; antitartaric; antiinflammatory; anti-HIV;
XX KW cytosaric; antiaslumatic; antiporiatic; hypotensive; osteopathic;
XX KW antitumor; anorectic; antidiabetic; antiallergic; haemostatic;
XX KW neuroleptic; antidepressant; antifertility; NOVA; human disease;
XX KW NOVA-associated disorder; trauma; viral; bacterial; fungal; protozoal;
XX KW parasitic infection; Alzheimer's disease; stroke; forensic biology;
XX KW immunogen; non-human transgenic animal; gene therapy; PCR; primer; ss.
XX OS Unidentified.
XX EN WO200281517-A2.
XX PD 17-OCT-2002.
XX PF 22-JAN-2002; 2002WO-US002064.
XX PR 19-JAN-2001; 2001US-0262892P.
XX PR 23-JAN-2001; 2001US-0263598P.
XX PR 24-JAN-2001; 2001US-0263799P.
XX PR 25-JAN-2001; 2001US-0264117P.
XX PR 25-JAN-2001; 2001US-0264139P.
XX PR 26-JAN-2001; 2001US-0264478P.
XX PR 30-JAN-2001; 2001US-0265351P.
XX PR 02-MAR-2001; 2001US-0272870P.
XX PR 14-MAR-2001; 2001US-0275927P.
XX PR 15-MAR-2001; 2001US-0276449P.
XX PR 20-MAR-2001; 2001US-0277358P.
XX PR 23-MAR-2001; 2001US-0278151P.
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PR 29-MAR-2001; 2001US-0279857P.  
 PR 20-APR-2001; 2001US-0285140P.  
 PR 20-APR-2001; 2001US-0285141P.  
 PR 30-APR-2001; 2001US-0287484P.  
 PR 17-MAY-2001; 2001US-0291701P.  
 PR 08-JUN-2001; 2001US-0296960P.  
 PR 10-JUL-2001; 2001US-0304353P.  
 PR 10-JUL-2001; 2001US-0304355P.  
 PR 12-JUL-2001; 2001US-0304886P.  
 PR 09-AUG-2001; 2001US-0311289P.  
 PR 13-AUG-2001; 2001US-0311975P.  
 PR 16-AUG-2001; 2001US-0312937P.  
 PR 18-OCT-2001; 2001US-0330257P.  
 PR 29-NOV-2001; 2001US-0334198P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Deciaotafaro MF, Padigaru M, Miller C, Tchernev V, Zhong H;  
 PI Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastelli L;  
 PI Kekuda R, Guo X, Zernhusen B, Andrew D, Mezes P, Paturajan M,  
 PI Burgess CE, Eileen A, Wolenc A, Baumgartner J, Shinkets RA, Gusev V,  
 PI Vermet CM, Taupier RJ, Pena C, Shenoy S, Li L, Caaman S, Boldog F,  
 PI Fernandes E, Smithson G, Malyankar U, Tallon B, Liu X;  
 XX  
 DR WPI; 2003-056504/05.  
 XX  
 PT New polypeptides, designated as NOVX, useful for diagnosing and treating  
 PT infections, neurological diseases, cancer, allergy, and bone,  
 PT immunological, skin, renal, brain, muscle and autoimmune disorders.  
 XX  
 PS Example 1; Page 215; 672pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide, designated NOVX  
 CC (NOVI - 33), consisting of a mature form of one of 61 sequences, given in  
 CC the specification, or its variant, where amino acid residue(s) in the  
 CC variant differ from the mature form, provided that the variant differs in  
 CC not more than 15 % of the amino acids from the sequence of the mature  
 CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and  
 CC an antibody to the polypeptides, are useful for treating or preventing a  
 CC NOVX-associated disorder in humans and for treating a syndrome associated  
 CC with a human disease (NOVX-associated disorder). NOVX polypeptides and  
 CC the encoding nucleic acids, are useful for determining the presence of or  
 CC predisposition to a disease associated with altered levels of NOVX.  
 CC polypeptide and polynucleotide, by measuring the level of polypeptide  
 CC expression or the amount of nucleic acid from a mammal and comparing it  
 CC with another mammal not having or not predisposed to the disease. NOVX  
 CC polypeptide is also useful for identifying an agent that binds to NOVX  
 CC and a cell expressing NOVX is useful for identifying an agent that  
 CC modulates the expression or activity of NOVX. The antibodies and a  
 CC polypeptide having 95 % sequence identity to NOVX polypeptides are useful  
 CC for treating a pathological state in a mammal. The antibodies are also  
 CC useful for determining the presence or amount of NOVX in a sample. NOVX  
 CC polypeptides, polynucleotides and antibodies specific for the  
 CC polypeptides are useful for treating or preventing disorders or syndromes  
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic  
 CC infections. They can also treat disorders such as e.g., Alzheimer's  
 CC disease or a stroke. The NOVX encoding nucleic acids are useful for  
 CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in  
 CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful  
 CC for identifying a cell or tissue type in a biological sample, to amplify  
 CC DNA sequences from very small biological samples such as tissues e.g.  
 CC hair or skin or body fluids in forensic biology and as primers and probes  
 CC for use in identifying and/or cloning NOVX homologues in other cell  
 CC types. The NOVX proteins are useful as an immunogen to generate  
 CC antibodies which are useful for diagnostically monitoring protein levels  
 CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are  
 CC useful for producing non-human transgenic animals which are useful for  
 CC studying the function and/or activity of NOVX protein and for identifying  
 CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic  
 CC acids can be used in gene therapy. This polynucleotide sequence  
 CC represents a NOVX PCR primer of the invention  
 CC  
 XX Sequence 21 BP; 4 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1608 CAGAACTTCACAGACAGCT 1628  
 Db 1 CATGGCTTCACAGACCTGCT 21  
 RESULT 3336  
 ABX56493/C  
 ID ABX56493 standard; DNA; 21 BP.  
 XX  
 AC ABX56493;  
 XX  
 DT 17-FEB-2003 (first entry)  
 XX  
 DE Human epidermal growth factor-like protein forward PCR primer #2.  
 KW Gamma-aminobutyric acid receptor-like protein; depression; stroke;  
 KW GABA receptor-like protein; Parkinson's disease; Huntington's disease;  
 KW Tourette's syndrome; amyotrophic lateral sclerosis; head trauma;  
 KW Alzheimer's disease; alcoholism; vigilance; anxiety; muscle tension;  
 KW epileptogenic activity; memory; cardiomyopathy; cancer; angiogenesis;  
 KW arrhythmogenic right ventricular dysplasia; renal disease; diabetes;  
 KW Epidermal growth factor like protein; leukaemia; lupus; anaemia; ulcer;  
 KW hematopoietic stem and progenitor cell like protein; cirrhosis;  
 KW sulfotransferase-like protein; cholangitis; hepatitis; hyperthyroidism;  
 KW developmental disorder; Syntaxin-like protein; myxoid liposarcoma;  
 KW asthma; Lambert-Eaton myasthenic syndrome; acute myeloidleukaemia;  
 KW transgenic animal; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 XX US2002123612-A1.  
 PN  
 XX 05-SEP-2002.  
 PD  
 XX  
 PP 03-JUL-2001; 2001US-00898570.  
 XX  
 XX 19-APR-2000; 2000US-0198293P.  
 PR 20-APR-2000; 2000US-0198645P.  
 PR 25-APR-2000; 2000US-0199476P.  
 PR 26-APR-2000; 2000US-0199880P.  
 PR 26-APR-2000; 2000US-0200024P.  
 PR 26-APR-2000; 2000US-0200025P.  
 PR 09-JUN-2000; 2000US-0210809P.  
 PR 03-JUL-2000; 2000US-0215855P.  
 PR 11-JUL-2000; 2000US-0218591P.  
 PR 11-AUG-2000; 2000US-0224610P.  
 PR 27-FEB-2001; 2001US-0271814P.  
 XX  
 XX (GERL/) GERLACH V L.  
 PA (ELLE/) ELLERMAN K.  
 PA (MACD/) MACDOUGALL J R.  
 PA (SMIT/) SMITHSON G.  
 XX  
 PI Gerlach VL, Ellerman K, Macdougall JR, Smithson G;  
 XX  
 DR WPI; 2003-066815/06.  
 XX  
 PT Novel polypeptides and nucleic acids which are members of epidermal  
 PT growth factor, complement receptor families for diagnosing and treating  
 PT psychiatric conditions, depression, stroke, Alzheimer's and Parkinson's  
 PT disease.  
 XX  
 PS Example 5A; Page 74; 91pp; English.  
 XX  
 CC The invention describes an isolated POLYX (POLY1-17) polypeptide and its  
 CC variant. POLYX polypeptides (especially POLY5, POLY6 and POLY7), the  
 CC polynucleotides encoding them (I) and an anti-POLYX-antibody (III) are  
 CC useful for treating or preventing a pathology associated with POLYX

CC polypeptide in humans and for treating a syndrome associated with human  
 CC disease. POLYX polypeptide is also useful for identifying an agent that  
 CC binds to POLYX and a cell expressing POLYX is useful for identifying a  
 CC therapeutic agent for use in treatment of a pathology related to aberrant  
 CC expression or physiological interactions of the polypeptide. (iii) is  
 CC useful for treating a pathological state in a mammal and for determining  
 CC the presence or amount of POLYX in a sample. POLYX-4 (GABA receptor-like  
 CC proteins) are useful for the treatment of psychiatric and medical  
 CC conditions, depression, stroke, Parkinson's disease, Huntington's  
 CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, head trauma,  
 CC Alzheimer's disease, alcoholism, vigilance, anxiety, muscle tension,  
 CC arthropogenic activity and memory functions, cardiomyopathy and  
 CC arrhythmogenic right ventricular dysplasia. POLYX-8 (Epidermal growth  
 CC factor like protein) may be useful for treating cancer, aberrant  
 CC angiogenesis, renal disease and diabetes. POLYX12 (haematopoietic stem and  
 CC progenitor cell like protein) may be useful for treatment of leukaemia,  
 CC lupus and anaemia. POLYX13 (sulfoltransferase-like protein) may be useful  
 CC for treating cirrhosis, cholangitis, hepatitis, ulcers, hyperthyroidism  
 CC and developmental disorders. POLYX14-16 (Synthaxin-like proteins) may be  
 CC useful in treatment of Lambert-Eaton myasthenic syndrome, asthma, myxoid  
 CC liposarcoma and acute myeloid leukaemia, and POLYX 18 may be useful in  
 CC treatment of cancer. Cells comprising (i) are useful for producing non-  
 CC human transgenic animals which are useful for studying the function  
 CC and/or activity of POLYX protein and for identifying and/or evaluating  
 CC modulators of POLYX protein activity. This sequence represents a PCR  
 CC primer used to isolate DNA encoding novel human proteins characterised in  
 CC the invention

XX  
 XX  
 SQ Sequence 21 BP; 4 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6523 GACTATTAGCTGCGCCATAGG 6543  
 Db 21 GATTATGAGCTGCGCCACAG 1

RESULT 3337  
 ADA13874/c  
 ID ADA13874 standard; RNA; 21 BP.

XX  
 AC ADA13874;

XX  
 DT 20-NOV-2003 (first entry)

XX  
 DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:211.

XX  
 KW double-stranded short interfering nucleic acid;  
 KW short interfering nucleic acid; siNA; expression; replication;  
 KW inhibition; RNA interference; virocid; anti-HIV; hepatotropic;  
 KW antinflammatory; plant; antiviral; vasotropic; neuroprotective;  
 KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
 KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
 KW herpes simplex; cytomegalovirus; human papillomavirus;  
 KW respiratory syncytial virus; influenza virus; reovirus;  
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
 KW chemical modification; ss.

XX  
 OS Synthetic.

XX  
 PN WO2003070918-A2.

XX  
 PD 28-AUG-2003.

XX  
 PF 20-FEB-2003; 2003WO-US005346.

XX  
 PR 20-FEB-2002; 2002US-0358580P.

XX  
 PR 11-MAR-2002; 2002US-0363124P.

XX  
 PR 06-JUN-2002; 2002US-036782P.

XX  
 PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX  
 XX (RIBO-) RIBOTYME PHARM INC.

XX  
 PI McWissen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
 PI Morrissey D, Fossnaugh K, Mokler V, Jamison S;  
 XX WPI; 2003-689785/65.

XX  
 XX New short interfering nucleic acid containing no ribonucleotides, useful  
 XX e.g. for treating viral infection, downregulates expression of target  
 XX gene or RNA.

XX  
 PS Example 4; Page 138; 204pp; English.

XX  
 CC The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that downregulates expression of a target gene, where  
 CC the siNA molecule comprises no ribonucleotides and each strand of the  
 CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
 CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
 CC molecule that inhibits replication of a virus and optionally does not  
 CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
 CC that inhibits expression of a target gene and does not require presence  
 CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
 CC expression of a target gene by mediating RNA interference; and (5) a  
 CC method for modulating expression of a gene in a cell using siNA  
 CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
 CC antinflammatory, plant antiviral, vasotropic, neuroprotective,  
 CC cytosolic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
 CC and endocrine activities. The siNA's are useful for downregulating  
 CC expression of target genes, inhibiting expression of target RNA, and  
 CC inhibiting replication of a virus. siNA molecules can be used: (a) for  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC reovirus, neurodegeneration, cancer, and cardiovascular, neurological,  
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.

XX  
 SQ Sequence 21 BP; 3 A; 7 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 221 CGGACCTTCGGAGCAGCTG 241  
 Db 21 CGGGGCCCTCCAGAGCATCTG 1

RESULT 3338  
 ADB78519/c  
 ID ADB78519 standard; DNA; 21 BP.

XX  
 AC ADB78519;

XX  
 DT 04-DEC-2003 (first entry)

XX  
 DE Probe sequence #22 related to the invention.

XX  
 KW human leukocyte antigen; HLA; probe; PCR; ss.

XX  
 OS Synthetic.

XX WO2003027309-A2.  
 PN 03-APR-2003.  
 PD 24-SEP-2002; 2002WO-US030238.  
 XX 24-SEP-2001; 2001US-0324421P.  
 PR (ONEL-) ONE LAMBDA.  
 XX Saito K, Lee J, Blair L;  
 PI WPI; 2003-363216/34.  
 DR Detecting the presence of a target nucleic acid sequence on a sample  
 XX nucleic acid strand, useful for human leukocyte antigen tissue typing,  
 PT comprises contacting a sample with a diagnostic probe under hybridizing  
 PT conditions.  
 XX Example 3; Page 29; 62pp; English.  
 PS The present invention relates to the detecting of a target nucleic acid  
 CC sequence on a sample nucleic acid strand. The methods are useful for  
 CC detecting the presence or absence of target nucleic acid sequences on  
 CC sample nucleic acid strands that are characteristic of pathogens or gene  
 CC variations and mutations relating to human leukocyte antigen (HLA) or T-  
 CC cell receptor gene sequences, e.g. for HLA tissue typing, detecting  
 CC genetically inherited diseases or detecting infectious organisms in  
 CC tissues. The diagnostic probes are useful for detecting the presence of  
 CC particular target nucleotide sequences. The present invention provides  
 CC improved methods of detecting sample/target nucleic acid sequences, where  
 CC the use of diagnostic probes having increased specificity reduces the  
 CC number of alleles detected, which increases the resolution of the method,  
 CC and does so at a lower cost. The present sequence represents a probe of  
 CC the invention.  
 XX Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2740 GCCGTGACGGTTCACAGGAT 2760  
 DB 21 GCCGCGCAGGTTCCCGACGCT 1  
 RESULT 3339  
 ADB78522/C  
 ID ADB78522 standard; DNA; 21 BP.  
 XX ADB78522;  
 AC  
 XX 04-DEC-2003 (first entry)  
 DT  
 XX Probe sequence #25 related to the invention.  
 DE human leukocyte antigen; HLA; probe; PCR; ss.  
 XX human leukocyte antigen; HLA; probe; PCR; ss.  
 OS Synthetic.  
 XX WO2003027309-A2.  
 PN 03-APR-2003.  
 PD 24-SEP-2002; 2002WO-US030238.  
 PF 24-SEP-2001; 2001US-0324421P.  
 PR (ONEL-) ONE LAMBDA.  
 XX Saito K, Lee J, Blair L;

XX WPI; 2003-363216/34.  
 DR Detecting the presence of a target nucleic acid sequence on a sample  
 XX nucleic acid strand, useful for human leukocyte antigen tissue typing,  
 PT comprises contacting a sample with a diagnostic probe under hybridizing  
 PT conditions.  
 XX Example 3; Page 29; 62pp; English.  
 PS The present invention relates to the detecting of a target nucleic acid  
 CC sequence on a sample nucleic acid strand. The methods are useful for  
 CC detecting the presence or absence of target nucleic acid sequences on  
 CC sample nucleic acid strands that are characteristic of pathogens or gene  
 CC variations and mutations relating to human leukocyte antigen (HLA) or T-  
 CC cell receptor gene sequences, e.g. for HLA tissue typing, detecting  
 CC genetically inherited diseases or detecting infectious organisms in  
 CC tissues. The diagnostic probes are useful for detecting the presence of  
 CC particular target nucleotide sequences. The present invention provides  
 CC improved methods of detecting sample/target nucleic acid sequences, where  
 CC the use of diagnostic probes having increased specificity reduces the  
 CC number of alleles detected, which increases the resolution of the method,  
 CC and does so at a lower cost. The present sequence represents a probe of  
 CC the invention.  
 XX Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2740 GCCGTGACGGTTCACAGGAT 2760  
 DB 21 GCCGCGCAGGTTCCCGACGCT 1  
 RESULT 3340  
 ADC16367  
 ID ADC16367 standard; RNA; 21 BP.  
 XX ADC16367;  
 AC  
 XX 18-DEC-2003 (first entry)  
 DT  
 XX Short interfering double-stranded RNA oligonucleotide SEQ ID NO:92.  
 DE expression interference; expression inhibition; target gene;  
 KW short interfering double stranded RNA; cytostatic; gene therapy;  
 XX proliferative disease; cancer; ds.  
 OS Synthetic.  
 XX WO2003012052-A2.  
 PN 13-FEB-2003.  
 PD 30-JUL-2002; 2002WO-US024226.  
 PF 30-JUL-2001; 2001US-0308640P.  
 PR 08-APR-2002; 2002US-0370970P.  
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA (CARN-) CARNEGIE INST WASHINGTON.  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX Caplen NJ, Morgan RA, Fire A, Parrish S, Mousaee S;  
 PI Kallionlehti O, Cornelison JR, Alton EW, Griesenbach U;  
 XX WPI; 2003-248169/24.  
 DR New RNA comprising double stranded RNA and a 3' or 5' overhang having a  
 PT length of 0-nucleotide to 5-nucleotide on each strand, useful as reverse  
 PT genetic and/or therapeutic tools for interfering or inhibiting expression

PT of a target gene.  
XX  
PS Claim 71; SEQ ID NO 92; 176pp; English.  
XX  
CC The present invention describes an RNA (1) used for the interference or  
CC inhibition of expression of a target gene, where (1) comprises double  
CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang  
CC having a length of 0-nucleotide to 5-nucleotides on each strand, where  
CC the sequence of the double stranded RNA is substantially identical to a  
CC portion of a mRNA or transcript of the target gene. Also described: (1)  
CC interfering with or inhibiting the expression of a target gene in a cell  
CC by exposing the cell to an amount of (1); (2) a gene silencing array  
CC comprising a substantially flat substrate, and addressably arrayed  
CC different double-stranded RNAs; (3) an array-based method of assessing a  
CC phenotypic effect of a double-stranded RNA on a target gene; (4)  
CC validating a gene as a potential drug target for a disease or condition;  
CC (5) selecting an optimised sequence of a double-stranded RNA for  
CC interference with or inhibition of expression of a target gene in a cell;  
CC and (6) a short double-stranded RNA effective for interfering with or  
CC inhibiting expression of a target gene comprising any of 311 20-78  
CC nucleotide sequences (see ADC16276 to ADC16586). (1) has cytostatic  
CC activity, and can be used in gene therapy. The RNAs are useful as reverse  
CC genetic and/or therapeutic tools for interfering or inhibiting expression  
CC of a target gene. They are useful for treating proliferative diseases,  
CC e.g. cancer.  
SQ Sequence 21 BP; 3 A; 7 C; 4 G; 0 T; 7 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 52.4%; Pred. No. 2.3e+03;  
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 2761 ACTCTGCCGACCACTACTTC 2781  
DB 1 AGUCUCCGCAUCGUGUACUUC 21  
RESULT 3341  
ADC42515  
ID ADC42515 standard; DNA; 21 BP.  
XX  
AC ADC42515;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE FANCD2 PCR primer MG763 SEQ ID NO:181.  
XX  
KW cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;  
KW chemosensitising; ss; PCR; primer.  
XX  
OS Synthetic.  
XX  
PN MO2003039327-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 06-JUN-2002; 2002WO-US018153.  
XX  
PR 02-NOV-2001; 2001US-00998027.  
XX  
PR 02-NOV-2001; 2001WO-US045561.  
XX  
PA (DAND ) DANA FARBEN CANCER INST.  
PA (UTOR-) UNIV OREGON HEALTH SCI.  
XX  
PI D'andrea AD, Taniguchi T, Timmers C, Grome M, Fox EA;  
XX  
DR WPI; 2003-441436/41.  
XX  
PT Diagnosing or determining cancer or increased risk of cancer in a  
PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a  
PT cancer-associated defect, that indicates cancer or increased risk of  
PT cancer.  
XX

PS Claim 11; SEQ ID NO 181; 160pp; English.  
XX  
CC The invention relates to a novel method of diagnosing or determining if a  
CC patient has cancer or is at increased risk of cancer, involving testing a  
CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a  
CC cancer-associated defect, where the presence of one or more cancer-  
CC associated defects is indicative of cancer or an increased risk of cancer  
CC in the patient. The method of the invention has cytostatic activity. The  
CC method is useful for determining if a patient has cancer, or is at  
CC increased risk of developing cancer, e.g. breast, ovarian or prostate  
CC cancer. A microarray of the invention is useful for determining if a  
CC patient has cancer, or is at increased risk of developing cancer, by  
CC hybridising a nucleic acid sample to the nucleic acid sequences from the  
CC array, and detecting the presence of mutations in FA/BRCA pathway genes  
CC in the nucleic acid sample from the patient, where detecting the presence  
CC of mutations is indicative of a patient who has cancer, or is at  
CC increased risk of developing cancer. A method of the invention is useful  
CC for screening a chemosensitising agent, and the agent obtained is useful  
CC for treating a patient having a cancer. The present sequence is used in  
CC the exemplification of the invention.  
SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2742 CGTGCAGTTCACCAGCATAC 2762  
DB 1 CATTGACATTCCACGAGACAC 21  
RESULT 3342  
ADC64837/C  
ID ADC64837 standard; DNA; 21 BP.  
XX  
AC ADC64837;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE RNaseA PCR primer SEQ ID NO:2.  
XX  
KW atopic dermatitis; steroid; RNaseA; RNase k6 precursor; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP2002291485-A.  
XX  
PD 08-OCT-2002.  
XX  
PF 03-APR-2001; 2001JP-00104621.  
XX  
PR 03-APR-2001; 2001JP-00104621.  
XX  
PA (GENO-) GENOX SOYAKU KENKUSHO KK.  
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.  
XX  
DR WPI; 2003-375782/36.  
XX  
PT Examination of responsiveness to steroids in patients with atopic  
PT dermatitis for improved treatment of patients suffering from allergic  
PT diseases.  
XX  
PS Example 2; Page 14; 24pp; Japanese.  
XX  
CC The present invention describes a method for examining the response of  
CC patients with atopic dermatitis to steroids. The method comprises: (a)  
CC determining the expression levels of an RNaseA gene or an RNase k6  
CC precursor gene in a living sample; and (b) comparing the response level  
CC with that of healthy subjects and steroid responsive patients, determined  
CC by PCR of cDNA. The present sequence represents an RNaseA PCR primer,  
XX which is used in an example from the present invention.  
XX





Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4708 TTACTTGAACCTAGCCAGG 4728  
 Db 21 TTCCCTTAGAGCTAGCCAGG 1

RESULT 3345  
 ADC84417  
 ID ADC84417 standard; DNA; 21 BP.

AC ADC84417;

DT 01-JAN-2004 (first entry)

DE HPV detection method-related oligonucleotide Gap21-5.

KW probe; human papilloma virus; HPV; detection; identification; ss;

KV Gap21-5.

OS Unidentified.

PN EPI302550-A1.

PD 16-APR-2003.

PF 10-OCT-2001; 2001EP-00123379.

PR 10-OCT-2001; 2001EP-00123379.

PA (KING-) KING CAR FOOD IND CO LTD.

P1 Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Fan C;

P1 Hsu H, Shih C, Yeh C, Kao Y, Pan C, Chan P;

DR WPI; 2003-432398/41.

FT Detector for identifying human papilloma virus subtypes, comprises

PT carrier having two parts carrying first and second oligonucleotides that

PT respectively hybridize with DNA contained in first and second subtypes of

PS Disclosure; SEQ ID NO 647; 221pp; English.

CC The invention comprises oligonucleotides for detecting and identifying

CC subtypes of human papilloma virus (HPV) contained in a sample. The

CC oligonucleotides of the invention are useful for simultaneously detecting

CC and identifying subtypes of HPV. The present DNA sequence represents an

CC oligonucleotide that was used in the exemplification of the invention.

SQ Sequence 21 BP; 5 A; 11 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1562 CCATCGCTGCTTGCACCCC 1582

Db 1 CCACCACTGCTTGCACCCC 21

RESULT 3346

ADD20200/C

ID ADD20200 standard; DNA; 21 BP.

AC ADD20200;

DT 15-JAN-2004 (first entry)

DE Orochromis niloticus microsatellite primer SEQ ID NO:835.

KW single nucleotide polymorphism; SNP; fish; Salmo salar;

KV Orochromis niloticus; Atlantic halibut; microsatellite; cod;

KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;

OS Synthetic.

PN WO2003060160-A2.

PD 24-JUL-2003.

PF 17-JAN-2003; 2003WO-IB000112.

PR 18-JAN-2002; 2002US-0349950P.

PR 16-AUG-2002; 2002US-0404200P.

PA (GENO-) GENOMAR ASA.

PI Lie O, Slettan A, Hoyum M, Lingaas F;

DR WPI; 2003-627388/59.

PT Novel isolated nucleic acid molecule comprising single nucleotide

PT polymorphism associated with fish, useful for forming PCR primers which

PT are used for detecting single nucleotide polymorphisms in fish nucleic

PS Claim 18; SEQ ID NO 835; 233pp; English.

CC The present invention describes an isolated nucleic acid (I) comprising a

CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of

CC Salmo salar SNPs, Orochromis niloticus SNPs or Atlantic halibut SNPs;

CC and (ii) a nucleic acid having nucleotide sequence that hybridizes to

CC (i), or its complement under highly stringent hybridisation conditions.

CC Also described: (1) an isolated oligonucleotide (II) comprising at least

CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.

CC niloticus SNPs, O. niloticus microsatellites; Atlantic halibut SNPs, cod

CC polymorphic sites and seabass polymorphic sites, or their complement; (2)

CC a primer pair (III) suitable for use in PCR, comprising two (II) capable

CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.

CC niloticus SNPs, O. niloticus microsatellites; Atlantic halibut SNPs, cod

CC polymorphic sites and seabass polymorphic sites; and determining (M1) the

CC origin of fish sample comprising providing a parentage genotype database

CC comprising a collection of candidate parent genotypes, where each of the

CC candidate parent genotype represents a distinct origin, and comparing a

CC sample genotype to the parentage genotype database, where a match between

CC the sample genotype and one of the candidate parent genotype identifies

CC to the origin of the sample. (M1) is useful for determining the origin of

CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,

CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for

CC detecting nucleic acid molecule comprising SNP in a sample, which

CC involves contacting the sample containing nucleic acids with one or more

CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus

CC SNPs, and identifying nucleic acid that hybridizes to (II). (II) is

CC useful for detecting nucleic acid molecule comprising a polymorphic

CC sequence in a sample, comprising contacting the sample containing nucleic

CC acids with one or more (II) which is derived from O. niloticus

CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic

CC sites or seabass polymorphic sites, and identifying a nucleic acid that

CC hybridises to (II). (III) is useful for detecting nucleic acid molecule

CC comprising a microsatellite sequence in sample. The present sequence is

CC used in the exemplification of the present invention.

SQ Sequence 21 BP; 9 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5318 CTCCTCTTCTCTCTTGGC 5338

Db 21 CTCCTCTTCTCTCTTGGC 1

```

RESULT 3347
ADD95120/c
ID ADD95120 standard; DNA; 21 BP.
XX
AC ADD95120;
XX
DT 29-JAN-2004 (first entry)
XX
DE BMP receptor type 1B upstream primer #SEQ ID 4.
XX
KM Pigmentation; skin; hair; wool; fur; bone morphogenetic protein 4; BMP-4;
KM PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO2003086313-A2.
XX
PD 23-OCT-2003.
XX
PF 11-APR-2003; 2003WO-US011376.
XX
PR 12-APR-2002; 2002US-0372523P.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Year M, Park H, Botchkarev V, Gilchrist BA;
DR WPI; 2003-903051/82.
XX
PT Decreasing skin, hair, wool or fur pigmentation in a mammal comprising
PT administering a composition comprising bone morphogenetic protein 4 (BMP-
PT 4), an active fusion protein or fragment of BMP-4, a BMP-4 mimic or its
PT combination.
XX
PS Example 8; SEQ ID NO 4; 42bp; English.
XX
CC The invention relates to decreasing pigmentation in the skin, hair, wool
CC or fur of a vertebrate or a mammal. This method comprises administering a
CC composition comprising bone morphogenetic protein 4 (BMP-4), an active
CC fusion protein of BMP-4, an active fragment of BMP-4, a BMP-4 mimic or a
CC combination of any of those. The method is useful for lightening or
CC decreasing pigmentation in the skin, hair, wool or fur of a vertebrate or
CC a mammal. The current sequence represents a PCR primer for the
CC amplification of BMP receptor type 1B DNA.
XX
SQ Sequence 21 BP; 6 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred.No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1915 AAACCTTGCGCATTACAC 1935
DB 21 AATGCTGCTGCATTACAC 1

```

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RESULT 3348
ADE16100/c
ID ADE16100 standard; DNA; 21 BP.
XX
AC ADE16100;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related forward PCR primer, SEQ ID No 130.
XX
KM G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KM vitruide; fungicide; cytostatic; neurotropic; neuroprotective;
KM antiparkinsonian; haemostatic; antihypaemic; neurogenesis;
KM cell differentiation; cell proliferation; hematopoiesis; wound healing;
KM angiogenesis; gene therapy; chromosome mapping; tissue typing;
KM preventive medicine; pharmacogenomics; human; PCR; primer; ss.
XX

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OS Homo sapiens.
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
PA (CURA-) CURAGEN CORP.
XX
PI IJ L, Gerlach V, Liu X, Miller CE, Spytek KA, Zernhusen BD;
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boidog FL;
PI Voss EZ, Vermet CAM, MacDougall JR, Kastelell L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Paturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
DR WPI; 2003-067574/06.
XX
PT New isolated NOX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
PS Example 27; SEQ ID NO 130; 320bp; English.
XX
CC The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC vitruide, fungicide, cytostatic, neurotropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antihypaemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing, and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,

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CC tissue typing, preventive medicine, and pharmacogenomics. This  
 CC polynucleotide sequence represents a primer relating to the novel G-  
 CC coupled protein receptor related polypeptides of the invention.

XX Sequence 21 BP; 1 A; 8 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2859 AGAGGAGCAAGAGAGGGA 2879  
 Db 21 AAAGCAGCAAGAGAGACTGA 1

RESULT 3349  
 ID AAQ14243  
 XX AAQ14243 standard; DNA; 22 BP.

AC AAQ14243;

DT 20-JAN-1992 (first entry)

DE Primer CMLI.

KW Acute lymphocytic leukaemia; chimeric; mRNA; ABL; breakpoint; cluster;  
 KM BCR; ALL; exon junction; PCR; ss.

OS Synthetic.

PN US5057410-A.

PD 15-OCT-1991.

PF 05-AUG-1988; 88US-00229604.

PR 05-AUG-1988; 88US-00229604.

XX (CERTU ) CERTUS CORP.

XX Kawasaki ES, McCormick BP, Witto OO;

DR WPI; 1991-324515/44.

PT Method for detecting chimeric mRNA - useful e.g. for distinguishing  
 PT between acute lymphocytic leukaemia and chronic myeloid leukaemia.

PS Claim 5; Page 13; 14pp; English.

CC The primer is used with primer CMLII (AAQ14244) to amplify chimeric mRNA  
 CC contg. a specific exon-exon junction associated with chronic myeloid  
 CC leukaemia (CML). It is complementary to cDNA sequences within the break  
 CC point cluster region (BCR) exon 2. It can distinguish between ALL BCR-ABL  
 CC chimeric mRNA and CML BCR-ABL mRNA. The CML DNA sequences used to design  
 CC the primer are reported by Heisterkamp, N., et al. Nature 315: 758 (1985)  
 CC ; Grosvel, G., et al Mol. Cell Biol. 6:607 (1987); and Shitvelman, E.,  
 CC et al Cell 47:277 (1986). See also AAQ14241-47

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2539 GAGCTCCAGATCTGACGCTAC 2559  
 Db 2 GAGCTGCAGATCTGACCAAC 22

RESULT 3350  
 ID AAQ32173  
 XX AAQ32173 standard; DNA; 22 BP.

AC AAQ32173;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 30-MAR-1993 (first entry)

DE Reverse PCR primer for novel nematode active genes eg BT toxins.  
 KM nematode worms; nematicide; nematicidal toxin; agriculture; plants;  
 KM crops; pests; CryV proteins.

OS Bacillus thuringiensis.

PN EP517367-A1.

PD 09-DEC-1992.

PF 01-MAY-1992; 92EP-00303969.

PR 03-MAY-1991; 91US-00693018.

PR 31-JAN-1992; 92US-00830050.

PR 23-APR-1992; 92US-00871510.

XX (MYCO ) MYCOGEN CORP.  
 PI Schnepf HE, Schwab GE, Payne JM, Narva KE, Foncecerra L;  
 KM WPI; 1992-408829/50.

DR WPI; 1992-408829/50.

PT Nematocidal toxins from *Bacillus thuringiensis* - useful for control of  
 PT animal or plant parasites, and DNA acid coding sequences, transformed  
 PT hosts and transgenic plants.

PS Claim 1(f); Page 53; 57pp; English.

CC This degenerate sequence represents a reverse PCR primer for the cloning  
 CC of a novel nematocidal toxin from BT as in AAQ32172. (Updated on 25-MAR-  
 CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 22 BP; 7 A; 2 C; 2 G; 7 T; 0 U; 4 Other;

Qy 4405 TTACAAATGAATTTTCC 4425

Db 22 TWGAYMDATTGAATTATTC 2

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;  
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4405 TTACAAATGAATTTTCC 4425  
 Db 22 TWGAYMDATTGAATTATTC 2

RESULT 3351  
 ID AAQ30933  
 XX AAQ30933 standard; DNA; 22 BP.

AC AAQ30933;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DE Reverse PCR primer for novel nematode active genes eg BT toxins.

KW nematode worms; nematicide; nematicidal toxin; agriculture; plants;  
 KM crops; pests; CryV proteins.

OS *Bacillus thuringiensis*.

PN W09219739-A1.

PD 12-NOV-1992.

PF 01-MAY-1992; 92WO-US003624.

XX

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PR 03-MAY-1991; 91US-00693018.
PR 31-JUN-1992; 92US-00830050.
PR 23-APR-1992; 92US-00871510.
XX
XX (MYCO ) MYCOGEN CORP.
XX
PI Schnopf HE, Schwab GE, Payne JM, Narva KE, Foncecerra L,
XX WPI; 1992-398866/48.
XX
XX New genes and toxins against nematodes - obt'd. from Bacillus
PT Thuringiensis isolates with nematocidal activity.
XX
XX Claim 1(f); Page 12; 77pp; English.
XX
XX This degenerate sequence represents a reverse PCR primer for the cloning
CC of a novel nematocidal toxin from BT as in AAQ01943. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 22 BP; 7 A; 2 C; 2 G; 7 T; 0 U; 4 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4405 TTTACAAAATGAAATTTTCC 4425
DB 22 TWGAYMRAATTGAATTAATTC 2

RESULT 3352
AAQ0300
ID AAQ0300 standard; DNA; 22 BP.
XX
XX AAQ0300;
XX
XX 25-MAR-2003 (revised)
DT 11-JUL-1995 (first entry)
XX
XX Human plasmin cDNA PCR primer.
DE
XX Human plasmin; haemopoietic cells; neoplastic; PCR primers;
KM nucleotide probes; anti-plasmin antibodies; ss.
XX
XX Synthetic.
OS
XX US5360715-A.
PN
XX 01-NOV-1994.
PD
XX 10-JAN-1991; 91US-00642983.
XX
XX 07-JUN-1988; 88US-00203434.
PR 16-MAR-1990; 90US-00495256.
XX
XX (CALY ) CALIFORNIA INST OF TECHN.
PA
XX Lin C, Hebersold RH, Leavitt JC;
PI
XX WPI; 1994-349444/43.
DR
XX DNA encoding leukocyte-plasmin and tissue-plasmin - used to develop
PT prods. for distinguishing human haemopoietic cells, normal tissue cells
PT and neoplastic cells.
XX
XX Example 2; Col 19; 17pp; English.
XX
XX AAQ0239 and AAQ0300 are a pair of upstream and AAQ0301 and AAQ0302
CC are a pair of downstream primers for the PCR amplification of AAQ3001
CC and AAQ73002, which encode AAR62657 and AAR62658 human tissue plasmin (t-
CC plasmin) and human leukocyte plasmin (l-plasmin) respectively. The
CC plasmin cDNA and amino acid sequences were used to develop isoform
CC specific plasmin nucleotide probes, and isoform specific anti-plasmin
```

```
CC antibodies. Using the fact that human cells that express only l-plasmin
CC are haemopoietic cells, and human cells that express both l-plasmin and t-
CC plasmin are neoplastic, the above probes and antibodies could be used to
CC distinguish between the above cell types. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 22 BP; 1 A; 18 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3388 CCCGAGCTGCCACCCCCACC 3408
DB 1 CTCGAGCTCCCCCCCCCCC 21

RESULT 3353
AAQ61522/c
ID AAQ61522 standard; cDNA; 22 BP.
XX
XX AAQ61522;
XX
XX 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 21-OCT-1994 (first entry)
XX
XX TCR delta E5 enhancer element comprising Ikaros binding site.
DE
XX Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
KM corpus striatum; regulatory gene; enhancer; regulatory element;
KM gene expression; ss.
XX
XX Nus sp.
OS
XX WO9406814-A1.
PN
XX 31-MAR-1994.
PD
XX 14-SEP-1993; 93WO-US008743.
XX
XX 14-SEP-1992; 92US-00946233.
PR
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX Georgopoulos K;
PI
XX WPI; 1994-118387/14.
DR
XX I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc
PT finger proteins, useful for treating immune system disorders.
XX
XX Disclosure; Page 28; 112pp; English.
XX
XX The Ikaros gene encodes a zinc finger protein which can be used in a
CC therapeutic composition to treat animals with an immune system disorder.
CC It may also be used for assessing whether a subject is at risk for an
CC immune disorder. It is of particular use in treating a disorder of the
CC corpus striatum. Heterologous genes may be expressed by placing them
CC under the control of an Ikaros responsive control element and contacting
CC the element with an Ikaros protein. Potential high affinity binding sites
CC for the Ikaros proteins were found in the enhancer and promoter regions
CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma
CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains
CC of other T cell restricted antigens. Related sequences to the Ikaros
CC motif were also found in the purine boxes of the IL2 gene in the in the
CC LTF site of the TDT promoter as well as in the NFkB variant sites of the
CC HIV long terminal repeat. See also AAQ61504-061543. (Updated on 10-MAR-
CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
CC field.)
SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
```

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5690 TACCACTGTTTGGCTTCCTT 5710  
 |||||  
 DB 21 TTCCCTGTTTGGTTTCCTT 1

## RESULT 3354

AA086634  
 ID AA086634 standard; DNA; 22 BP.

XX  
 AC AA086634;

XX 25-MAR-2003 (revised)  
 DT 16-NOV-1995 (first entry)

XX Non-promoter primer for the CML major breakpoint region.

XX Primer; autocatalytic; PCR; target; sequence; ss.

XX Synthetic.

XX US5399491-A.

XX 21-MAR-1995.

XX 19-MAR-1992; 92US-00855732.

XX 11-JUL-1989; 89US-00379501.

XX 10-JUL-1990; 90US-00550837.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

XX WPI; 1995-130686/17.

XX Amplification of nucleic acid targets - using a reverse transcriptase  
 PT with RNase H activity and a RNA polymerase at constant temp.

XX Example 18; Col 47; 58pp; English.

XX The oligonucleotide AA086634 is a non-promoter primer for the CML major  
 CC breakpoint amplification region. It is used to illustrate that small  
 CC changes in the NA sequence result in large changes in the amplification  
 CC efficiency. AA086634 is capable of serving as a primer for the synthesis  
 CC of autocatalytic oligonucleotides which require no change in the PCR  
 CC conditions i.e. constant temperature, pH and ionic strength. This sequence  
 CC is useful in generating multiple copies of specific nucleic acid target  
 CC sequences. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2539 GAGCTCGAGATCGTACGTAC 2559  
 |||||  
 DB 2 GAGCTCGAGATCGTACCAAC 22

## RESULT 3355

AA086627  
 ID AA086627 standard; DNA; 22 BP.

XX  
 AC AA086627;

XX 25-MAR-2003 (revised)  
 DT 15-NOV-1995 (first entry)

DE CML chromosomal translocation plus strand primer.

XX Primer; autocatalytic; target; CML; translocation; ss.

XX Synthetic.

XX US5399491-A.

XX 21-MAR-1995.

XX 19-MAR-1992; 92US-00855732.

XX 11-JUL-1989; 89US-00379501.

XX 10-JUL-1990; 90US-00550837.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

XX WPI; 1995-130686/17.

XX Amplification of nucleic acid targets - using a reverse transcriptase  
 PT with RNase H activity and a RNA polymerase at constant temp.

XX Disclosure; Col 9; 58pp; English.

XX AA086626-28 are primers and a probe for the CML chromosomal  
 CC translocation. They are used to produce autocatalytic oligonucleotides  
 CC which require no change in the experimental conditions i.e. constant  
 CC temperature, pH and ionic strength. These sequences are useful in  
 CC generating multiple copies of specific nucleic acid target sequences.  
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2539 GAGCTCGAGATCGTACGTAC 2559  
 |||||  
 DB 2 GAGCTCGAGATCGTACCAAC 22

## RESULT 3356

AAT15572  
 ID AAT15572 standard; DNA; 22 BP.

XX  
 AC AAT15572;

XX 25-MAR-2003 (revised)

XX 17-JUL-1996 (first entry)

XX CML-2 chromosomal translocation major breakpoint t(9;22) (+) primer.

XX CML-2 chromosomal translocation major breakpoint; t(9; 22); primer;  
 KW auto-catalytic; synthesis; RNA target sequence; assay; detection;  
 KW quantification; ss.

XX Synthetic.

XX US5480784-A.

XX 02-JAN-1996.

XX 10-JUL-1990; 90US-00550837.

XX 11-JUL-1989; 89US-00379501.

XX (GENP-) GEN-PROBE INC.

XX Fultz TJ, Kacian DL;

DR WPI; 1996-068248/07.  
XX  
XX Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
PT uses cooperative action of a DNA and RNA polymerase in presence of RNase  
PT H; useful for detection of target sequence e.g. in clinical or  
PT environmental sample.  
XX  
PS Example; Col 9-10; 51pp; English.  
XX  
XX The present sequence is a primer for the CML-2 chromosomal translocation  
CC major breakpoint t(9;22), which was used to demonstrate an improved  
CC method for synthesizing multiple copies of a RNA target sequence. The  
CC method comprises combining the target with a primer which hybridises to  
CC the 3'-terminal portion of the target, a promoter primer which hybridises  
CC with a portion of the DNA primer extension prod., reverse transcriptase,  
CC RNase H and transcriptase. It can be used as a component of an assay to  
CC detect and/or quantitate specific target sequences in clinical,  
CC environmental or forensic samples. It also has the advantages of being  
CC autocatalytic, using the cooperative action of a DNA polymerase, e.g. a  
CC reverse transcriptase and avoids repetitive manipulations of reaction  
CC conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 2539 GAGCTCCAGATCCTGACGTAC 2559  
Db 2 GAGCTGCAGATGCTGACCAAC 22  
XX  
RESULT 3357  
AAT42418  
ID AAT42418 standard; DNA; 22 BP.  
XX  
XX AAT42418;  
AC  
XX 25-MAR-2003 (revised)  
DT 28-APR-1997 (first entry)  
XX  
XX CML chromosomal translocation primer #2.  
DE  
XX HIV; probe; primer; amplify; polymerase chain reaction; microorganism;  
KM BCL-2; PCR; hepatitis B virus; HBV; CML; ss.  
XX  
XX Synthetic.  
OS  
XX EP731175-A2.  
PN  
XX 11-SEP-1996.  
PD  
XX 10-JUL-1990; 96EP-00101621.  
PF  
XX 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90EP-00307503.  
XX  
XX (GENP-) GEN-PROBE INC.  
PA  
XX McDonough S;  
PI  
XX WPI; 1996-403995/41.  
DR  
XX  
XX Detection of HIV nucleic acids in samples - using new specific oligo-  
PT nucleotide(s) for the amplification and detection of target sequences.  
XX  
XX Disclosure; Page 8; 66pp; English.  
PS  
XX AAT42417-T42419 represent primers and a probe for the CML chromosomal  
CC translocation t(9;22). These sequences can be used in modified versions  
CC of the kits of the invention. The kits of the invention, are for

CC detecting the presence of HIV nucleic acid sequences in a sample. The  
CC kits comprise two amplification primers (such as AAT40182 and AAT40183),  
CC and a probe (such as AAT42404) for detection of HIV nucleic acid sequences  
CC by using these sequences, the amplification of HIV nucleic acid sequences  
CC is improved. The kits can also be used for the detection of other  
CC microorganisms, by using different probe sequences. Other sequences that  
CC can be detected using this method include those from HBV (using the  
CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).  
CC The samples can be clinical, environmental or forensic samples, and the  
CC method produces large amounts of the target sequence for a variety of  
CC uses. The method can also be used to produce multiple copies of a target  
CC sequence for use in cloning, and sequencing, and to produce probes for  
CC the target sequence. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
XX  
QY 2539 GAGCTCCAGATCCTGACGTAC 2559  
Db 2 GAGCTGCAGATGCTGACCAAC 22  
XX  
RESULT 3358  
AAX83079  
ID AAX83079 standard; DNA; 22 BP.  
XX  
XX AAX83079;  
AC  
XX 31-AUG-1999 (first entry)  
DT  
XX  
XX Primer SES to detect mutations in the human WRN gene.  
DE  
XX Human; WRN; Werner's syndrome; detection; diagnosis; autosomal; mutation;  
KM recessive disorder; phenotype; primer; PCR; amplification; ss.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX WC9724435-A1.  
PN  
XX 10-JUL-1997.  
PD  
XX 30-DEC-1996; 96WC-US020785.  
PF  
XX 29-DEC-1995; 95US-0009409P.  
PR 29-DEC-1995; 95US-00580539.  
XX 30-JAN-1996; 96US-0010835P.  
PR 30-JAN-1996; 96US-00594242.  
XX 12-APR-1996; 96US-00632175.  
PR  
XX (DARW-) DARWIN MOLECULAR CORP.  
PA  
XX  
XX Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;  
PI  
XX WPI; 1997-363671/33.  
DR  
XX  
XX Isolated nucleic acid molecule encoding the WRN gene product - useful for  
PT detection and treatment of Werner's syndrome, and related diseases.  
XX  
XX Example 5; Page 48; 153pp; English.  
PS  
XX Primers AAX83071-X83082 were used to PCR amplify, detect and identify  
CC mutations in the human WRN gene (AAX83003) which encodes a protein  
CC related to Werner's syndrome. The products can be used for the detection  
CC and treatment of Werner's syndrome (ws), an autosomal recessive disorder  
CC with a complex phenotype, as well as related diseases  
XX  
SQ Sequence 22 BP; 2 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4149 CTGATTGTTCTCTGACCTGG 4169  
 |||||  
 DB 2 CTGATTGTTCTCTGACCTGG 22

## RESULT 3359

AAK83072  
 ID AAK83072 standard; DNA; 22 BP.

AC AAK83072;

DT 31-AUG-1999 (first entry)

XX Primer 5EU to detect mutations in the human WRN gene.

XX Human; WRN; Werner's syndrome; detection; diagnosis; autosomal; mutation;  
 KW recessive disorder; phenotype; primer; PCR; amplification; ss.

OS Synthetic.

OS Homo sapiens.

PN M09724435-A1.

PD 10-JUL-1997.

PF 30-DEC-1996; 96WO-US020785.

PR 29-DEC-1995; 95US-0009409P.

PR 29-DEC-1995; 95US-0058053P.

PR 30-JAN-1996; 96US-0010835P.

PR 30-JAN-1996; 96US-00594242.

PR 12-APR-1996; 96US-00632175.

XX (DARW-) DARWIN MOLECULAR CORP.

PI Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;

DR WPI; 1997-363671/33.

XX Isolated nucleic acid molecule encoding the WRN gene product - useful for  
 PT detection and treatment of Werner's syndrome, and related diseases.

XX Example 5; Page 48; 153pp; English.

CC Primers AAK83071-X83082 were used to PCR amplify, detect and identify  
 CC mutations in the human WRN gene (AAK83003) which encodes a protein  
 CC related to Werner's syndrome. The products can be used for the detection  
 CC and treatment of Werner's syndrome (WS), an autosomal recessive disorder  
 CC with a complex phenotype, as well as related diseases

XX Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7337 AGCTGTACCTGTGCAGTCCA 7357  
 |||||  
 DB 1 AGCTGTACCTGTGCAGTCCA 21

## RESULT 3360

AAK68896  
 ID AAK68896 standard; DNA; 22 BP.

AC AAK68896;

DT 06-APR-1998 (first entry)

DE Human BCR 5' RT-PCR primer.

XX Drug-resistance; neoplastic disease; non-malignant hematopoietic cell;  
 KW progenitor; gene rearrangement; RT-PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

PN M09718305-A2.

PD 22-MAY-1997.

PF 13-NOV-1996; 96WO-US018273.

PR 14-NOV-1995; 95US-0006692P.

XX (MINU) UNIV MINNESOTA.

PI Verfallle CM, McIvor RS, Zhao RC;

DR WPI; 1997-289281/26.

XX Expression cassette for forming drug resistant hematopoietic stem cells -  
 PT decreases RNA or protein found only in malignant cells; for treating  
 PT leukaemia(s), such as chronic myelogenous leukaemia.

XX Example 2; Fig 1; 52pp; English.

CC This RT-PCR 5' primer is designed to a human breakpoint cluster region  
 CC (BCR) and is used in a novel method of preparing drug-resistant, non-  
 CC malignant haematopoietic cells. This method involves the construction of  
 CC a new expression cassette comprising a first nucleic acid molecule which  
 CC encodes resistance of a host cell to a cytotoxic agent, operably linked  
 CC to a first promoter which functions in the host cell and a second nucleic  
 CC acid molecule operably linked to a second promoter which functions in the  
 CC host cell. The second nucleic acid molecule encodes an RNA molecule or a  
 CC polypeptide whose expression decreases the expression of an RNA or a  
 CC polypeptide present in a malignant cell only. This method can eliminate  
 CC residual neoplastic disease in a patient, where the disease has an  
 CC immature hematopoietic progenitor cell with a well-defined gene  
 CC rearrangement. Diseases such as chronic myelogenous leukaemia which is  
 CC associated with a BCR/ABL gene rearrangement, acute lymphoblastic  
 CC leukaemia and acute promyelocytic leukaemia may be treated using this  
 CC method

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2539 GAGCTCCAGTCTGTGACGTAC 2559  
 |||||  
 DB 2 GAGCTCCAGTCTGTGACGTAC 22

## RESULT 3361

AAT91777  
 ID AAT91777 standard; DNA; 22 BP.

AC AAT91777;

DT 25-MAR-2003 (revised)

DT 08-JAN-1998 (first entry)

DE Primer B3300b for bcr2-abl2 and bcr3-abl2 translocation regions.

XX PCR; primer; amplify; polymerase chain reaction; haematopoietic cell;  
 KW chronic myelogenous leukaemia; human; bcr2-abl2; translocation region;  
 KW cytogenetic remission; Ph chromosome; bcr3-abl2; CML cell;  
 KW acute lymphocytic leukaemia; ss.

OS Synthetic.

XX	M09706339-A1.
FN	
XX	
PD	06-MAR-1997.
XX	
PF	28-AUG-1995; 95MO-US010919.
XX	
PR	25-AUG-1995; 95US-00296258.
XX	
PA	(DADE-) DADE INT INC.
XX	
PI	Brown J, LockhartBruce C;
XX	
DR	WPI, 1997-179294/16.
PT	Detection of chronic myelogenous leukaemia cells - by amplification of RNA from haematopoietic cells with primers for the bcr2-abl2 and bcr3-
PR	abl2 trans-location regions.
XX	
PS	Example 1; Page 10; 79pp; English.
XX	
CC	AA191749-T91763, and AA191765-T91792 are primers used in the method of
CC	the invention. AA191754-T91759 can also be used as capture
CC	oligonucleotides (ON), while AA191760-T91763, AA191791 and AA191792 can
CC	also be used as detector agents. The method of the invention is for
CC	detecting or monitoring chronic myelogenous leukaemia (CML) cells in a
CC	human patient. The method comprises obtaining RNA from haematopoietic
CC	cells of the patient, and amplifying it using a pair of primers that
CC	amplify both the bcr2-abl2 and bcr3-abl2 translocation regions. The
CC	amplified sequence is contacted with a capture agent comprising a capture
CC	ON and a binding ligand to form a capture mixture. The capture ON is
CC	specific for the bcr2-abl2 and bcr3-abl2 translocation regions. The
CC	mixture is contacted with a solid phase coupled to a receptor specific
CC	for the binding ligand. The solid phase is washed, then contacted with a
CC	detector agent comprising a detector ON specific for the bcr2-abl2 or
CC	bcr3-abl2 translocation regions and a label. The amount of labelled
CC	detector ON bound to the solid phase is then correlated with the presence
CC	or quantity of CML cells in the patient. The method is to detect or
CC	monitor CML cells in patients. It can also be used prognostically to
CC	assess cytogenetic remission in patients with CML. The method detects
CC	both the bcr2-abl2 and the bcr3-abl2 translocations associated with CML.
CC	The assay does not detect CML in the absence of the Ph chromosome, nor
CC	does it detect acute lymphotropic leukaemia (ALL) even if the ALL
CC	patient has the Ph chromosome. (Updated on 25-MAR-2003 to correct FI
CC	field.)
XX	
SQ	Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match	0.2%; Score 14.6; DR 1; Length 22;
Best Local Similarity	81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	2539 GAGCTCGACATCTGACGTAC 2559
Db	 2 GAGCTGCAGATCTGACCAAC 22
RESULT 3362	
AAV29432	
ID	AAV29432 standard; DNA; 22 BP.
XX	
AC	AAV29432;
XX	
DT	31-JUL-1998 (first entry)
XX	
DE	Calcium ion channel alpha subunit exon 28 specific reverse primer.
XX	
KW	Calcium ion channel alpha subunit; human; episodic ataxia type 2; familial hemiplegic migraine; FHM; EA-2; treatment; diagnosis; PCR primer; ss.
XX	
KS	Synthetic.
OS	Homo sapiens.

XX	FN	EP834561-A1.
XX	PD	08-APR-1998.
XX	PE	27-SEP-1996; 96EP-00202707.
XX	PR	27-SEP-1996; 96EP-00202707.
XX	PA	(UYLE-) RIUKSUNIV LEIDEN.
XX	WP1,	1998-195461/18.
XX	PT	New human nucleic acid associated with migraine and episodic ataxia type 2.
XX	PS	Disclosure: Page 9; 157pp; English.
CC	XX	This primer is used for the PCR amplification of an exon of the human calcium ion channel alpha 1 subunit. The channel is related to familial hemiplegic migraine (FHM) and/or episodic ataxia type 2 (EA-2) and is derived from, related to or associated with a gene present in humans on chromosome 19p13.1-13.2. The encoding nucleic acid can be used to localise or identify genes related to episodic neurological disorders, specifically migraine, FHM or EA-2, but also epilepsy. It can also be used to distinguish between alleles of the corresponding gene. Cells and animals containing recombinant expression vectors comprising the nucleic acid can be useful in study, development and treatment of migraine, FHM, EA-2 and epilepsy. Proteins or peptides encoded by the nucleic acid and natural or synthetic antibodies against the proteins can be used to diagnose FHM, EA-2, migraine and other neurological conditions associated with cation channel dysfunction
CC	CC	Sequence 22 BP; 1 A; 10 C; 2 G; 9 T; 0 U; 0 Other;
CC	CC	Query Match 0.2%; Score 14.6; DB 1; Length 22; Best Local Similarity 81.0%; Pred. No. 2.4e+03; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY		4602 TTTTCCTGCCCCACGTCTTG 4622 1 TTTCCTGCCCATCTTCTTG 21
ID	AAV52673/C	RESULT 3363
XX	AAV52673	standard; DNA, 22 BP.
DT	AAV52673;	
XX	21-DEC-1998	(first entry)
DE	Hepatocyte nuclear factor 4 alpha gene exon 4 forward PCR primer.	
XX	Hepatocyte nuclear factor 4 alpha; HNF-4 alpha; MODY1; human;	
KW	transcription factor; maturity onset diabetes of the young; TCF14;	
OS	diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.	
OS	Synthetic.	
OS	Homo sapiens.	
PN	WO9811254-A1.	
XX	19-MAR-1998.	
PF	10-SEP-1997;	97WO-USO16037.
XX	10-SEP-1996;	96US-0025719P.
PR	02-OCT-1996;	96US-0028056P.
PR	30-OCT-1996;	96US-0029679P.
PA	(ARCH-) ARCH DEV CORP.	



CC (see AAV/0963-71). It includes the core motif GGGAA found in consensus  
CC recognition sequences for murine Ikaros protein isoforms mlk-1, mlk-2 and  
CC ,mlk-3 (see AAV52830-32). High affinity binding sites for Ikaros have been  
CC found in enhancer and promoter regions of the regulatory domains of the  
CC TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal repeat  
CC and in the regulatory domains of other T cell restricted antigens (see  
CC AAV5358-402) by gel retardation assay. Ikaros is involved in early  
CC differentiation of lymphocytes. The invention provides Ikaros nucleic  
CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host  
CC cells. These are used to treat T and B cell diseases, to control  
CC expression of heterologous genes placed under control of an Ikaros-  
CC responsive element, to treat nervous system diseases and to modulate cell  
CC division, amplification or differentiation, especially in haematopoietic  
CC cells  
CC XX  
SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2,4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 5690 TACCACGTTTGCCTTCCT 5710  
Db 21 TTCCCCGTTTGGTTTCCT 1  
RESULT 3365  
AAV66352  
AAV66352 standard; DNA; 22 BP.  
XX AC  
XX AAV66352;  
XX DT  
XX 06-JAN-1999 (first entry)  
DE CML-2 chromosomal translocation major breakpoint non-promoter primer.  
XX KM  
XX CML-2 chromosomal translocation t(14;18) major breakpoint;  
XX KM block splice template; autocatalytic RNA amplification; primer; ss.  
XX OS  
XX Synthetic.  
XX US5824518-A.  
XX PD  
XX 20-OCT-1998.  
XX PF  
XX 06-JUN-1995; 95US-00469067.  
XX PR  
XX 11-JUL-1989; 89US-00379501.  
XX PR 10-JUL-1990; 90US-00550837.  
XX PA  
XX (GENE-) GEN-PROBE INC.  
XX Pultz TU, Kacian DJ;  
XX Pultz TU, Kacian DJ;  
XX WPI; 1998-582557/49.  
XX  
XX Block splice template useful for amplification of nucleic acids -  
XX PT comprises two nucleic acid regions, the first region located 3' of the  
XX PT second region and blocked at its 3' terminus to inhibit primer extension  
XX PT by a DNA polymerase.  
XX  
XX Example 18; Col 43; 51pp; English.  
AAV6352-55 represent CML-2 chromosomal translocation t(14;18) major  
CC breakpoint amplification region non-promoter primers. The primers are  
CC used to exemplify the invention. The specification describes methods of  
CC synthesising multiple copies of a target nucleic acid sequence  
CC autocatalytically under conditions of substantially constant temperature,  
CC ionic strength and pH are provided in which multiple RNA copies of the  
CC target sequence autocatalytically generate additional copies. The target  
CC sequence is a block splice template which comprises two nucleic acid  
CC regions. The first region is located 3' of the second region and is  
CC blocked at its 3' terminus to inhibit primer extension by a DNA

CC polymerase, and the second region comprises a promoter sequence  
CC recognised by an RNA polymerase. The methods are used to amplify nucleic  
CC acids, especially RNA, for analysis, cloning or probe production  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2539 GAGCTCCAGATCCTGACGTAC 2559  
Db 2 GAGCTGCAGATGCTGACCAAC 22  
RESULT 3366  
AAV6350  
ID AAV6350 standard; DNA; 22 BP.  
XX  
AC AAV66350;  
XX  
DT 06-JAN-1999 (first entry)  
XX  
DE CML-2 chromosomal translocation t(9;22) primer.  
XX  
KM CML-2 chromosomal translocation t(9;22); block splice template;  
KM autocatalytic RNA amplification; primer; ss.  
XX  
OS Synthetic.  
XX  
PN US5824518-A.  
XX  
PD 20-OCT-1998.  
XX  
PF 06-JUN-1995; 95US-00469067.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Fullz TJ, Kacian DJ;  
XX  
DR WPI; 1998-582557/49.  
XX  
PT Block splice template useful for amplification of nucleic acids -  
PT comprises two nucleic acid regions, the first region located 3' of the  
PT second region and blocked at its 3' terminus to inhibit primer extension  
PT by a DNA polymerase.  
XX  
PS Example 15; Col 9; 51pp; English.  
XX  
CC AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,  
CC for the (+) and (-) strands respectively. The primers are used to  
CC exemplify the invention, together with probe AAV6351. The specification  
CC describes methods of synthesising multiple copies of a target nucleic  
CC acid sequence autocatalytically under conditions of substantially  
CC constant temperature, ionic strength and pH are provided in which  
CC multiple RNA copies of the target sequence autocatalytically generate  
CC additional copies. The target sequence is a block splice template which  
CC comprises two nucleic acid regions. The first region is located 3' of the  
CC second region and is blocked at its 3' terminus to inhibit primer  
CC extension by a DNA polymerase, and the second region comprises a promoter  
CC sequence recognised by an RNA polymerase. The methods are used to amplify  
CC nucleic acids, especially RNA, for analysis, cloning or probe production  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2539 GAGCTCCAGATCCTGACGTAC 2559

Db 2 GAGCTGCAGATGCTGACCAAC 22  
RESULT 3367  
AAV45541  
ID AAV45541 standard; DNA; 22 BP.  
XX  
AC AAV45541;  
XX  
DT 15-FEB-1999 (first entry)  
XX  
DE Helicobacter pylori babB gene PCR primer.  
XX  
KM Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;  
KM stomach cancer; babB gene; PCR; primer; ss.  
XX  
OS Synthetic.  
OS Helicobacter pylori.  
XX  
PN WO9844130-A1.  
XX  
PD 08-OCT-1998.  
XX  
PF 31-MAR-1998; 98WO-KR000073.  
XX  
PR 31-MAR-1997; 97KR-00011950.  
PR 31-MAR-1997; 97KR-00011951.  
XX  
PA (DAEW-) DAEWONG PHARM CO LTD.  
XX  
PI Kim B, Shin S, Yu Y, Park M, Choi D, Jung H;  
XX  
DR WPI; 1998-568279/48.  
XX  
PT New chimeric proteins for use against Helicobacter pylori - comprising an  
PT antigenic protein of H. pylori and A1 and B subunits of Vibrio cholerae  
PT toxin, preferably produced by recombinant techniques.  
XX  
PS Example 2-21; Page 15; 102pp; English.  
XX  
CC PCR primers (see AAV45541 and AAV45542) are designed for the PCR  
CC amplification of the Helicobacter pylori babB gene. The invention relates  
CC to recombinant DNA (see AAV62460-61) comprising a fusion gene prepared by  
CC ligating an antigenic determinant coding gene (e.g. the babB gene) of H.  
CC pylori and A2 and B subunit genes of Vibrio cholerae. Also claimed are  
CC chimeric proteins (see AAW80599-600) encoded by such recombinant DNA,  
CC methods for the recombinant production of the chimeric proteins, and use  
CC of the chimeric proteins in preventative and therapeutic vaccines for H.  
CC pylori-associated diseases such as gastritis, gastric ulcer, duodenal  
CC ulcer and gastric cancer  
XX  
SQ Sequence 22 BP; 9 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2015 GAGCGATGGGAAAAAACCTT 2035  
Db 1 CCGTGCATGAAAAAACCTT 21  
RESULT 3368  
AAV67083/C  
ID AAV67083 standard; cDNA; 22 BP.  
XX  
AC AAV67083;  
XX  
DT 14-JAN-1999 (first entry)  
XX  
DE Mouse TCR-delta enhancer deltaE5.  
XX

KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;  
 KW differentiation marker; immune system; corpus striatum; AIDS;  
 XX Alzheimer's disease; ss.  
 OS Mus sp.  
 XX Synthetic.  
 XX US5824770-A.  
 XX 20-OCT-1998.  
 XX 05-JUN-1995; 95US-00465590.  
 XX 14-SEP-1992; 92US-00946233.  
 PR 14-SEP-1993; 93US-00121438.  
 PR 02-MAY-1994; 94US-00238212.  
 XX (GHEO ) GEN HOSPITAL CORP.  
 XX Georgopoulos K;  
 PI WPI; 1998-582621/49.  
 DR Ikaros poly:peptide(s) - useful for treating disorders of immune system  
 XX or corpus striatum.  
 PT Disclosure; Col 26; 11pp; English.  
 XX  
 PS The present invention describes a purified peptide having at least one of  
 CC the following properties: (a) it stimulates transcription of a DNA  
 CC sequence under the control of a delta A element, an NFKB element or an  
 CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of  
 CC a delta A element, an NFKB element or an Ikaros binding oligonucleotide  
 CC consensus sequence; (c) it competitively inhibits the binding of a  
 CC naturally occurring Ikaros isoform to any of a delta A element, an NFKB  
 CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it  
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
 CC (e) it inhibits protein-protein interactions of transcriptional complexes  
 CC formed with naturally occurring Ikaros isoforms. The proteins, provided  
 CC that they stimulate gene transcription under the control of delta A  
 CC elements, NFKB elements and/or Ikaros-binding oligonucleotides, bind to  
 CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
 CC delta A elements, NFKB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
 CC inhibit protein-protein interactions of transcriptional complexes with  
 CC naturally occurring Ikaros isoforms, can be used to treat immune system  
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
 CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
 CC given in the present invention  
 XX  
 SQ Sequence 22 BP; 12 A; 3 C; 7 G; 0 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No.2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5690 TACCACTGTTTGGCTTCTT 5710  
 DB 21 TTCCCTGTGTTGGTTCCTT 1  
 RESULT 3369  
 AAT99486  
 ID AAT99486 standard; DNA; 22 BP.  
 XX  
 AC AAT99486;  
 XX  
 XX 21-MAY-1998 (first entry)  
 DT Human ST receptor PCR primer.  
 XX  
 DE ST receptor; heat stable toxin receptor; colorectal cancer; tumour;  
 KW

KW metastasis; diagnosis; human; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX Homo sapiens.  
 XX WO9742506-A1.  
 XX 13-NOV-1997.  
 XX 02-MAY-1997; 97WO-US007467.  
 XX 03-MAY-1996; 96US-0016564P.  
 XX (UYJE-) UNIV JEFFERSON THOMAS.  
 XX Waldman SA, Carrithers SL;  
 PI WPI; 1998-008454/01.  
 DR  
 XX  
 XX Determining whether an individual has metastasised colorectal cancer  
 PT cells and origin of tumour cells - by detecting presence of heat-stable  
 PT toxin receptor on cells in a sample.  
 XX  
 PS Claim 14; Page 53; 62pp; English.  
 XX  
 CC Claimed PCR primers (see AAT99462-199531) hybridise to sequences that  
 CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
 CC protein (see AAW37371), a highly specific marker for metastasised  
 CC colorectal cancer cells. PCR using these primers provides specific and  
 CC sensitive detection of human ST receptor expression. A specific primer  
 CC pair comprises the primers given in AAT99486 and AAT99487. Claimed in  
 CC vitro methods for determining whether or not (i) an individual has  
 CC metastasised colorectal cancer cells, or (ii) a tumour cell is a  
 CC colorectal cancer cell comprise the steps of examining a sample of  
 CC extraintestinal tissue and/or body fluids or tumour cells from an  
 CC individual to determine whether ST receptor protein is being expressed by  
 CC cells in the sample. Expression is determined by immunoassay or by PCR  
 CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
 CC AAT97229)  
 XX  
 SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No.2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3199 AGTGAGGGGCTTGGAAGTG 3219  
 DB 2 AATGAGGGGCTTGGAATATG 22  
 RESULT 3370  
 AAT99484  
 ID AAT99484 standard; DNA; 22 BP.  
 XX  
 AC AAT99484;  
 XX  
 XX 21-MAY-1998 (first entry)  
 DT Human ST receptor PCR primer.  
 XX  
 DE Human ST receptor PCR primer.  
 XX  
 KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;  
 KW metastasis; diagnosis; human; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX Homo sapiens.  
 XX WO9742506-A1.  
 XX 13-NOV-1997.  
 PD 02-MAY-1997; 97WO-US007467.  
 PF

PR 03-MAY-1996; 96US-0016564P.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Waldman SA, Carrithers SL;  
 XX  
 DR WPI; 1998-008454/01.  
 XX  
 PT Determining whether an individual has metastasised colorectal cancer  
 PT cells and origin of tumour cells - by detecting presence of heat-stable  
 PT toxin receptor on cells in a sample.  
 PS  
 XX Claim 14; Page 53; 62pp; English.  
 CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that  
 CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
 CC protein (see AAW37371), a highly specific marker for metastasised  
 CC colorectal cancer cells. PCR using these primers provides specific and  
 CC sensitive detection of human ST receptor expression. A specific primer  
 CC pair comprises the primers given in AAT99484 and AAT99485. Claimed in  
 CC vitro methods for determining whether or not (i) an individual has  
 CC metastasised colorectal cancer cells, or (ii) a tumour cell is a  
 CC colorectal cancer cell comprise the steps of examining a sample of  
 CC extraintestinal tissue and/or body fluids or tumour cells from an  
 CC individual to determine whether ST receptor protein is being expressed by  
 CC cells in the sample. Expression is determined by immunosassay or by PCR  
 CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
 CC AAT97229)  
 XX  
 SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3199 AGTGGGGGCTTGAGAAAGTG 3219  
 Db 2 AATGAGGGGCTGGAATAGTG 22  
 RESULT 3371  
 AAT99494  
 ID AAT99494 standard; DNA; 22 BP.  
 XX  
 AC AAT99494;  
 XX  
 DT 21-MAY-1998 (first entry)  
 XX  
 DE Human ST receptor PCR primer.  
 XX  
 KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;  
 KW metastasis; diagnosis; human; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09742506-A1.  
 PD 13-NOV-1997.  
 XX  
 PF 02-MAY-1997; 97WO-US007467.  
 XX  
 PR 03-MAY-1996; 96US-0016564P.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Waldman SA, Carrithers SL;  
 XX  
 DR WPI; 1998-008454/01.  
 XX  
 PT Determining whether an individual has metastasised colorectal cancer  
 PT cells and origin of tumour cells - by detecting presence of heat-stable  
 PT toxin receptor on cells in a sample.

XX  
 PS Claim 14; Page 53; 62pp; English.  
 XX  
 CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that  
 CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
 CC protein (see AAW37371), a highly specific marker for metastasised  
 CC colorectal cancer cells. PCR using these primers provides specific and  
 CC sensitive detection of human ST receptor expression. A specific primer  
 CC pair comprises the primers given in AAT99494 and AAT99495. Claimed in  
 CC vitro methods for determining whether or not (i) an individual has  
 CC metastasised colorectal cancer cells, or (ii) a tumour cell is a  
 CC colorectal cancer cell comprise the steps of examining a sample of  
 CC extraintestinal tissue and/or body fluids or tumour cells from an  
 CC individual to determine whether ST receptor protein is being expressed by  
 CC cells in the sample. Expression is determined by immunosassay or by PCR  
 CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
 CC AAT97229)  
 XX  
 SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3201 TGAAGGGGCTTGAGAAAGTG 3221  
 Db 2 TGAAGGGGCTGGAATAGTG 22  
 RESULT 3372  
 AAT99490  
 ID AAT99490 standard; DNA; 22 BP.  
 XX  
 AC AAT99490;  
 XX  
 DT 21-MAY-1998 (first entry)  
 XX  
 DE Human ST receptor PCR primer.  
 XX  
 KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;  
 KW metastasis; diagnosis; human; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09742506-A1.  
 PD 13-NOV-1997.  
 XX  
 PF 02-MAY-1997; 97WO-US007467.  
 XX  
 PR 03-MAY-1996; 96US-0016564P.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Waldman SA, Carrithers SL;  
 XX  
 DR WPI; 1998-008454/01.  
 XX  
 PT Determining whether an individual has metastasised colorectal cancer  
 PT cells and origin of tumour cells - by detecting presence of heat-stable  
 PT toxin receptor on cells in a sample.  
 PS  
 XX Claim 14; Page 53; 62pp; English.  
 CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that  
 CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
 CC protein (see AAW37371), a highly specific marker for metastasised  
 CC colorectal cancer cells. PCR using these primers provides specific and  
 CC sensitive detection of human ST receptor expression. A specific primer  
 CC pair comprises the primers given in AAT99490 and AAT99491. Claimed in  
 CC vitro methods for determining whether or not (i) an individual has  
 CC metastasised colorectal cancer cells, or (ii) a tumour cell is a

CC colorectal cancer cell comprise the steps of examining a sample of  
CC extraintestinal tissue and/or body fluids or tumour cells from an  
CC individual to determine whether ST receptor protein is being expressed by  
CC cells in the sample. Expression is determined by immunosassay or by PCR  
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
CC AA1972229)

XX  
SQ Sequence 22 BP; 8 A; 1 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3199 AGTGGGGGCTTGGAAGTG 3219  
DB 1 AATGAGGGGCTGGAATAGTG 21

RESULT 3373

AAT99496  
ID AAT99496 standard; DNA; 22 BP.

XX  
AC AAT99496;

DT 21-MAY-1998 (first entry)

XX  
DE Human ST receptor PCR primer.

XX  
KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;

KW metastasis; diagnosis; human; PCR; primer; ss.

XX  
OS Synthetic.

OS Homo sapiens.

XX  
PN WO9742506-A1.

PD 13-NOV-1997.

XX  
PF 02-MAY-1997; 97WO-US007467.

XX  
PR 03-MAY-1996; 96US-0016564P.

XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.

XX  
PI Waldman SA, Carrithers SL;

XX  
DR WPI; 1998-008454/01.

PT Determining whether an individual has metastasised colorectal cancer  
PT cells and origin of tumour cells - by detecting presence of heat-stable  
PT toxin receptor on cells in a sample.

XX  
PS Claim 14; Page 53; 62pp; English.

CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that  
CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
CC protein (see AA197371), a highly specific marker for metastasised  
CC colorectal cancer cells. PCR using these primers provides specific and  
CC sensitive detection of human ST receptor expression. A specific primer  
CC pair comprises the primers given in AAT99496 and AAT99497. Claimed in  
CC vitro methods for determining whether or not (i) an individual has  
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a  
CC colorectal cancer cell comprise the steps of examining a sample of  
CC extraintestinal tissue and/or body fluids or tumour cells from an  
CC individual to determine whether ST receptor protein is being expressed by  
CC cells in the sample. Expression is determined by immunosassay or by PCR  
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
CC AA1972229)

XX  
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3201 TGAAGGGGCTTGGAAGTG 3221  
DB 2 TGAAGGGGCTGGAATAGTG 22

RESULT 3374

AAT99488  
ID AAT99488 standard; DNA; 22 BP.

XX  
AC AAT99488;

DT 21-MAY-1998 (first entry)

XX  
DE Human ST receptor PCR primer.

XX  
KW ST receptor; heat stable toxin receptor; colorectal cancer; tumour;

KW metastasis; diagnosis; human; PCR; primer; ss.

XX  
OS Synthetic.

OS Homo sapiens.

XX  
PN WO9742506-A1.

PD 13-NOV-1997.

XX  
PF 02-MAY-1997; 97WO-US007467.

XX  
PR 03-MAY-1996; 96US-0016564P.

XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.

XX  
PI Waldman SA, Carrithers SL;

XX  
DR WPI; 1998-008454/01.

PT Determining whether an individual has metastasised colorectal cancer  
PT cells and origin of tumour cells - by detecting presence of heat-stable  
PT toxin receptor on cells in a sample.

XX  
PS Claim 14; Page 53; 62pp; English.

CC Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that  
CC encode the extracellular domain of human heat-stable toxin (ST) receptor  
CC protein (see AA197371), a highly specific marker for metastasised  
CC colorectal cancer cells. PCR using these primers provides specific and  
CC sensitive detection of human ST receptor expression. A specific primer  
CC pair comprises the primers given in AAT99488 and AAT99489. Claimed in  
CC vitro methods for determining whether or not (i) an individual has  
CC metastasised colorectal cancer cells, or (ii) a tumour cell is a  
CC colorectal cancer cell comprise the steps of examining a sample of  
CC extraintestinal tissue and/or body fluids or tumour cells from an  
CC individual to determine whether ST receptor protein is being expressed by  
CC cells in the sample. Expression is determined by immunosassay or by PCR  
CC using primers that selectively amplify ST receptor cDNA or mRNA (see also  
CC AA1972229)

XX  
SQ Sequence 22 BP; 7 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3199 AGTGGGGGCTTGGAAGTG 3219  
DB 2 AATGAGGGGCTGGAATAGTG 22

RESULT 3375

AAT99492  
ID AAT99492 standard; DNA; 22 BP.

XX

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AC AAT99492;
XX
XX 21-MAY-1998 (first entry)
XX
XX Human ST receptor PCR primer.
XX
XX ST receptor; heat stable toxin receptor; colorectal cancer; tumour;
XX metastasis; diagnosis; human; PCR; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9742506-A1.
XX
XX 13-NOV-1997.
XX
XX 02-MAY-1997; 97WO-US007467.
XX
XX 03-MAY-1996; 96US-0016564P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Waldman SA, Carrithers SL;
XX
XX WPI; 1998-008454/01.
XX
XX Determining whether an individual has metastasised colorectal cancer
XX PT cells and origin of tumour cells - By detecting presence of heat-stable
XX PT toxin receptor on cells in a sample.
XX
XX
XX Claim 14; Page 53; 62pp; English.
XX
XX Claimed PCR primers (see AAT99462-T99531) hybridise to sequences that
XX encode the extracellular domain of human heat-stable toxin (ST) receptor
XX protein (see AAW37371), a highly specific marker for metastasised
XX colorectal cancer cells. PCR using these primers provides specific and
XX sensitive detection of human ST receptor expression. A specific primer
XX pair comprises the primers given in AAT99492 and AAT99493. Claimed in
XX vitro methods for determining whether or not (i) an individual has
XX metastasised colorectal cancer cells, or (ii) a tumour cell is a
XX colorectal cancer cell comprise the steps of examining a sample of
XX extraintestinal tissue and/or body fluids or tumour cells from an
XX individual to determine whether ST receptor protein is being expressed by
XX cells in the sample. Expression is determined by immunosassay or by PCR
XX using primers that selectively amplify ST receptor cDNA or mRNA (see also
XX AAT97229)
XX
XX
XX Sequence 22 BP; 8 A; 1 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3199 AGTGGGGCTTGGAGAAAGTG 3219
XX | | | | | | | | | | | | | | | | | | | |
XX 1 AATGAGGGGCTGAAATAGTG 21
XX
XX
XX RESULT 3376
XX AAV27972
XX ID AAV27972 standard; DNA; 22 BP.
XX
XX AAV27972;
XX
XX 25-SEP-1998 (first entry)
XX
XX Ataxia telangiectasia exon 8 primer 1.
XX
XX ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
XX radiation; breast cancer.
XX
XX Synthetic.
XX Homo sapiens.
XX

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XX
XX WO9822621-A1.
XX
XX 28-MAY-1998.
XX
XX 17-NOV-1997; 97WO-US020953.
XX
XX 20-NOV-1996; 96US-00753147.
XX
XX (VIRG-) VIRGINIA MASON RES CENT.
XX
XX Concanon P;
XX
XX WPI; 1998-312503/27.
XX
XX Method of detecting ataxia telangiectasia - comprises use of primers
XX PT based on intron-exon boundaries, useful for diagnosing disease in
XX PT heterozygotes.
XX
XX
XX Claim 6; Page 5; 47pp; English.
XX
XX The primers AAV27964-V28086 are used to amplify ataxia telangiectasia
XX CC (ATM) exons and their adjacent splice junction sites. These can be used
XX CC as a method of detecting a mutation in the ATM gene by comparing the PCR
XX CC products of amplification from a sample from a patient suspected of
XX CC having an ATM mutation with a sample from a non-mutated ATM patient. This
XX CC method is especially useful for diagnosing ataxia telangiectasia in
XX CC heterozygotes and can be used to locate the positions of the mutation.
XX CC The diagnosis of ataxia telangiectasia in patients needing therapeutic
XX CC radiation will prevent fatal radiation burns and the development of
XX CC breast cancer which can occur
XX
XX
XX Sequence 22 BP; 4 A; 1 C; 6 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 6469 TTTTCTGTTGTAATAGG 6489
XX | | | | | | | | | | | | | | | | | | | |
XX 1 TTTTCTGTAATAGGATTAGG 21
XX
XX
XX RESULT 3377
XX AAV16099/c
XX ID AAV16099 standard; DNA; 22 BP.
XX
XX AAV16099;
XX
XX 07-JUL-1998 (first entry)
XX
XX PGST97-delta-N238 primer.
XX
XX Glutathione-S-transferase-U97 fusion Protein; GST; ss; primer;
XX KM amplification; PCR; CMV; protein kinase.
XX
XX Synthetic.
XX OS Human herpesvirus 5.
XX
XX WO9804747-A1.
XX
XX 05-FEB-1998.
XX
XX 25-JUL-1997; 97WO-US013340.
XX
XX 26-JUL-1996; 96US-0022888P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Coen D;
XX
XX WPI; 1998-130727/12.
XX

```

PT Assay for detecting modulating agents of UL97 protein kinase - useful  
CC for, e.g. preparation of therapeutics for treatment of cytomegalovirus  
PT infections.  
XX  
XX Disclosure: Page 15; 57pp; English.  
XX  
CC The pGST97-delta-N238 primer was used with pGST97 reverse primer  
CC (AAV16101) to amplify the corresponding fragments by PCR, using  
CC linearised pGST-UL97 as a template. The PCR product would encode for a  
CC glutathione-S-transferase (GST)- human cytomegalovirus (CMV) UL97 fusion  
CC protein in which the N-terminal region of the latter protein was  
CC truncated by 238 residues. Truncation of the N-terminal region of UL97  
CC protein kinase (see also AAV16098 and AAV16100) was carried out to  
CC investigate any changes in enzyme activity. It was determined that  
CC truncation of the first 303 N-terminal residues totally abolished  
CC enzymatic activity indicating that the N-terminal region was involved in  
CC kinase activity. The invention provides an assay method for the detection  
CC of agents that inhibit or enhance activity of the CMV UL97 protein  
CC kinase. GST-UL97 fusion protein confers an advantage in this method as it  
CC is more soluble, without loss of enzymatic activity, than UL97 protein.  
CC The invention claims that by using an optionally modified polypeptide  
CC which contains a UL97 phosphorylation consensus sequence, the assay  
CC method can be extended for usage in therapeutic compositions which can be  
CC used for treating CMV infections  
CC  
SQ Sequence 22 BP; 1 A; 11 C; 9 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Oy 109 CGAGCCCGCCCGGATCCCG 129  
Db 21 CGGCCCGGCGCCGCGATCCG 1  
  
RESULT 3378  
AA81911  
ID AA81911 standard; DNA; 22 BP.  
XX  
XX AA81911;  
XX  
XX 02-SEP-1999 (first entry)  
XX  
XX PCR primer used to amplify human TCR V beta genes.  
XX  
XX Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;  
XX V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 8;  
XX multiple sclerosis; PCR primer; ss.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX MO9927957-A1.  
XX  
XX 10-JUN-1999.  
XX  
XX 03-DEC-1997; 97WO-US023147.  
XX  
XX 03-DEC-1997; 97WO-US023147.  
XX  
XX 03-DEC-1997; 97WO-US023147.  
XX  
XX (IMMU-) IMMUNE RESPONSE CORP.  
XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.  
XX  
XX Brostoff SW, Wilson DB, Smith LR, Gold DP, Carlo DJ;  
XX WPI; 1999-404801/34.  
XX  
XX DR WPI; 1999-404801/34.  
XX  
XX T0 cell receptor peptide-derived vaccines.  
XX  
XX Example 10; Page 41; 104pp; English.  
XX  
XX The specification describes vaccines which comprise immunologically

CC effective amounts of T cell receptor (TCR) peptides. The TCRs are present  
CC on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta  
CC 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta  
CC TCR peptide-based vaccines are useful for prevention or treatment of  
CC multiple sclerosis. The presence of V beta 6.7 appears to be particularly  
CC associated with multiple sclerosis and can be used to determine an  
CC individual's susceptibility to multiple sclerosis. Vaccinating, rather  
CC than passively administering heterologous antibodies, allows the host's  
CC own immune system to mobilize and suppress auto aggressive T cells.  
CC Therefore, the suppression is persistent and may involve any and all  
CC immunological mechanisms in effecting that suppression. Such a multi-  
CC faceted response is more effective than the uni-dimensional suppression  
CC achieved by passive administration of monoclonal antibodies or extant-  
CC derived regulatory T cell clones. PCR primers AA81982-X81914 were used  
CC to amplify and analyse human TCR V beta genes, in the course of the  
CC invention  
CC  
SQ Sequence 22 BP; 4 A; 6 C; 5 G; 7 T; 0 U; 0 Other;  
  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Oy 4141 CTGTGACCTGATTGTTCTC 4161  
Db 1 CAGTGACCTGAGTTGTTCTC 21  
  
RESULT 3379  
AA239210/c  
ID AA239210 standard; DNA; 22 BP.  
XX  
XX AA239210;  
XX  
XX 11-FEB-2000 (first entry)  
XX  
XX HLA allele DRB1\*0820 exon 2 amplifying primer.  
XX  
XX  
XX Human leukocyte antigen; HLA; allele; HLA-B\*3913; HLA-B\*1406; human;  
XX HLA-B\*51; HLA-DRB1\*0820; HLA-DRB1\*04; allele typing; exon;  
XX major histocompatibility complex; MHC; PCR primer; ss.  
XX  
XX Synthetic.  
XX OS Homo sapiens.  
XX  
XX MO9954496-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 19-APR-1999; 99WO-EP002614.  
XX  
XX 20-APR-1998; 98EP-00870088.  
XX  
XX (INNO-) INNOGENETICS NV.  
XX  
XX De Canck I, Merssch G, Rousseau R;  
XX WPI; 1999-634008/54.  
XX  
XX New polynucleotides for human leukocyte antigen, HLA, allele fragments,  
XX useful for typing HLA alleles.  
XX  
XX Claim 4; Page 7; 62pp; English.  
XX  
XX The invention provides polynucleotides corresponding to exon 2 and exon 3  
XX of human leukocyte antigen (HLA) alleles HLA-B\*3913, HLA-B\*1406 and HLA-  
XX B\*51 and exon 2 of HLA alleles HLA-DRB1\*0820, HLA-DRB1\*04 and HLA-  
XX DRB4\*01. The polynucleotides are useful for typing the above HLA alleles  
XX in a sample, especially by a method that comprises (a) amplifying  
XX all/part of the relevant sequence using at least one primer pair; and (b)  
XX hybridizing the amplified product to a set of probes specifically  
XX hybridizing to target regions comprising one or more polymorphic  
XX nucleotides of the sequence, to determine the absence or presence of the





```
RESULT 3382
AA30126
ID AAX30126 standard; DNA; 22 BP.
XX
AC AAX30126;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human APRIL PCR primer #1.
XX
KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
KW immune disorder; cancer; PCR primer; ss.
XX
OS Synthetic.
XX
PN MO9912965-A2.
XX
PD 18-MAR-1999.
XX
PP 11-SEP-1998; 98MO-US019191.
XX
PR 12-SEP-1997; 97US-0058786P.
PR 26-MAR-1998; 98US-0079384P.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Techopp J;
PI 1999-215028/18.
XX
DR WPI; 1999-215028/18.
XX
PT A Proliferating Inducing Agent (APRIL), a member of the Tumour Necrosis
PT Factor Family - useful as diagnostic agents and for prevention or
PT treatment of immune disorders and cancer.
XX
PS Example 1; Page 30; 47pp; English.
XX
CC The present sequence represents a PCR primer for human APRIL (a
CC proliferating inducing agent). APRIL is a member of the tumour necrosis
CC factor family, and essentially free of normally associated proteins.
CC APRIL and APRIL antibodies are useful in pharmaceutical compositions for
CC preventing or reducing severity of an autoimmune disease or an immune
CC response to tissue graft. The composition is also useful for stimulating
CC or suppressing the immune system, and treating cancer. APRIL is also
CC useful for treating APRIL-related disorders by delivering via a vector
CC (preferably viral vector) (gene therapy) into a mammalian (preferably
CC human) cell. Labeled APRIL and fragments are useful for identifying APRIL
CC receptors by screening compositions. Antisense DNA and antibodies and
CC modified APRIL (preferably an anti-APRIL receptor antibody) are useful as
CC blocking agents for inducing cell death by interfering with APRIL
CC receptors. The blocking agent is preferably administered with interferon-
CC c, and treats, suppresses or alters an immune response involving a
CC signalling pathway between APRIL and its receptor (preferably involving
CC human carcinoma cells); and also treats, suppresses or alters the
CC progression of cancer (preferably at least one chemotherapeutic agent is
CC also administered, and radiation therapy is also given to the patient
XX
SQ Sequence 22 BP; 2 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 5651 CCAGCCTCAGCTCTTACTTG 5671
DB 1 CCAGCCTCAGCTCTTCTTG 21
XX
RESULT 3383
AAX34398
ID AAX34398 standard; DNA; 22 BP.
XX
AC AAX34398;
XX
```

```
XX
DT 16-JUL-1999 (first entry)
XX
DE S. aureus 3-hydroxyacyl-CoA dehydrogenase gene hcd probe.
XX
KW 3-hydroxyacyl-CoA dehydrogenase; hcd; infection; Helicobacter pylori;
KW tissue; wound; skin; connective tissue; implant; mucous membrane; mouth;
KW throat; mammary gland; urethra; vagina; probe; hybridisation; ss.
XX
OS Synthetic.
XX
PN MO9918117-A1.
XX
PD 15-APR-1999.
XX
PP 02-OCT-1998; 98MO-US020636.
XX
PR 03-OCT-1997; 97US-0060983P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (BGHM ) BRIGHAM & WOMEN'S HOSPITAL.
PA (VIRU-) VIRUS RES INST.
XX
PI Palmer L, Pratt JM, Lometto MA, Hodgson JE, Nicholas RO;
PI Beattie DT, Deresiewicz RL, Lowe A;
PI 1999-263995/22.
XX
DR WPI; 1999-263995/22.
XX
PT New isolated 3-hydroxyacyl-CoA dehydrogenase polynucleotides.
PT Example 2; Page 55; 75pp; English.
XX
PS This sequence represents a probe used to detect the coding region for a
PS novel 3-hydroxyacyl-CoA dehydrogenase (hcd) from Staphylococcus aureus
PS (AAX34393). The products can be used to prevent or treat bacterial
PS infection, e.g. S. aureus infection or Helicobacter pylori infection.
CC They can also be used for preventing invasion of bacteria in damaged
CC tissue including wounds in skin or connective tissue caused, e.g. by
CC mechanical, chemical, thermal or radiation damage or by implantation of
CC indwelling devices, or wounds in the mucous membranes, such as the mouth,
CC throat, mammary glands, urethra or vagina
XX
SQ Sequence 22 BP; 5 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2158 ATCCATTCACAGTCCACC 2178
DB 1 AGCCATTTCGCAAGGCCACC 21
XX
RESULT 3384
AAX32149/c
ID AAX32149 standard; DNA; 22 BP.
XX
AC AAX32149;
XX
DT 14-JUN-1999 (first entry)
XX
DE BRCA2 gene specific primer.
XX
KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW CTRR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW BAP1 gene; PCR primer; ss.
XX
OS Synthetic.
XX
```

PN W0906598-A2.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 04-AUG-1998; 98WO-US016574.  
 XX  
 PR 04-AUG-1997; 97US-00905772.  
 XX 22-MAY-1998; 98US-00084471.  
 PA (ONCO-) ONCOMED INC.  
 XX  
 PI Murphy PD;  
 XX  
 DR WPI; 1999-153820/13.  
 XX  
 PT Determining common functional alleles in a population - useful in the  
 PT diagnosis of disease associated with allelic heterogeneity.  
 XX  
 PS Example 5; Page 37; 78pp; English.  
 XX  
 CC The invention relates to methods of determining a functional allele  
 CC profile of a gene in a population. Functional allele profiles comprise  
 CC the commonly occurring alleles in a population, and the relative  
 CC frequencies at which such alleles of a given gene occur. The methods are  
 CC used to identify and determine the frequency of the functional alleles of  
 CC genes which display extensive allelic heterogeneity, particularly those  
 CC implicated in disease or conditions, such as the BRCA1 gene associated  
 CC with breast cancer, CTR associated with cystic fibrosis, dystrophin  
 CC associated with Duchenne muscular dystrophy and Becker muscular  
 CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can  
 CC also be employed for diseases where allelic and genetic heterogeneity  
 CC exist, such as breast cancer, neurofibromatosis, and hereditary non-  
 CC polyposis colorectal cancer. Identification of functional alleles is  
 CC necessary for identification of mutations which may be implicated in the  
 CC disease. Sequences AA032001-172 represent primers for determining the  
 CC functional allele profiles of various genes. The primers are specific for  
 CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene  
 XX  
 SQ Sequence 22 BP; 13 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 7307 CTTGAGATTGCTTGTGCT 7327  
 DB 22 CTTGAGATTGCTTGTGCT 2  
 RESULT 3385  
 AA0209309/c  
 ID AA0209309 standard; DNA; 22 BP.  
 XX  
 AC AA0209309;  
 XX  
 DT 26-OCT-1999 (first entry)  
 XX  
 DE Human macrophage stimulating protein PCR primer 1.  
 XX  
 KW Macrophage stimulating protein; MSP; human; modulator; proliferation;  
 KW differentiation; intestinal epithelium; colon crypt; treatment; cancer;  
 KW haematopoietic disorder; megakaryocyte deficiency; gastrointestinal;  
 KW chemotherapeutic agent; gut toxicity; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5948892-A.  
 XX  
 PD 07-SEP-1999.  
 XX  
 PF 16-DEC-1996; 96US-00766982.  
 XX

PR 16-DEC-1996; 96US-00766982.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Wahl RC;  
 XX  
 DR WPI; 1999-517975/43.  
 XX  
 PT Analogues of macrophage stimulating protein for treating gastrointestinal  
 PT or haematopoietic disorders.  
 XX  
 PS Example 5; Col 23-24; 23pp; English.  
 XX  
 CC This invention describes a novel purified and isolated analogue of mature  
 CC macrophage stimulating protein (MSP) having at least one unpaired  
 CC cysteine residue substituted with another amino acid which modulates the  
 CC proliferation or differentiation of the intestinal epithelium. The  
 CC product of the invention binds to RON (a cell membrane protein tyrosine  
 CC kinase which is a member of the c-met family) to promote the formation of  
 CC colon crypts. MSP analogues are useful for the treatment of conditions  
 CC requiring the administration of MSP, such conditions include  
 CC haematopoietic disorders such as those involving a deficiency of  
 CC megakaryocytes and gastrointestinal disorders such as ulcerative colitis,  
 CC Crohn's disease and infections. The MSP analogues are useful for  
 CC maintaining and repairing the epithelial lining in the treatment of  
 CC cancer, where the aggressive use of chemotherapeutic agents or the use of  
 CC whole body radiation may lead to gut toxicity. The MSP analogues, which  
 CC have a higher activity than normal human MSP are effective at smaller  
 CC dosages, or optionally, they may be administered less frequently than  
 CC human MSP. This sequence represents a PCR primer used to amplify the  
 CC human MSP described in the method of the invention  
 XX  
 SQ Sequence 22 BP; 5 A; 7 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2826 TTCCAGACCCGAGGCTGTG 2846  
 DB 21 TTCCAGACCCGAGGCTGTG 1  
 RESULT 3386  
 AA027795/c  
 ID AA027795 standard; DNA; 22 BP.  
 XX  
 AC AA027795;  
 XX  
 DT 23-DEC-1999 (first entry)  
 XX  
 DE PCR primer for human DNA marker clone G212.  
 XX  
 KW Tandem repeat sequence; DNA isolation; intermediate tandem repeat;  
 KW ITR sequence; pentanucleotide tandem repeat; stutter artifact;  
 KW DNA typing; DNA profiling; linkage analysis; criminal justice;  
 KW paternity testing; animal lineage analysis; microsatellite loci;  
 KW polymorphism detection; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09940194-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 04-FEB-1999; 99WO-US002345.  
 XX  
 PR 04-FEB-1998; 98US-00018584.  
 XX  
 PA (FROM-) PROMEGA CORP.  
 XX  
 PI Schumm JW, Bacher JW;  
 XX

XX DR WPI; 1999-590696/50.  
 XX XX Isolating DNA containing intermediate tandem repeat sequences, useful in  
 PT DNA profiling.  
 XX PS Claim 30; Page 21; 111pp; English.  
 XX CC This sequence is a PCR primer for a human DNA marker clone used in the  
 CC method of the invention. The method is for isolating a fragment of DNA  
 CC containing an intermediate tandem repeat (ITR) sequence using  
 CC hybridization selection, and comprises: (a) providing several DNA  
 CC fragments, at least one of which contains an ITR sequence, a region of  
 CC the DNA fragment which contains at least one repeat unit consisting of a  
 CC sequence of five, six or seven bases repeated in tandem at least two  
 CC times; (b) providing a stationary support having at least one  
 CC oligonucleotide associated with it, where the oligonucleotide includes a  
 CC sequence of nucleotides which is complementary to a portion of the ITR  
 CC sequence; and (c) combining the DNA fragments with the support under  
 CC conditions where the DNA fragments including the DNA fragment containing  
 CC the ITR sequence hybridize to the support. The method is particularly  
 CC well suited to isolate DNA containing pentanucleotide tandem repeat sequences as  
 CC well as to detect target ITR DNA sequences having a low incidence of  
 CC stutter artifacts (no more than 2.4%). The method is useful in DNA  
 CC profiling for linkage analysis, criminal justice, paternity testing and  
 CC other forensic and medical uses. DNA typing is also useful for confirming  
 CC the lineage of horses, dogs and other prize animals. The invention  
 CC overcomes problems related to the use of microsatellite loci in DNA  
 CC profiling. The method can detect polymorphisms with a low incidence of  
 CC stutter artifacts, which has previously been a problem in interpreting  
 CC allelic content of loci. The development of markers based on larger  
 CC repeat units, enables easier separation of the fragments on larger  
 CC electrophoretic gels. This allows the simultaneous analysis of more loci  
 CC XX  
 SQ Sequence 22 BP; 1 A; 9 C; 3 G; 9 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Db 2861 AGAAGCAGAGGAGGAGG 2881  
 |||||  
 22 AGAAGCAGAGGAGGAGG 2  
 RESULT 3387  
 AAX21479  
 ID AAX21479 standard; DNA; 22 BP.  
 XX AC AAX21479;  
 XX DT 21-MAY-1999 (first entry)  
 XX DE 5' RACE primer for Turnip mosaic virus genome.  
 XX KM Primer; PCR; amplification; infection; plant; Arabidopsis thaliana;  
 KM animal virus; epitope; edible vaccine; ss.  
 XX OS Synthetic.  
 OS Turnip mosaic virus.  
 XX PN W09902718-A1.  
 PD 21-JAN-1999.  
 XX PF 09-JUL-1998; 98WO-ES000200.  
 XX PR 09-JUL-1997; 97ES-00001522.  
 XX PA (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.  
 CC CC Ponz Ascaso F., Torres Pascual V., Sanchez Sanchez F;  
 PI Martinez Herrera D;

XX DR WPI; 1999-120919/10.  
 XX XX New infectious clone of turnip mosaic virus - useful for virological  
 PT research and for expressing genes or proteins, particularly for oral  
 PT vaccines.  
 XX PS Example 1; Page 29; 37pp; Spanish.  
 XX CC This primer was used in a 5' RACE (rapid amplification of cDNA ends)  
 CC method to construct the complete turnip mosaic virus (TUMV) genome. The  
 CC invention relates to the isolation of an infectious clone of TUMV. The  
 CC clones, and vectors containing them, are used to infect susceptible  
 CC plants, specifically Arabidopsis thaliana, for basic virological research  
 CC and for expression of genes or epitopes of interest, particularly  
 CC expression of animal virus epitopes for production of edible vaccines  
 CC XX  
 SQ Sequence 22 BP; 6 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
 QY Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Db 296 GCATTGGCACTGTGGGAAC 316  
 |||||  
 2 GCATTGGCACTGTGGGAAC 22  
 RESULT 3388  
 AAV83869  
 ID AAV83869 standard; DNA; 22 BP.  
 XX AC AAV83869;  
 XX DT 09-MAR-1999 (first entry)  
 XX DE Reverse primer SSCex4 used to amplify IB3089A gene coding sequence.  
 XX KM Tumour suppressor gene; IB3089A; DBCR1; 9q32-33; hypermethylation;  
 KM Deleted in Bladder Cancer Chromosome Region candidate 1; cancer;  
 KM bladder cancer; ovarian cancer; skin cancer; squamous carcinoma;  
 KM renal cell carcinoma; squamous cell oesophageal carcinoma;  
 KM prenatal testing; heterozygosity loss; PCR primer; ss.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX PN W09854318-A1.  
 PD 03-DEC-1998.  
 XX PF 26-MAY-1998; 98WO-GB001515.  
 XX PR 28-MAY-1997; 97GB-00010995.  
 XX PA (CUR1-) CURIE RES INST MARIE.  
 XX PI Knowles M., Habuchi T;  
 XX DR WPI; 1999-070216/06.  
 XX PT New human gene, DBCR1, associated with bladder and other cancers - used  
 PT for diagnosis, treatment and prevention of cancer.  
 XX PS Disclosure; Page 78; 106pp; English.  
 XX CC PCR primers AAV83864-83 were used to amplify the coding region from the  
 CC exons of the genomic DNA of tumour suppressor gene IB3089A, also known as  
 CC DBCR1 (Deleted in Bladder Cancer Chromosome Region candidate 1). The  
 CC gene is located at 9q32-33. Although the gene is expressed in multiple  
 CC human tissues, lack of expression of the gene was found in several  
 CC bladder cancer cells. The DBCR1 gene is involved in the development of  
 CC sporadic cancer, probably by the deletion of one allele of the gene



CC XLIS gene from a sample for comparison to normal samples in the in vitro  
CC diagnosis regime. This may also be performed by amplifying XLIS cDNA from  
CC the mRNA in the sample. Antibodies to XLIS may be used to detect XLIS in  
CC a biological sample or can be administered to patients to prevent or  
CC treat the above disorders. They may also be used to purify XLIS from a  
CC biological sample. XLIS may also be administered to patients to prevent  
CC or treat the above neurological disorders. In addition XLIS may be used  
CC as a marker of neuronal cells at an early stage of development; its  
CC discovery increases understanding of both the neuronal movement which  
CC leads to development of the cortical region of the brain and of the  
CC pathogenesis of the group of neuronal disorders mentioned above  
XX  
XX  
SQ Sequence 22 BP; 0 A; 10 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5701 TGCCTCTTCTTCCTCTC 5721  
1 TCCTCTCTTTTTCCTCTC 21

Db

RESULT 3391  
AAx81831/c  
ID AAx81831 standard; DNA; 22 BP.  
XX  
AC AAx81831;  
XX  
DT 02-SEP-1999 (first entry)  
XX  
DE PCR primer used to amplify human malignancy-associated gene (MAG).  
XX  
KW Liver neoplastic disease; malignancy-associated gene; MAG; liver disease;  
KW neoplastic disease; cirrhosis; hepatocellular carcinoma; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9929859-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 11-DEC-1998; 98WO-US026461.  
XX  
PR 12-DEC-1997; 97US-00989750.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Black K, Ljubimova JY, Demetrio AA;  
XX  
DR WPI; 1999-404942/34.  
XX  
PT Liver-associated malignancy-associated gene (MAG), useful for screening  
PT for cirrhosis and hepatocellular carcinoma.  
XX  
PS Example 11; Page 17; 42pp; English.  
XX  
CC PCR primers AAx81830-31 were used to amplify human malignancy-associated  
CC gene (MAG) proteins. The polypeptide is useful for detecting antibodies  
CC associated with liver disease. Probes derived from the MAG gene are  
CC useful for detecting the presence of sequences associated with neoplastic  
CC disease, e.g. liver diseases such as cirrhosis and hepatocellular  
CC carcinoma, and therefore can be used in disease diagnosis. The sequences  
CC can be used for development of therapeutics that are useful for  
CC inhibition of the development of neoplastic liver disease  
XX  
SQ Sequence 22 BP; 4 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 616 ATTGTGAGCTGGCGAATGCTG 636  
22 ATAGTAGCTGGCCAAAGCTG 2

Db

RESULT 3392  
AAx81837/c  
ID AAx81837 standard; DNA; 22 BP.  
XX  
AC AAx81837;  
XX  
DT 02-SEP-1999 (first entry)  
XX  
DE PCR primer used to amplify cDNA sequences isolated from liver tissue.  
XX  
KW Liver neoplastic disease; malignancy-associated gene; MAG; liver disease;  
KW neoplastic disease; cirrhosis; hepatocellular carcinoma; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9929859-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 11-DEC-1998; 98WO-US026461.  
XX  
PR 12-DEC-1997; 97US-00989750.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Black K, Ljubimova JY, Demetrio AA;  
XX  
DR WPI; 1999-404942/34.  
XX  
PT Liver-associated malignancy-associated gene (MAG), useful for screening  
PT for cirrhosis and hepatocellular carcinoma.  
XX  
PS Example 16; Page 23; 42pp; English.  
XX  
CC The specification describes a liver neoplastic disease polynucleotide and  
CC malignancy-associated gene (MAG) proteins. The polypeptide is useful for  
CC detecting antibodies associated with liver disease. Probes derived from  
CC the MAG gene are useful for detecting the presence of sequences  
CC associated with neoplastic disease, e.g. liver diseases such as cirrhosis  
CC and hepatocellular carcinoma, and therefore can be used in disease  
CC diagnosis. The sequences can be used for development of therapeutics that  
CC are useful for inhibition of the development of neoplastic liver disease.  
CC PCR primers AAx81836-37 were used in the course of the invention  
XX  
SQ Sequence 22 BP; 4 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 616 ATTGTGAGCTGGCGAATGCTG 636  
22 ATAGTAGCTGGCCAAAGCTG 2

Db

RESULT 3393  
AAx99208  
ID AAx99208 standard; DNA; 22 BP.  
XX  
AC AAx99208;  
XX  
DT 23-JAN-2001 (first entry)  
XX  
DE Human apoptosis related protein CCR9 related primer #4.  
XX  
KW Human; apoptosis; CCR9; anti-tumour; tumour; cancer; diagnosis; primer;  
KW ss.

```

OS Homo sapiens.
XX JP2000210089-A.
XX
XX 02-AUG-2000.
XX
XX 18-NOV-1999; 99JP-00327885.
XX
XX 20-NOV-1998; 98JP-00330302.
XX
XX (ASAKI) ASAHI BREWERIES LTD.
XX
XX WPI; 2000-614556/59.
XX
XX Gene and its encoded protein that induce apoptosis, useful for producing
XX a malignant tumor gene treating agent and for the diagnosis on the
XX resistance of cancer cells against an anticancer agent.
XX
XX Example 2, Page 5; 13pp; Japanese.
XX
XX The present invention describes the human CCR9 protein, which is an
XX apoptosis related protein having apoptosis-inducing activity. Human CCR9
XX has anti-tumor activity, and can be used to produce a malignant tumor
XX gene treating agent. The CCR9 gene and protein can be used for the
XX diagnosis of the resistance of cancer cells against an anticancer agent.
XX the present sequence represents a primer which is used in an example from
XX
XX Sequence 22 BP; 10 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
XX
XX 1236 CATGATTAAGGCCACAGCTAG 1316
XX |||||
XX 2 CAAGAAAATGCCACAGCCAG 22
XX
XX RESULT 3394
XX AA239687/C
XX ID AA239687 standard; DNA; 22 BP.
XX
XX AA239687;
XX
XX 28-FEB-2000 (first entry)
XX
XX Human V $\alpha$ H aggregation factor gene specific FPCR-SSCP primer.
XX
XX Gene polymorphism; human; V $\alpha$ H aggregation factor; genetic diagnosis;
XX diabetes; FPCR; SSCP; fluorescence-based polymerase chain reaction;
XX single strand conformation polymorphism; PCR primer; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX JP1313676-A.
XX
XX 16-NOV-1999.
XX
XX 30-APR-1998; 98JP-00120217.
XX
XX 30-APR-1998; 98JP-00120217.
XX
XX (SAKA) OTSUKA PHARM CO LTD.
XX
XX WPI; 2000-057352/05.
XX
XX Discrimination of human V aggregation factor gene polymorphism.
XX
XX Disclosure; Page 10; 34pp; Japanese.
XX
XX The invention provides a method for the discrimination of the gene
XX

```

CC polymorphism of human Vth aggregation factor, where one of the following  
CC (1) to (6) residues/nucleotides in the aggregation gene is discriminated  
CC in the patient to be tested : (1) residue 495: guanine (G) or adenine (A),  
CC (2) residue 642: (G) or thymine (T), (3) residue 2663: (G) or (A), (4)  
CC residue 2763: (G) or (A), (5) residue 2863: (A) or (G), (6) residue 5112:  
CC (A) or (G). The method is useful in the genetic diagnosis of a diabetes  
CC patient. The method uses PCR-SSCP (fluorescence-based polymerase chain  
CC reaction-single strand conformation polymorphism) for analyzing DNA  
CC samples for polymorphisms. Sequences AA39632-717 represent primers used  
CC for the PCR-SSCP analysis of the human Vth aggregation factor gene  
CC  
XX  
SQ Sequence 22 BP; 5 A; 4 C; 4 G; 9 T; 0 U; 0 Other;  
QY  
Db 7398 TGAAGCAGCAACATCAGCAG 7418  
22 TGAATCAACATCATGAGCAG 2  
RESULT 3395  
AAZ49922  
ID AAZ49922 standard; DNA; 22 BP.  
AC AAZ49922;  
DT 02-MAY-2000 (first entry)  
XX  
DE Human tumour suppressor gene IB3089A exon 4 reverse primer SSCPex4.  
XX  
KM Human; tumour suppressor; IB3089A; cytostatic; promoter; 9q32-33;  
KM Deleted in Bladder Cancer Chromosome Region candidate 1; DBCCR1;  
KM diagnostic; prophylactic; therapeutic treatment; cancer; skin; ovarian;  
KM bladder; squamous carcinoma; renal cell; oesophageal; PCR primer; 88.  
XX  
OS Homo sapiens.  
XX  
PN WO200001816-A1.  
XX  
PD 13-JAN-2000.  
PF 02-JUL-1998; 98WO-GB001958.  
PR 02-JUL-1998; 98WO-GB001958.  
XX  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
PI Knowles M, Habuchi T;  
PI  
DR WPI; 2000-171014/15.  
PT  
PT Novel promoter sequence, useful for identifying a predisposition to  
PT cancer or the presence of a tumor.  
XX  
XX Claim 22; Page 78; 101pp; English.  
CC The patent relates to the identification of a novel gene IB3089A, also  
CC referred as DBCCR1 (Deleted in Bladder Cancer Chromosome Region candidate  
CC 1), and its promoter in a tumour suppressor region at 9q32-33 between  
CC D9S1848 and APM2339X9 of human chromosome 9q. The DBCCR1 sequence can be  
CC used in the diagnostic, prophylactic and therapeutic treatment of cancer  
CC particularly bladder cancer. The promoter can be used to design DBCCR1  
CC amplifying primers and screen compounds that activate production of  
CC DBCCR1. It can also be used in methods for determining inactivation of  
CC the DBCCR1 gene in a patient, where inactivation indicates the presence  
CC of a tumour or a predisposition to cancer, especially a cancer associated  
CC with loss of heterozygosity involving 9q32-33 e.g. bladder cancer,  
CC squamous carcinoma, skin cancer, renal cell carcinoma, oesophageal and  
CC ovarian cancers. The present sequence is a reverse primer SSCPex4 used to  
CC amplify exon 4 of IB3089A from the genomic DNA for SSCP (single-stranded  
CC conformational polymorphism) analysis

```
XX
SQ Sequence 22 BP; 7 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 5904 AGAACCTGTCTCCCAAGCCCA 5924
Db 2 AGAACCTGTCTCCCAATCCA 22
RESULT 3396
AAZ44367
ID AAZ44367 standard; DNA; 22 BP.
XX
AC AAZ44367;
XX
DT 06-APR-2000 (first entry)
XX
DB Human G protein-coupled receptor primer 106R1.
XX
KW G protein-coupled receptor; human; lysophosphatidic acid; diagnosis;
KW treatment; prostate cancer; prostatic hyperplasia; inflammation; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO967383-A1.
XX
PD 29-DEC-1999.
XX
PP 21-JUN-1999; 99WO-JP003306.
XX
PR 22-JUN-1998; 98JP-00174731.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Nozaki Y, Naito T;
XX
DR WPI; 2000-106293/09.
XX
PT G-protein coupled receptor protein binding to lysophosphatidic acid used
PT for treatment of prostate cancer.
XX
PS Example 1; Page 60; 67pp; Japanese.
XX
CC This invention describes a novel human G-protein coupled receptor protein
CC capable of binding lysophosphatidic acid, and proteins derived from it by
CC addition, deletion and/or substitution of one or more amino acid
CC residues. Antibodies to the protein are used for diagnosis of, and
CC agonists/antagonists to the protein are used for the treatment of,
CC prostatic disorders such as prostate cancer, benign prostatic
CC hyperplasia, and inflammation of the prostate. This sequence represents a
CC primer used in the isolation of the human G protein-coupled receptor
CC protein described in the method of the invention
XX
SQ Sequence 22 BP; 7 A; 7 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 7414 AGCAGCAGCAGCAGCAGCAGC 7434
Db 2 AGCAGCAGCAGCAGCAGCAGC 22
RESULT 3397
AAA11724/C
ID AAA11724 standard; DNA; 22 BP.
XX
AC AAA11724;
XX
```

```
XX
DT 14-JUL-2000 (first entry)
XX
DE Human prothrombin 20210 A allele PCR primer #2.
XX
KW Prothrombin; human; thrombosis; mutation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6043035-A.
XX
PD 28-MAR-2000.
XX
PP 03-NOV-1997; 97US-00962790.
XX
PR 03-NOV-1997; 97US-00962790.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bertina RM, Reitsma PH, Rosendaal FR, Poort SR;
XX
DR WPI; 2000-270338/23.
XX
PT Determining increased risk for thrombosis by determining prothrombin
PT level, or by detecting the presence or absence of genetic mutation
PT correlated with elevated prothrombin levels.
XX
PS Example 2; Col 11-12; 11pp; English.
XX
CC This invention describes a novel method for determining an increased risk
CC for thrombosis in an individual by determining the prothrombin level, or
CC by detecting the presence or absence of a genetic mutation correlated
CC with elevated prothrombin levels in individuals with the mutation, and
CC where an increased prothrombin level indicates increased risk for
CC thrombosis. INDEPENDENT CLAIMS are also included for the following: (1) a
CC kit for determining whether an individual is at an increased risk for
CC thrombosis comprising at least one primer which specifically hybridizes
CC adjacent to the region of the prothrombin gene that contains a G to A
CC mutation at position 20210, and suitable amplification reagents; and (2)
CC an isolated polynucleotide comprising a mutated prothrombin gene, in
CC which G at position 20210 is replaced by A, or a fragment of the gene
CC which includes the G to A transition mutation at position 20210. The
CC method is also used for screening and diagnosis of thrombophilia,
CC especially, hereditary thrombophilia. AAA11723-A11726 represent PCR
CC primers used in the method of the invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 5842 GCTGCATGATCCCACTGTTA 5862
Db 2 GCTGCATGCTCCCACTGCTA 2
RESULT 3398
AAA95380
ID AAA95380 standard; DNA; 22 BP.
XX
AC AAA95380;
XX
DT 12-FEB-2001 (first entry)
XX
DB Rat G11 coding sequence PCR primer #1.
XX
KW Rat; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
KW Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.
XX
OS Rattus norvegicus.
XX
PN WO200058451-A1.
```

```

XX 05-OCT-2000.
PD
XX
XX 21-MAR-2000; 2000WO-US007544.
PF
XX
XX 26-MAR-1999; 99US-00277078.
PR
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
PA
XX Sakurada K, Palmer T, Gage FH;
PI
XX WPI; 2000-656165/63.
DR
XX
XX Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase
PT expression useful for treating catecholamine-related diseases such as
PT Parkinson's disease, manic depression and schizophrenia.
XX
XX
XX Example 1; Page 20; 68pp; English.
PS
XX
XX The present invention describes the rat Nurrl coding and protein
CC sequences. The Nurrl protein is involved in the induction of tyrosine
CC hydroxylase expression in adult rat-derived hippocampal progenitor cells.
CC The Nurrl gene and protein can be used in the treatment of catecholamine-
CC related diseases such as Parkinson's disease, manic depression and
CC schizophrenia. They can also be used to induce tyrosine hydroxylase
CC expression and identify tyrosine hydroxylase related deficiencies, which
CC are linked to the same diseases. The present sequence is a PCR primer
CC used in a method to differentiate adult neural progenitor cells
XX
XX Sequence 22 BP; 6 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6583 CATGTGTAACACAGGTTG 6603
| | | | | | | | | | | | | | | | | |
Db 1 CATGTGTGACGACAGAGGTTG 21
RESULT 3399
AAA37706
ID AAA37706 standard; DNA; 22 BP.
XX
XX AAA37706;
AC
XX
XX 22-NOV-2000 (first entry)
DT
XX
XX Human Rad51 antisense inhibitor AS6.
DE
XX
XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KM radiation sensitivity; therapy; AS6; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200047231-A2.
PN
XX
XX 17-AUG-2000.
PD
XX
XX 03-FEB-2000; 2000WO-US002881.
PF
XX
XX 10-FEB-1999; 99US-0119578P.
PR
XX 06-DEC-1999; 99US-00454495.
PA
XX (PANG-) PANGENE CORP.
XX
XX Reddy G;
PI
XX
XX WPI; 2000-506091/45.
DR
XX
XX Inhibiting cell proliferation useful for cancer therapy, comprises
PT administering Rad51 inhibitor in vivo.
XX

```

```

PS Claim 8; Page 26; 42pp; English.
XX
XX This sequence represents an antisense inhibitor of human Rad51,
CC designated AS6 (also referred to as R51AS6). The antisense inhibitors can
CC be used in a method of the invention, for inhibiting cell proliferation.
CC They can also be used in methods for inducing sensitivity to radiation
CC and DNA damaging chemotherapeutics in an individual and in a method for
CC prolonging survival in an individual with cancer. The methods and
CC antisense molecules are useful for inhibiting cell proliferation,
CC especially cancerous cell proliferation, for inducing sensitivity to
CC radiation and DNA damaging chemotherapeutics in individuals and for
CC prolonging survival in an individual with cancer. Kits for carrying out
CC the methods may be used to diagnose and/or treat cancer and for
CC adjunctive therapy
XX
XX Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3477 CCTTACTAATCTTAAGGCAC 3497
| | | | | | | | | | | | | | | | | |
Db 1 CCCAGTCAATCTCTTAAGGCAC 21
RESULT 3400
AAA74138
ID AAA74138 standard; DNA; 22 BP.
XX
XX AAA74138;
AC
XX
XX 29-NOV-2000 (first entry)
DT
XX
XX Reverse PCR primer for loblolly pine locus R1PPT815.
DE
XX
XX PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
KM microsatellite DNA repeat; genetic marker; mapping; inheritance study;
KM population genetics study; plant breeding programme; ss.
XX
XX Pinus taeda.
OS
XX
XX WO200042210-A2.
PN
XX
XX 20-JUL-2000.
PD
XX
XX 06-JAN-2000; 2000WO-US000325.
PF
XX
XX 15-JAN-1999; 99US-00232884.
PR
XX 19-JAN-1999; 99US-00232785.
PA
XX (INTO ) INT PAPER CO.
PA (ECHR/) ECHR C S.
PA (NELS/) NELSON C D.
PA (USDA ) US SEC OF AGRIC.
XX
XX Echt CS, Nelson CD;
PI
XX
XX WPI; 2000-482836/42.
DR
XX
XX Polynucleotide having simple sequence repeat useful as markers in plants
PT for genetic characterization e.g. genetic mapping study, an inheritance
PT study of a commercially important trait in a plant breeding program.
XX
XX Claim 6; Page 24; 57pp; English.
PS
XX
XX The present invention relates to loblolly pine polynucleotides with one
CC or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
CC also known as microsatellite DNA repeats. The SSRs are useful as genetic
CC markers for genetic mapping, population genetics studies and inheritance
CC studies in various plant breeding programmes. The present sequence is a
CC PCR primer used for detecting the presence of a SSR locus in a pine
CC genomic DNA sample

```



XX SQ Sequence 22 BP; 3 A; 3 C; 6 G; 10 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 7282 TGTGACTGTTGATGTTGT 7302  
 DB 1 TGTACTTGATGATGTTGT 21  
 RESULT 3401  
 ID AAS01199 standard; cDNA; 22 BP.  
 AC AAS01199;  
 AT 04-JUL-2001 (first entry)  
 DE Human RAD51 antisense oligonucleotide, AS6.  
 KW Human; Rad51; antisense; drug screening; cancer; autoimmune disease;  
 KW arthritis; graft rejection; inflammatory bowel disease; surgery;  
 KW angioplasty; ss.  
 OS Homo sapiens.  
 PN WO200119397-A1.  
 PD 22-MAR-2001.  
 PE 18-SEP-2000; 2000WO-US025838.  
 PR 17-SEP-1999; 99US-0154616P.  
 PR 06-DEC-1999; 99US-00455300.  
 PA (PANG-) PANGENE CORP.  
 PI Reddy G;  
 DR WPI; 2001-244704/25.  
 XX PT Inhibiting cell proliferation for treating arthritis, graft rejection,  
 PT inflammatory bowel disease, cancer, proliferation induced after medical  
 PT procedure, involves administering Rad51 antibody or its fragment to cell.  
 PS Example 6; Fig 16C; 102pp; English.  
 XX CC The sequence represents the human Rad51 antisense oligonucleotide, AS6.  
 CC The antisense oligonucleotide is used to study down-regulation of Rad51  
 CC protein in human brain, breast and prostate cells. Rad51 protein is  
 CC defective in repair of damaged DNA, genetic recombination and the  
 CC recombinational repair of DNA lesions, and plays a central role in  
 CC cancer. Inhibiting cell proliferation involves administering to a cell a  
 CC Rad51 antibody or its fragment. The Rad51 antibody or its fragment is  
 CC useful for inhibiting cell proliferation, for treating disease states  
 CC such as cancer, autoimmune disease, arthritis, graft rejection,  
 CC inflammatory bowel disease, proliferation induced after medical  
 CC procedures such as surgery, angioplasty etc. in humans and animals  
 XX SQ Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3477 CCTAGNATATCTTAAGGCAC 3497  
 DB 1 CCAGATCATTCCTTAAGGCAC 21  
 RESULT 3402

AAD14949  
 ID AAD14949 standard; DNA; 22 BP.  
 AC AAD14949;  
 AT 01-NOV-2001 (first entry)  
 DE Oligo #20 used for mutagenesis of humanised KS antibody-IL-2 fusion DNA.  
 KW Fusion protein; immunoglobulin; serum half-life; FcR; Fc receptor;  
 KW Fc protection receptor; FcR; cancer; viral infection; immune disorder;  
 KW cell proliferation; human; KS antibody; BCGAM;  
 KW Epithelial cell adhesion molecule; mutagenesis; interleukin-2; IL-2; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT mlec\_feature 22  
 FT /\*tag= a  
 FT /label= Cohesive end  
 FT /note= "The 5' end of the complementary strand overhangs  
 FT the 3' end of this sequence by 5'-CGC-3'."  
 PN WO200158957-A2.  
 PD 16-AUG-2001.  
 PE 09-FEB-2001; 2001WO-US004455.  
 PR 11-FEB-2000; 2000US-0181768P.  
 PA (LEXT-) LEXIGEN PHARM CORP.  
 PI Gallies SD, Burger C, Lo KM;  
 DR WPI; 2001-514646/56.  
 XX PT Antibody-based fusion protein comprises mutations near the fusion  
 PT junction for enhancing circulating half-life.  
 PS Example 3; Page 17; 48pp; English.  
 XX CC The invention relates to antibody-based fusion proteins having one or  
 CC more mutations in the junction between an immunoglobulin (Ig) and a non-  
 CC Ig moiety, which increases the circulating half-life of the fusion  
 CC protein. The serum half-life of the mutant fusion protein is improved  
 CC without affecting the interaction of the antibody moiety with the Fc  
 CC receptor (FcR) and Fc protection receptor (FcRp). The antibody-based  
 CC fusion proteins of the invention are useful to treat cancer, viral  
 CC infections, immune disorders, and to enhance growth (including  
 CC proliferation) of specific cell types. The present sequence is an  
 CC oligonucleotide used for generating mutant humanised KS antibody  
 CC (recognises epithelial cell adhesion molecule) and interleukin-2 fusion  
 CC protein with Pro to Leu substitution at the fusion junction  
 XX SQ Sequence 22 BP; 5 A; 4 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 6998 GGGAAAGGAGATTTCTTCT 7018  
 DB 2 GGGACAGGGAGAGGCTCTTCT 22  
 RESULT 3403  
 ID AAC92055/c  
 AC AAC92055; standard; DNA; 22 BP.  
 AT AAC92055;  
 AT 21-MAR-2001 (first entry)

```

XX Rat PER1 PCR primer #1.
DE Rat; PER1; circadian rhythm; period protein; PCR primer; ss.
XX
XX Rattus sp.
OS
XX WO200075669-A1.
PN
XX 14-DEC-2000.
PD
XX
XX 07-JUN-2000; 2000WO-US015633.
PF
XX 08-JUN-1999; 99US-00327745.
PR
XX (AVET ) AVENTIS PHARM INC.
PA
XX Keesler G, Mondadori C, Yao Z, Camacho F;
PI
XX WPI; 2001-061769/07.
DR
XX
XX Identifying compounds that alter circadian rhythm of a mammal by altering
PT the phosphorylation or degradation of human period proteins, comprises
PT adding test compound to screening system comprising period proteins.
XX
XX Example 10; Page 33; 55pp; English.
PS
XX The present invention relates to a method for determining the ability of
CC a test compound to alter the circadian rhythm of a mammal by its ability
CC to alter phosphorylation or degradation of one or more period proteins.
CC The present sequence is a PCR primer for one such period protein (rat
CC PER1), that was used in the method of the present invention
XX
SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
QY
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 3239 TTTTGGAGCGCTTAATCACA 3259
21 TTGTGACGAGCGCTTAACACAGA 1
RESULT 3404
AAFS870/c
ID AAF58870 standard; DNA; 22 BP.
XX
XX AAF58870;
AC
XX
XX 06-JUN-2001 (first entry)
DT
XX Human metastasis-associated antigen C4-4A PCR primer #2.
DE
XX Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200123553-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-EP009567.
PF
XX
XX 29-SEP-1999; 99US-00407784.
PR
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Zoeller M, Roessel M, Wuerfel J;
PI
XX WPI; 2001-258133/26.
DR
XX New nucleic acid encoding rat or human metastasis-associated antigen
PT

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```

PT C4.4A for treating cell proliferative disorder associated with a
PT metastasizing tumor.
XX
XX Example 1; Page 29; 63pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of the
CC human and rat metastasis-associated antigen C4.4A. The protein is
CC expressed rarely in the adult, except on metastasizing cancer cells.
CC Because of this, the sequences are useful in cancer diagnosis and
CC treatment of cell proliferation diseases. The present sequence is a PCR
CC primer used to isolate the human C4.4A coding sequence
XX
XX
SQ Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;
QY
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 3611 CTTGGGGAATGGCGTGGCGG 3631
21 CTTGGAGCGTGGCGTGGCGG 1
RESULT 3405
AAFS876/c
ID AAF58876 standard; DNA; 22 BP.
XX
XX AAF58876;
AC
XX
XX 06-JUN-2001 (first entry)
DT
XX Human metastasis-associated antigen C4-4A PCR primer #4.
DE
XX Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200123553-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000WO-EP009567.
PF
XX
XX 29-SEP-1999; 99US-00407784.
PR
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA
XX Zoeller M, Roessel M, Wuerfel J;
PI
XX WPI; 2001-258133/26.
DR
XX
XX New nucleic acid encoding rat or human metastasis-associated antigen
PT C4.4A for treating cell proliferative disorder associated with a
PT metastasizing tumor.
XX
XX Example 1; Page 31; 63pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of the
CC human and rat metastasis-associated antigen C4.4A. The protein is
CC expressed rarely in the adult, except on metastasizing cancer cells.
CC Because of this, the sequences are useful in cancer diagnosis and
CC treatment of cell proliferation diseases. The present sequence is a PCR
CC primer used to isolate the human C4.4A coding sequence
XX
XX
SQ Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;
QY
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 3611 CTTGGGGAATGGCGTGGCGG 3631
21 CTTGGAGCGTGGCGTGGCGG 1

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```
RESULT 3406
AAFS878/C
ID AAF5878 standard; DNA; 22 BP.
XX
XX
AC AAF5878;
XX
XX 06-JUN-2001 (first entry)
XX
XX Human metastasis-associated antigen C4-4A PCR primer #6.
XX
XX Rat; human; metastasis-associated antigen; C4.4A; cancer; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200123553-A2.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-EP009567.
XX
XX 29-SEP-1999; 99US-00407784.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Zoeller M, Roessel M, Wuerfel J;
XX
XX WPI; 2001-258133/26.
XX
XX New nucleic acid encoding rat or human metastasis-associated antigen
XX C4.4A for treating cell proliferative disorder associated with a
XX metastasizing tumor.
XX
XX Example 1; Page 32; 63pp; English.
XX
XX The present invention provides the protein and coding sequences of the
XX human and rat metastasis-associated antigen C4.4A. The protein is
XX expressed rarely in the adult, except on metastasizing cancer cells.
XX Because of this, the sequences are useful in cancer diagnosis and
XX treatment of cell proliferation diseases. The present sequence is a PCR
XX primer used to isolate the human C4.4A coding sequence
XX
XX Sequence 22 BP; 6 A; 12 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3611 CTTTGGGGAATGGGGTGGGG 3611
XX DB 21 CTTTGAGCGTGGGGTGGTG 1
XX
XX RESULT 3407
XX AAF99703
XX ID AAF99703 standard; DNA; 22 BP.
XX
XX AAF99703;
XX
XX 12-JUN-2001 (first entry)
XX
XX Immunoestimulatory nucleic acid #819.
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX immunoestimulatory; tumor; viral infection; bacterial infection;
XX fungal infection; parasitic infection; cancer; asthma;
XX infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX WO200122972-A2.
XX
```

```
PD 05-APR-2001.
XX
XX 25-SEP-2000; 2000WO-US026383.
XX
XX 25-SEP-1999; 99US-0156113P.
XX
XX 27-SEP-1999; 99US-0156135P.
XX
XX 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunoestimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 56; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunoestimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunoestimulatory
XX nucleic acid. The immunoestimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Tn2 to a Th1 immune response and to activate immune cells. Note: the
XX present sequence may have a phosphorothioate backbone
XX
XX Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5328 CTCCTCTTGGCTCACTCTCTC 5348
XX DB 1 CTCCTCTCTCTCTCTCTCTC 21
XX
XX RESULT 3408
XX AAH79377/C
XX ID AAH79377 standard; DNA; 22 BP.
XX
XX AAH79377;
XX
XX 04-DEC-2001 (first entry)
XX
XX Human RNA uncoiling enzyme 44 coding sequence PCR primer #1.
XX
XX Human; RNA uncoiling enzyme 44; cancer; nervous system disease;
XX gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX CN1302893-A.
XX
XX 11-JUL-2001.
XX
XX 29-OCT-1999; 99CN-00119928.
XX
XX 29-OCT-1999; 99CN-00119928.
XX
XX (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
```

DR WPI; 2001-566052/64.  
XX  
PT Polypeptide-human RNA uncoiling enzyme 44 and polynucleotide for coding  
PT it.  
XX  
PS Example 3; Page 14 (Disclosure); 24pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC RNA uncoiling enzyme 44. The sequences can be used in the treatment of  
CC cancer and nervous system diseases. The present sequence is a PCR primer  
CC for the coding sequence of the invention  
XX  
SQ Sequence 22 BP; 9 A; 0 C; 4 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4405 TTACCAAAATGATTTTCC 4425  
DB 21 TTTTCAAAAACAAATTTCC 1  
XX  
RESULT 3409  
AAH74500  
ID AAH74500 standard; DNA; 22 BP.  
XX  
AC AAH74500;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE PCR primer used to amplify a marker SW782 from pig genome.  
XX  
XX Pig; boar taint; genetic marker; SW1057; SW782; S0121; SW322;  
KM chromosome 6; SW857; SW2496; SW295; SW210; S0007; SW761; SW1557;  
KM chromosome 14; PCR primer; ss.  
XX  
OS Sus sp.  
XX  
PN WO200157250-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 05-FEB-2001; 2001WO-GB000448.  
XX  
PR 04-FEB-2000; 2000GB-00002451.  
XX  
PA (ROSL-) ROSLIN INST.  
XX  
PI Haley CS, Archibald AL;  
XX  
DR WPI; 2001-496928/54.  
XX  
PT Determining if a pig is predisposed to boar taint for exhibiting  
PT desirable flavor properties, involves assaying for the presence of  
PT alleles conveying susceptibility to boar taint using specific genetic  
PT markers.  
XX  
PS Example 1; Page 32; 71pp; English.  
XX  
CC PCR primers AAH74499-AAH74500 were used to amplify a fragment of the pig  
CC genome, comprising the marker SW782. The primers were used in the method  
CC of the invention. The specification describes a method for determining if  
CC a pig is predisposed to a boar taint. The method comprises assaying for  
CC the presence of alleles conveying susceptibility to boar taint using  
CC genetic markers selected from SW1057, SW782, S0121, SW322 or regions of  
CC chromosome 6 spanning in between, or SW857, SW2496, SW295, SW210, S0007,  
CC SW761, SW1557 or regions of chromosome 14 spanning in between. The method  
CC is useful for determining the predisposition of pigs to boar taint which  
CC is a strong unpleasant odour given off upon heating or cooking of meat  
CC from uncastrated male pigs, and for exhibiting desirable flavour  
CC properties  
XX

SQ Sequence 22 BP; 6 A; 1 C; 9 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4435 ACTAGGCGATGAGGCGGTG 4455  
DB 1 AATAGGCGATGAGGCGGTG 21  
XX  
RESULT 3410  
AAH74340  
ID AAH74340 standard; DNA; 22 BP.  
XX  
AC AAH74340;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE PCR primer used to amplify a fragment of the human ATIP gene.  
XX  
XX Human; ATIP; hATIP2; hATIP3; hATIP4; hATIP5; hATIP6; hAT2 receptor;  
KM human; ATIP; hATIP2; hATIP3; hATIP4; hATIP5; hATIP6; hAT2 receptor;  
KM angiotensin II receptor; anticoncogenic; 8p21.3-p22; cancer; PCR primer;  
KM ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157209-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 07-FEB-2001; 2001WO-FR000359.  
XX  
PR 07-FEB-2000; 2000FR-00001504.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Nahmias C, Strosberg AD, Nouet S;  
XX  
DR WPI; 2001-488880/53.  
XX  
PT New protein family, designated hATIP, which interacts with the AT2  
PT receptor of angiotensin II are anti-oncogenic and useful to detect and  
PT treat cancer or precancerous conditions.  
XX  
PS Claim 7; Page 100; 118pp; French.  
XX  
CC PCR primers AAH74330-41 were used to amplify a fragment of the human ATIP  
CC gene. ATIP has isoforms designated hATIP2, hATIP3, hATIP4, hATIP5 and  
CC hATIP6. All ATIP proteins comprise in their C-terminal a common fragment  
CC which interacts with the angiotensin II (AT2) receptor. ATIP proteins  
CC have anticoncogenic functions. The human ATIP gene has 17 exons, and is  
CC located at chromosome region 8p21.3-p22. ATIP polynucleotides and  
CC polypeptides are used to detect, evaluate or give prognosis for a cancer  
CC condition, and as an anti-tumour medicament  
XX  
SQ Sequence 22 BP; 11 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 7401 AGCAAGCAATCAGCAGCG 7421  
DB 2 AACAGACACATTAAGCAGCG 22  
XX  
RESULT 3411  
AAH78021  
ID AAH78021 standard; DNA; 22 BP.  
XX  
AC AAH78021;  
XX

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DT 26-NOV-2001 (first entry)
XX PCR primer for human alpha subunit of prollyl 4-hydroxylase cDNA.
DE
XX
XX Human; alpha subunit; prollyl 4-hydroxylase; alpha (III) subunit;
KW collagen; kidney fibrosis; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX W0200168868-A2.
XX
XX
XX 20-SEP-2001.
XX
XX
XX 15-MAR-2001; 2001MO-US008267.
XX
XX 15-MAR-2000; 2000US-0189373P.
XX
XX (FIBR-) FIBROGEN INC.
XX
XX Kivirikko K, Myllyharju J, Kukkola L, Hietala R;
XX
XX WPI; 2001-570871/64.
XX
XX
XX New alpha subunit of prollyl 4-hydroxylase and polynucleotide encoding the
PT subunit, useful for diagnosis, prevention and treatment of diseases and
PT disorders associated with increased or decreased expression of the
XX subunit.
XX
XX Example 1; Page 52; 75pp; English.
XX
XX PCR primers AAH78021-22 were used to amplify cDNA encoding a human alpha
CC subunit of prollyl 4-hydroxylase, designated alpha (III) subunit. The
CC alpha (III) subunit is useful for the production of recombinant collagen,
CC and for the diagnosis, prevention and treatment of various diseases and
CC disorders associated with decreased or increased production of the
CC subunit in specific tissues. The polynucleotide is a source of probes and
CC primers, which are useful for diagnosis, prevention and treatment of
CC diseases and disorders associated with increased or decreased expression
CC or activity of various prollyl 4-hydroxylase enzymes and to identify alpha
CC or beta prollyl 4-hydroxylase or fragments in tissue, e.g. biopsies from
CC specific tissues, etc or other biological samples. Small molecules that
CC modulate, regulate and inhibit prollyl 4-hydroxylase activity are useful
CC for treating and preventing kidney fibrosis and various other diseases
CC and disorders
XX
XX
XX Sequence 22 BP; 5 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 6437 TTACCTAGCAGCAGTGTTT 6457
DB 2 TTAGGATGCAGCACTGTTT 22

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PN W0200078802-A2.
XX
XX PD -28-DEC-2000.
XX
XX 23-JUN-2000; 2000MO-US017328.
XX
XX
XX 23-JUN-1999; 99US-0140584P.
XX
XX 20-JUL-1999; 99US-0144722P.
XX
XX 16-SEP-1999; 99US-0154520P.
XX
XX 22-JUN-2000; 2000US-00604286.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX
XX Shinkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;
XX
XX Herrmann JL;
XX
XX WPI; 2001-071385/08.
XX
XX
XX Polynucleotides encoding SECK proteins useful for treating disease
PT characterized by an aberrant level of cell proliferation and/or
PT differentiation like cancer or immune associated disorders.
XX
XX
XX Example 10; Page 84; 132pp; English.
XX
XX The invention relates to human SECK polypeptides and polynucleotides
CC encoding them. The SECK polypeptides can be expressed by standard
CC recombinant methodology. The SECK polypeptides are useful for treating or
CC preventing a SECK-associated disorder. The invention is useful in
CC screening assays; detection assays (e.g. chromosomal mapping, cell and
CC tissue typing, forensic biology); predictive medicine (diagnostic assays,
CC prognostic assays, monitoring clinical trials, and pharmacogenomics); and
CC methods of treatment (e.g. therapeutic and prophylactic), especially
CC disorders characterized by aberrant cell proliferation and/or
CC differentiation like cancer or immune associated disorders or gestational
CC disease. Sequences AAC94904-906 represent primer-probe sets employed in
CC the expression analysis of SECK clone
XX
XX
XX Sequence 22 BP; 5 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4299 CATCTTTTCTCTTCCCTGGA 4319
DB 1 CATCTCTCTCTTCCCAAGA 21

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RESULT 3412
AAC84905
ID AAC84905 standard; DNA; 22 BP.
XX
XX AAC84905;
XX
XX 20-APR-2001 (first entry)
XX
XX
XX Primer Ag 36 (R) employed in expression analysis of SECK (3445452).
XX
XX SECK; cytostatic; gynecological; gene therapy; screening assay; human;
KW chromosomal mapping; forensic biology; cell proliferation; cancer;
KW cell differentiation; immune associated disorder; gestational disease;
KW SECK; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX

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RESULT 3413
AAS11868/c
ID AAS11868 standard; DNA; 22 BP.
XX
XX AAS11868;
XX
XX 24-OCT-2001 (first entry)
XX
XX
XX Human PCNA random mutagenesis PCR primer #2.
XX
XX
XX Human; PCNA; PCR primer; HIS tag; iminodiscetic acid cellulose; IDAC;
KW immobilised protein; proliferating cell nuclear antigen; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX US6232083-B1.
XX
XX
XX 15-MAY-2001.
XX
XX 12-MAR-1999; 99US-00268536.
XX
XX 12-MAR-1999; 99US-00268536.
XX
XX
XX (UTNY ) UNIV NEW YORK STATE RES FOUND.
XX
XX

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XX PI Fisher PA, Zaika A,
XX XX
XX DR WPI; 2001-440150/47.
XX PT Determining protein expression and function by genetically expressing
XX PT proteins having polypeptide regions, immobilizing the protein on metal
XX PT charged iminodiacetic acid cellulose and detecting protein or its
XX PT activity.
XX PS Example 5; Col 10; 23pp; English.
XX XX
XX CC The invention relates to determining expression or functional activity of
XX CC a protein, comprises expressing the protein having a polypeptide region
XX CC in genetically engineered cells, transferring the protein to metal
XX CC charged iminodiacetic acid cellulose (IDAC), immobilizing the protein on
XX CC the metal charged IDAC and detecting the protein or its functional
XX CC activity immobilised on the IDAC. The method is useful for determining
XX CC the expression of a protein and functional activity of a protein, which
XX CC includes binding specificity, enzyme activity, stimulation of enzyme
XX CC activity or stimulation of delta-polymerase activity. The protein is
XX CC especially human or Drosophila melanogaster proliferating cell nuclear
XX CC antigen (PCNA). Metal charged IDAC allows easy screening of a large
XX CC number of proteins following mutagenesis and can rapidly ascertain which
XX CC mutants have desired functional activity or binding capacity. The present
XX CC sequence is a mutagenic PCR primer for random mutagenesis of human PCNA
XX SQ
XX Sequence 22 BP; 5 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4743 GGAGGAGAGAGGCTTAATC 4763
XX 22 GGATGAGAGAGGATCTTAAC 2
XX
XX RESULT 3414
XX AAF76175/c
XX ID AAF76175 standard; DNA; 22 BP.
XX AC AAF76175;
XX XX
XX DT 05-JUN-2001 (first entry)
XX DE Human M-CSF PCR primer, SEQ ID NO:41.
XX XX
XX KM Transgenic mouse; immunodeficient; tissue recipient;
XX KM lymphocyte deficient; human cytokine; interleukin; IL-7; IL-6; SCF; LIF;
XX KM stem cell factor; leukemia inhibitory factor; GM-CSF; M-CSF;
XX KM granulocyte macrophage-colony stimulating factor;
XX KM macrophage-colony stimulating factor; human MHC class II; DR3;
XX KM major histocompatibility complex; allergenicity determination;
XX KM human monoclonal antibody generation; haematopoietic cell development;
XX KM human immune system animal model; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200115521-A1.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000WO-US023971.
XX PR 31-AUG-1999; 99US-0151688P.
XX PA (GENM ) GENENCOR INT INC.
XX PI Huang MA, Harding PA;
XX PF WPI; 2001-169001/17.
XX XX

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PT PT New transgenic mice, useful as non-human mammalian models of human
PT disease, comprise recombination activation gene mutations and donor
PT specific transgenes encoding cytokines.
XX PS Example 2; Page 37; 68pp; English.
XX XX
XX CC The invention relates to a transgenic immunodeficient recipient mouse
XX CC which is capable of supporting the growth of donor cells. In the mouse,
XX CC both alleles of a gene activated in early lymphocyte development are
XX CC disrupted, causing it to lack mature B and T cells. In particular, both
XX CC alleles of the recombination activation gene-2 (RAG-2) gene are
XX CC disrupted, which in turn prevents VDJ recombination. The mouse also
XX CC comprises donor (e.g., human) specific transgenes encoding the cytokines
XX CC interleukin-7 (IL-7), stem cell factor (SCF), leukemia inhibitory factor
XX CC (LIF), granulocyte macrophage-colony stimulating factor (GM-CSF),
XX CC macrophage-colony stimulating factor (M-CSF), and IL-6, which enable it
XX CC to support the growth of transplanted donor cells. In another embodiment
XX CC of the invention, the mouse comprises DNA encoding the human major
XX CC histocompatibility complex (MHC) class II DR3 molecule, where the
XX CC transgene has naturally linked Drab and Dqab alleles. The transgenic
XX CC mouse may be used as a model for determining the allergenicity of non-
XX CC donor, e.g., non-human, macromolecules, to determine the effect compounds
XX CC have on a human immune system; to generate fully human polyclonal or
XX CC monoclonal antibodies to specific antigens; to determine whether
XX CC humanised or other monoclonal antibodies will raise a response in a human
XX CC immune system; to investigate the human cell mediated response to
XX CC pathogens and other immunomodulatory compounds; and to determine the
XX CC factors involved in regulating the development and function of human
XX CC haematopoietic cells. The transgenic mouse supports the functional
XX CC properties of human haematopoietic cells, unlike previous animal models
XX CC which produce functionally impaired haematopoietic cells or are
XX CC immunologically dysfunctional. In addition the transgenic mouse provides
XX CC a unique model system which supports T cell development in a manner which
XX CC more closely resembles normal ontogeny, as they possess CD4+ T cells in
XX CC the periphery that exhibit MHC-restricted antigen- specific responses.
XX CC Sequences AAF76133-AAF76192 represent human cytokine PCR primers used in
XX CC the development of human cytokine-expressing transgenic mice
XX SQ
XX Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4803 CTGCCCTTGATGACCCGGAT 4823
XX 22 CTGCCCTTGATGACCTTGCT 2
XX
XX RESULT 3415
XX AAF31837/c
XX ID AAF31837 standard; DNA; 22 BP.
XX AC AAF31837;
XX XX
XX DT 12-APR-2001 (first entry)
XX DE Human MAT II beta subunit-specific PCR primer.
XX XX
XX KM Human; methionine adenosyltransferase II; MAT II; MAT II beta subunit;
XX KM cytosolic; immunosuppressive; gene therapy; antisense therapy;
XX KM livestock feed additive; cancer; autoimmune disease; transplantation;
XX KM PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200102420-A1.
XX PD 11-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018269.
XX PR 01-JUL-1999; 99US-0142020P.
XX XX

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XX (UTTE-) UNIV TENNESSEE RES CORP.
XX
XX Koch M, Legros HL, Geller AM;
XX
XX WPI; 2001-080980/09.
XX
XX Nucleic acid encoding a biologically active methionine
XX adenosyltransferase II (MAT II) beta subunit, useful in screening assays
XX for identifying MAT II modulating compounds which can be used to treat
XX cancer and autoimmune diseases.
XX
XX Example 2; Page 92; 176bp; English.
XX
XX The present sequence is given in a specification relating to an isolated
XX and purified nucleic acid encoding a biologically active methionine
XX adenosyltransferase II (MAT II) beta subunit polypeptide capable of
XX modulating MAT II biological activity. The MAT II beta subunit nucleic
XX acid and polypeptide are useful in screening assays for identifying
XX compounds that affect or modulate MAT II biological activity. The MAT
XX II beta subunit polypeptides have utility as feed additives for
XX livestock. The MAT II beta subunit polypeptide, anti-MAT II beta
XX subunit antibody and antisense oligonucleotide are useful for treating a
XX disorder associated with MAT II biological activity, e.g. cancer,
XX autoimmune diseases and transplantation
XX
XX Sequence 22 BP; 4 A; 3 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3379 TTGCTCTCCGCCAGCTGCCA 3399
XX |||||
XX 22 TTCTCTCTCCAGCCGCGACA 2
XX
XX RESULT 3416
XX ABA94871/C
XX ID ABA94871 standard; DNA; 22 BP.
XX
XX AC ABA94871;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX DE Unmethylated RASSF1A promoter fragment detecting reverse primer.
XX
XX KM Tumour suppressor gene; chromosome 3p21.3; Gene 26; PL6; Beta*; LUCA-1;
XX LUCA-2; 123F2; Fusi1; 101F6; Gene 21; SEM A3; cancer; tumour; BLU; human;
XX cyclostatic; gene therapy; protein therapy; RASSF1A; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200204511-A2.
XX
XX PD 17-JAN-2002.
XX
XX PF 10-JUL-2001; 2001WO-US021781.
XX
XX PR 10-JUL-2000; 2000US-0217112P.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX P1 Ji L, Minna J, Roth J, Lerman M;
XX
XX DR WPI; 2002-179699/23.
XX
XX New tumor suppressor genes and proteins, useful for detecting, diagnosing
XX and treating various human cancers, e.g. spleen cancer, kidney cancer,
XX lymph node cancer, small intestine cancer, blood cell cancer or
XX pancreatic cancer.
XX
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PS Example 15; Page 99; 206bp; English.
XX
XX The invention relates to tumour suppressor genes at chromosome 3p21.3
XX (Gene 26, PL6, Beta*, LUCA-1, LUCA-2, 123F2, Fusi1, 101F6, Gene 21, or
XX SEM A3). The tumour suppressor genes play a major role in the
XX pathogenesis of human lung cancer and other cancers. The polypeptide and
XX polynucleotides are useful for detecting, diagnosing and treating various
XX human cancers. These are particularly useful for inhibiting
XX tumorigenicity, suppressing tumour or restricting metastatic processes
XX in various tumours such as lung, colon, breast, stomach, cervix, and head
XX and neck, prostate or pancreas. In particular, the cancer is brain
XX cancer, lung cancer, liver cancer, spleen cancer, kidney cancer, lymph
XX node cancer, small intestine cancer, blood cell cancer, pancreatic
XX cancer, colon cancer, stomach cancer, cervix cancer, breast cancer,
XX endometrial cancer, prostate cancer, testicle cancer, ovarian cancer,
XX skin cancer, head and neck cancer, esophageal cancer, oral tissue cancer
XX or bone marrow cancer. The present sequence represents a primer for
XX detecting an unmethylated RASSF1A promoter fragment by methylation-
XX specific PCR
XX
XX Sequence 22 BP; 13 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 3167 GTTAGGTTTGCGTTGACT 3187
XX |||||
XX 22 GTTGTGTTGCGTTGTTACT 2
XX
XX ABL92904
XX ID ABL92904 standard; DNA; 22 BP.
XX
XX AC ABL92904;
XX
XX DT 06-JUN-2002 (first entry)
XX
XX DE G protein-coupled receptor GPCR23 PCR primer SEQ ID NO:186.
XX
XX KM Human; G protein-coupled receptor; antidiabetic; anorectic; cytostatic;
XX immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;
XX immunosuppressive; ophthalmological; antibacterial; virucide; fungicide;
XX protozoacide; hypertensive; hypotensive; analgesic; osteopathic;
XX anticancer; antistatic; antiallergic; anti-HIV; antipneumic; vaccine;
XX antifertility; antiinflammatory; haemostatic; cell signal processing;
XX cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;
XX gene therapy; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200212343-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 07-AUG-2001; 2001WO-US024787.
XX
XX PR 07-AUG-2000; 2000US-0223138P.
XX 07-AUG-2000; 2000US-0223472P.
XX 11-AUG-2000; 2000US-0224613P.
XX 11-AUG-2000; 2000US-0224815P.
XX 05-JAN-2001; 2001US-0260003P.
XX 05-JAN-2001; 2001US-0260072P.
XX 08-JAN-2001; 2001US-0260283P.
XX 09-JAN-2001; 2001US-0260450P.
XX 10-JAN-2001; 2001US-0261156P.
XX 22-JAN-2001; 2001US-0263358P.
XX 23-JAN-2001; 2001US-0263434P.
XX 01-FEB-2001; 2001US-0265704P.
XX 20-FEB-2001; 2001US-0265964P.
XX 09-MAR-2001; 2001US-0274873P.
XX 15-MAR-2001; 2001US-0276406P.
XX
```

PR 01-MAY-2001; 2001US-0287916P.

PA (CUPRA-) CUPRAGEN CORP.

PX

XX Spytsek KA, Padigar M, Zerhusen BD, Baumgartner JC, Li L,  
PI Caaman SJ, Vernet CAM, Ballinger RA, Shenoy SG, Kexuda R;  
PI Burgess CE, Mezes PS, Grosse WM, Alsbrook JP, Gorman LJ,  
PI Larochalle WJ, Taupier RJ, Colman SD, Szekeres ES;  
XX  
XX WPI; 2002-217180/27.

DR

XX New G-protein coupled receptor polypeptides and nucleic acids, useful for  
PT diagnosis, prevention or treatment of hepatocellular carcinoma, neurodegenerative,  
PT immune and signal transduction pathway disorders.

PX

XX Example 2; Page 407, 492pp; English.

PS

XX The present invention describes novel human G protein-coupled receptors  
CC (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have  
CC activities such as: antidiabetic; anorectic; immunomodulator; cytostatic;  
CC neuroprotective; nootropic; antiparkinsonian; analgesic; osteoprotective;  
CC immunosuppressive; metabolic; ophthalmological; antibacterial; virocidic;  
CC fungicide; protozoacide; hypertensive; hypotensive; anti-HIV; anticler;  
CC antitubercular; antihypertensive; antiallergic; antifertility; haemostatic;  
CC production. The GPCR proteins can be used in gene therapy and vaccine  
CC production. The GPCR proteins can be used for treating or preventing GPCR  
CC associated disorders such as cardiomyopathy, atherosclerosis, or a  
CC disorder related to cell signal processing and metabolic pathway  
CC modulation, in humans. GPCR proteins and the polynucleotides encoding  
CC them are useful for determining the presence of or predisposition to a  
CC disease, especially cancer associated with altered levels of GPCR  
CC proteins and polynucleotides, by measuring the level of protein  
CC expression or the amount of nucleic acid from a mammal and comparing it  
CC with another mammal not having or not predisposed to the disease. GPCR  
CC proteins are also useful for identifying an agent, especially cellular  
CC receptor or a downstream effector that binds to GPCR, for screening of a  
CC candidate substance interacting with an olfactory receptor polypeptide,  
CC its fragments or variants. The present sequence represents a PCR primer  
CC used in the isolation of a novel human GPCR in the present invention

XX

SQ Sequence 22 BP; A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

OY 3641 AGGTAGATGGGAGAATAATAC 3661  
||| ||| ||| ||| ||| ||| |||  
Db 2 AGCTGGCTGAGGAAGAACTTC 22

RESULT 3418  
ABL92913  
ID ABL92913 standard; DNA; 22 BP.  
AC ABL92913;  
DT 06-JUN-2002 (first entry)  
DE G protein-coupled receptor GPCR25 PCR primer SEQ ID NO:395.  
XX  
XX Human; G protein-coupled receptor; antidiabetic; anorectic; cytostatic;  
KW immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;  
KW immunosuppressive; ophthalmological; antibacterial; virocidic; fungicide;  
KW procoagulant; hypertensive; hypotensive; analgesic; osteopathic;  
KW anticancer; antitubercular; antiallergic; anti-HIV; antiparasitic; vaccine;  
KW antifertility; antineoplastic; haemostatic; cell signal processing;  
KW cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;  
KW gene therapy; PCR primer; ss.  
XX  
OS Homo sapiens.  
PN WO200212343-A2.

XX 14-FEB-2002.  
XX  
PD  
XX  
PF  
07-AUG-2001; 2001WO-US024787.  
XX  
PR  
07-AUG-2000; 2000US-0223138P.  
XX  
PR  
07-AUG-2000; 2000US-0223472P.  
PR  
11-AUG-2000; 2000US-0224613P.  
PR  
11-AUG-2000; 2000US-0224815P.  
PR  
05-JAN-2001; 2001US-0260003P.  
PR  
05-JAN-2001; 2001US-0260072P.  
PR  
08-JAN-2001; 2001US-0260283P.  
PR  
09-JAN-2001; 2001US-0260450P.  
PR  
10-JAN-2001; 2001US-0261156P.  
PR  
22-JAN-2001; 2001US-0263338P.  
PR  
23-JAN-2001; 2001US-0263434P.  
PR  
01-FEB-2001; 2001US-0265704P.  
PR  
20-FEB-2001; 2001US-0269964P.  
PR  
09-MAR-2001; 2001US-0274873P.  
PR  
15-MAR-2001; 2001US-0276406P.  
PR  
01-MAY-2001; 2001US-0287916P.  
XX  
PA  
(CURA-) CURAGEN CORP.  
XX  
PI  
Spytek KA, Padigaru M, Zerhusen BD, Baumgartner UC, Li L;  
PI  
Caman SJ, Vernet CM, Ballinger RA, Shenoy SG, Kekuda R;  
PI  
Burgess CE, Mezes PS, Grose WM, Alsbrook JP, Gorman L;  
PI  
Iarochelle WJ, Taupier RJ, Colman SD, Sekeres ES;  
XX  
XX  
WPI; 2002-217180/27.  
XX  
PT  
New G-protein coupled receptor polypeptides and nucleic acids, useful for  
PT  
diagnosis, prevention or treatment of hematopoietic, neurodegenerative,  
PT  
immune and signal transduction pathway disorders.  
PS  
Example 2; Page 417; 492pp; English.

The present invention describes novel human G protein-coupled receptors (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have activities such as: antidiabetic; anorectic; immunomodulator; cytostatic; neuroprotective; nootropic; antiparkinsonian; analgesic; osteopathic; immunosuppressive; metabolic; ophthalmological; antibacterial; virucide; fungicide; protozoal; hypertensive; hypotensive; anti-HIV; anticancer; antiasthmatic; antidiabetic; antiallergic; antineuritis; haemostatic; and antiinflammatory. They can be used in gene therapy and vaccine production. The GPCR proteins can be used for treating or preventing GPCR-associated disorders such as cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway modulation, in humans. GPCR proteins and the polynucleotides encoding them are useful for determining the presence of or predisposition to a disease, especially cancer associated with altered levels of GPCR proteins and polynucleotides, by measuring the level of protein expression or the amount of nucleic acid from a mammal and comparing it with another mammal not having or not predisposed to the disease. GPCR proteins are also useful for identifying an agent, especially cellular receptor or a downstream effector that binds to GPCR, for screening of a candidate substance interacting with an olfactory receptor polypeptide, its fragments or variants. The present sequence represents a PCR primer used in the isolation of a novel human GPCR in the present invention

Sequence 22 BP; 3 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5801 TGCGTGCCTGTCGTGCAATGTT 5821  
|||||  
Db 1 TGCGTCCCTTTCTGACTAACT 21

RESULT 3419  
AESK52319/C



ID ABK52319 standard; DNA; 22 BP.  
 AC ABK52319;  
 XX  
 DT 13-AUG-2002 (first entry)  
 DE Vascular smooth muscle cell proliferation associated PCR primer #7.  
 XX  
 KW Vascular smooth muscle; cell proliferation; proliferation inhibitor; PCR;  
 KM primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2002112798-A.  
 PD 16-APR-2002.  
 XX  
 PF 20-SEP-2000; 2000JP-00284973.  
 XX  
 PR 03-AUG-2000; 2000JP-00235459.  
 XX  
 PA (SUMO) SUMITOMO CHEM CO LTD.  
 XX  
 DR WPI; 2002-448760/48.  
 XX  
 PT Measurement of the inhibitory activity for vascular smooth muscle cell  
 proliferation, and a method for screening a substance with inhibitory  
 activity for vascular smooth muscle cell proliferation.  
 XX  
 PS Example 8; Page 22; 24pp; Japanese.  
 XX  
 CC The invention describes a measurement of inhibitory activity on vascular  
 smooth muscle cell proliferation and a method for screening a substance  
 having inhibitory activity on vascular smooth muscle cell proliferation.  
 CC This sequence represents a PCR primer associated with the method of  
 measuring, and screening for compounds responsible for, inhibition of  
 vascular smooth muscle cell proliferation  
 CC  
 XX  
 SQ Sequence 22 BP; 8 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4646 TGGATTTCCTTCTTGAGAG 4666  
 DB 21 TGGATTTCCTTCTTGAGAG 1  
 RESULT 3420  
 ID ABS58924/C  
 AC ABS58924 standard; DNA; 22 BP.  
 XX  
 AC ABS58924;  
 XX  
 DT 05-NOV-2002 (first entry)  
 DE Human G-protein coupled receptor, reverse primer #24.  
 XX  
 KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;  
 diabetes; cell signal processing; metabolic pathway modulation; cancer;  
 adenocarcinoma; lymphoma; prostate cancer; uterine cancer; asthma;  
 immune response; neurodegenerative disorder; inflammatory disorder;  
 Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;  
 primer; PCR; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200259313-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-US049394.

XX  
 PR 18-DEC-2000; 2000US-0256635P.  
 PR 21-DEC-2000; 2000US-0257876P.  
 PR 04-JAN-2001; 2001US-0259743P.  
 PR 10-JAN-2001; 2001US-0260718P.  
 PR 12-JAN-2001; 2001US-0261498P.  
 PR 24-JAN-2001; 2001US-0263669P.  
 PR 08-FEB-2001; 2001US-0267464P.  
 PR 22-FEB-2001; 2001US-0271021P.  
 PR 14-MAR-2001; 2001US-0275946P.  
 PR 23-MAR-2001; 2001US-0278150P.  
 PR 18-APR-2001; 2001US-0284591P.  
 PR 23-APR-2001; 2001US-0285718P.  
 PR 19-JUN-2001; 2001US-0299327P.  
 PR 16-AUG-2001; 2001US-0312902P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA,  
 Caeman SJ, Vernet CM, Shenoy SG, Gusev V, Malysankar UM, Edinger S,  
 Gerlach V, Smithson G, Stone DV, Sclaire P, McDougall JR, Gunther E,  
 Peyman JA, Ellerman K, Gangoli EA, Millet I;  
 XX  
 DR WPI; 2002-599789/64.  
 XX  
 PT New G protein coupled receptor polypeptides and polynucleotides, useful  
 in gene therapy, particularly for treating or preventing cardiomyopathy,  
 atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer  
 in humans.  
 XX  
 PS Claim 9; Page 300; 685pp; English.  
 XX  
 CC The invention relates to novel isolated G-protein coupled receptor (GPCR)  
 polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid  
 and antibody are useful for treating, preventing or alleviating a GPCR-  
 associated disorder or a pathological state in a subject, particularly a  
 human. In particular, the disorder is cardiomyopathy, atherosclerosis,  
 diabetes, or a disorder related to cell signal processing and metabolic  
 pathway modulation. The GPCR polypeptide and nucleic acid are also useful  
 for diagnosing the presence of or predisposition to a disease associated  
 with altered levels of GPCR, particularly cancer. The GPCR nucleic acid  
 and polypeptide are especially useful in therapeutic or prophylactic  
 applications for disorders associated with aberrant GPCR expression or  
 activity. The DNA encoding the protein is useful in gene therapy for  
 treating the above conditions. Furthermore, the nucleic acids and  
 polypeptides are useful in treating adenocarcinoma, lymphoma, prostate  
 cancer, uterine cancer, immune response, neurodegenerative disorders,  
 asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or  
 Albright hereditary osteodystrophy. These are also useful in developing a  
 powerful assay system for functional analysis of various human disorders,  
 CC as well as in diagnostic applications. ABS58747-ABS59231 represent human  
 GPCR coding sequences, primers and probes of the invention  
 CC  
 XX  
 SQ Sequence 22 BP; 12 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 0.2%; Score 14.6; DB 1; Length 22;  
 Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3921 CTCCTGGCTTCTTCTTCCT 3941  
 DB 21 CTCCTGGCTTCTTCTTCCT 1  
 RESULT 3421  
 ID AAD43245  
 AC AAD43245 standard; DNA; 22 BP.  
 XX  
 AC AAD43245;  
 XX  
 DT 14-NOV-2002 (first entry)  
 DE Antisense oligonucleotide R51A56.

```

XX Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;
KM hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;
KM leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;
KM inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;
KM antisense; phosphorothioate backbone; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN US2002086840-A1.
XX
PD 04-JUL-2002.
XX
PF 26-JAN-2001; 2001US-00771355.
XX
PR 26-JAN-2000; 2000US-0178561P.
XX
PA (ZARL/) ZARLING D A.
XX (REDD/) REDDY G.
XX
PI Zarling DA, Reddy G;
XX WPI; 2002-635686/68.
XX
DR Inhibiting/reducing tumor cell proliferation in individual in vivo, for
PT treating cancer; arthritis, involves contacting tumor cell in vivo with
PT Rad51 inhibitor, and polynucleotide expressing functional p53 protein.
XX
PS Disclosure; Page 5; 12pp; English.
XX
CC The invention relates to a method for inhibiting or reducing tumour cell
CC proliferation in an individual in vivo. The method comprising contacting
CC a tumour cell in vivo with a Rad51 inhibitor and a polynucleotide capable
CC of expressing functional p53 protein. The method is useful for inhibiting
CC or reducing tumour cell proliferation in an individual in vivo. The
CC method is useful for treating hyperproliferative disorders, especially
CC cancer (such as Hodgkin's disease, squamous cell carcinoma and
CC leukaemia), premature aging, autoimmune disease, arthritis, graft
CC rejection, inflammatory bowel disease, and proliferation induced after
CC medical procedures such as surgery and angioplasty. The invention is
CC useful in gene therapy. The present sequence is an antisense
CC oligonucleotide used to illustrate the method of the invention
XX
SQ Sequence 22 BP; 6 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3477 CCTAGTAATCTTACGAC 3497
Db 1 CCCAGTCATCTCTAGGAC 21
XX
RESULT 3422
ABL35690
ID ABL35690 standard; DNA; 22 BP.
XX
AC ABL35690;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 616.
XX
KM DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KM infection; allergy; cancer; hypersensitivity; bio-warfare;
KM immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KM
OS

```

```

KM immunosuppressive; protozoacide; viroicide; hepatotropic; gene therapy;
KM antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..22
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Kliman DM;
XX WPI; 2002-130570/17.
XX
DR New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 63; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 22 BP; 0 A; 3 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 4463 CTTTTTTTTTTTTTTTTTTT 4483
Db 2 CGTTGTCTCTTTTTTTTT 22
XX
RESULT 3423
AAD38021
ID AAD38021 standard; DNA; 22 BP.
XX
AC AAD38021;
XX
DT 10-SEP-2002 (first entry)
XX
DE FGF10 amplifying reverse RT PCR primer.
XX
KM Lung cancer; homeodomain; homeobox; HOX; wingless/int-1; WNT; tumour;
KM diagnosis; prognosis; therapeutic; real time PCR; RT-PCR; FGF10; primer;
KM ss.
XX
OS Unidentified.

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```
XX MO200231210-AL.
XX
XX 18-APR-2002.
XX
XX 11-OCT-2001; 2001WO-US031960.
XX
XX 11-OCT-2000; 2000US-0239596P.
XX
XX (UTRE-) UNIV TECHNOLOGY CORP.
XX
XX Drabkin HA, Gemm11 RM;
XX
XX WPI; 2002-454557/48.
XX
XX Evaluating a lung cell sample of a lung cancer patient for diagnosis to
XX determine clinical prognosis including tendency to metastasize comprises
XX screening for expression of homeodomain containing genes HOX or WNT.
XX
XX Example; Page 16; 37pp; English.
XX
XX The invention relates to evaluating a lung cell sample of a lung cancer
XX patient comprising screening for expression of a homeodomain containing
XX homeobox (HOX) or wingless/int-1 (WNT) gene and comparing the screen to a
XX sample of non-malignant lung cell. The method is useful for evaluating a
XX lung cell sample of a lung cancer patient. The method is useful for
XX determining the prognosis of a lung cancer and for assessing a lung
XX cancer for a tendency to metastasize, where decreased expression of a WNT
XX gene or HOXA1 gene, or increased expression of HOX gene other than HOXA1,
XX or both, indicates poor prognosis, increased rate of tumour growth, and
XX increased tendency to metastasize. The method is useful for obtaining
XX data for diagnosis, to determine clinical prognosis, including rate of
XX growth, tendency to metastasize, to assess the efficacy of treatment and
XX to determine the efficacy of a therapeutic agent. The present sequence is
XX a real time (RT)-PCR primer used to amplify FGF10. This sequence is used
XX in the exemplification of the invention
XX
XX Sequence 22 BP; 2 A; 10 C; 0 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5740 TCCCTTTCTCTATCACTC 5760
XX |||||
XX 1 TCCATTTCTCTATCTCTC 21
XX
XX RESULT 3424
XX ABS78424
XX ID ABS78424 standard; DNA; 22 BP.
XX
XX ABS78424;
XX
XX 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #908.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularization; telangiectasia; haemophilic joint;
XX angiodiroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
```

```
PF 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 35; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
XX having a condition characterised by unwanted angiogenesis. The method is
XX useful for inhibiting angiogenesis associated with solid tumour growth,
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
XX neovascularization, telangiectasia, haemophilic joints, angiodiroma,
XX wound granulation, intestinal adhesion, atherosclerosis, scleroderma and
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention
XX
XX Sequence 22 BP; 0 A; 11 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 14.6; DB 1; Length 22;
XX Best Local Similarity 81.0%; Pred. No. 2.4e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 5328 CTCCTTGCTCCTCACTCTC 5348
XX |||||
XX 1 CTCCTCTCTCTCTCTCTC 21
XX
XX RESULT 3425
XX ABK97133
XX ID ABK97133 standard; DNA; 22 BP.
XX
XX ABK97133;
XX
XX 07-OCT-2002 (first entry)
XX
XX Alfa1fa mosaic virus DNA RT-PCR primer #1.
XX
XX Virus-encoded coat protein; primer; AMV; CVV; WGMV; leguminous plant;
XX viral replicase; intron ribonucleic acid; rRNA; hairpin RNA; virucide;
XX pathogenic plant virus; SSU promoter; 35S promoter; gene therapy; RT-PCR;
XX reverse transcriptase PCR; ss.
XX
XX Alfa1fa mosaic virus.
XX
XX Synthetic.
XX
XX WO200239808-AL.
XX
XX 23-MAY-2002.
XX
XX 16-NOV-2001; 2001WO-AU001496.
XX
XX 17-NOV-2000; 2000AU-00001558.
XX
XX (CSIR ) COMMONWEALTH SCT & IND RES ORG.
XX (DAIR-) DAIRY RES & DEV CORP.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX
XX Chu PWG, Garrett RG, Kalla SR, Spangenberg GC, Larkin PJ,
XX Higgins TJ;
```

XX  
DR WPI; 2002-519361/55.  
XX  
PT Conferring immunity to pathogenic plant virus on leguminous plant by  
PT introducing nucleic acid sequence encoding virus-encoded coat protein,  
PT dysfunctional viral replicase or tRNA comprising hairpin RNA, to plant.  
XX  
XX Example 1; Page 49; 283pp; English.  
XX  
CC The invention relates to a method for conferring immunity to a pathogenic  
CC plant virus on a leguminous plant comprising introducing an isolated  
CC nucleic acid molecule encoding a virus-encoded coat protein, a  
CC dysfunctional viral replicase or an intron ribonucleic acid (tRNA)  
CC comprising a hairpin RNA to the plant so the plant is immune to the plant  
CC virus under field conditions. The invention also relates to a method for  
CC transforming a leguminous plant by introducing to a leguminous plant  
CC cell, tissue or organ, an isolated nucleic acid molecule comprising an  
CC SSU promoter or a 35S promoter operably linked to a nucleic acid encoding  
CC a virus-encoded coat protein and regenerating a transformed leguminous  
CC plant from the plant cell, tissue or organ, where the transformed  
CC leguminous plant is immune to a pathogenic plant virus. The method is  
CC useful for producing a leguminous plant with enhanced viral resistance or  
CC crossing two parent plants each having enhanced viral resistance or  
CC immunity against one or more different viruses. This sequence represents  
CC a reverse transcriptase PCR (RT-PCR) primer used in the method of the  
CC invention  
XX  
SQ Sequence 22 BP; 5 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2238 CCAGATCTCCATATGAGCT 2258  
DB 1 CCAGATCTTCATCATGAGTT 21  
XX  
RESULT 3426  
ABN84449  
ID ABN84449 standard; DNA; 22 BP.  
XX  
AC ABN84449;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Bcr/abl forward PCR primer used in whole cell RT-PCR.  
XX  
KM RNA polymer; ribonuclease; RNase; inhibitor; bcr; abl; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200259366-A2.  
XX  
PD 01-AUG-2002.  
XX  
PE 28-NOV-2001; 2001WO-US044644.  
XX  
PR 28-NOV-2000; 2000US-0253451P.  
XX  
PR 28-NOV-2001; 2001US-00955912.  
XX  
PA (PROM-) PROMEGA CORP.  
XX  
PI Schultz JW, Lewis MK, Andrews CA;  
XX  
DR WPI; 2002-599806/64.  
XX  
XX Reducing the activity of a ribonuclease, useful for inhibiting tumor  
XX growth or for removing RNA binding proteins from a solution, comprises  
XX mixing a sample containing an RNase with a preparation containing at  
XX least one RNA polymer.  
XX  
XX Example 7; Page 45; 61pp; English.

XX  
CC The present sequence is that of a bcr/abl forward PCR primer. The primer  
CC was used in an example from the invention demonstrating the inhibition of  
CC RNase enzymes in RT-PCR reactions using polyG or polyT attached to  
CC resins. RT-PCR was conducted without prior RNA isolation using K562  
CC (human erythroleukemia cell line) whole cell lysates. The reverse primer  
CC for the PCR is given in ABN84450. Results were compared with the effect  
CC of adding RNASIN ribonuclease inhibitor. Addition of RNASIN to cells  
CC during lysis allowed for the sensitive detection of the bcr/abl signal  
CC down to as low as 1 cell, with increasing signal intensity with  
CC increasing cell number. The addition of 1 uL, but not 3 uL, of polyG  
CC resin allowed detection of the bcr/abl signal down to approximately 1-10  
CC cells (with or without spin). The signal in the presence of polyG was  
CC weaker than with RNASIN. It is concluded that RNA polymers can replace  
CC RNASIN in single-tube, whole cell RT-PCR. The example illustrates the  
CC present invention, which relates to compositions and methods for using  
CC RNA polymers to inhibit RNase enzymes (e.g. those involved in  
CC angiogenesis such as in tumour growth and proliferation, and in other  
CC biological processes), for removing RNA binding proteins from a solution,  
CC and for enhancing certain enzymatic reactions. The RNA polymers may also  
CC be used in drug testing, or in screening for RNA binding proteins  
CC involved in disease states  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.2%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2539 GAGCTCCAGATCTGACGATC 2559  
DB 2 GAGCTGCAGATGCTGACCAAC 22  
XX  
RESULT 3427  
ABS64779  
ID ABS64779 standard; DNA; 22 BP.  
XX  
AC ABS64779;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE GPCR15 real time forward PCR primer.  
XX  
KM G protein coupled receptor related protein; ss; primer; human; GPCR;  
KM cardiomyopathy; atherosclerosis; diabetes; cancer; stroke; human; GPCR;  
KM Von Hippel-Lindau syndrome; Alzheimer's disease; tubercous sclerosis;  
KM hypercalcaemia; Parkinson's disease; Huntington's disease;  
KM cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis;  
KM ataxia-telangiectasia; leukodystrophy; addiction; anxiety; depression;  
KM pain; obesity; Crohn's disease; osteoporosis; haemophilia; asthma;  
KM inflammatory bowel disease; infertility; hypertension; scleroderma;  
KM arthritis; human immunodeficiency virus; autoimmune disease; HIV;  
KM infection; graft-versus-host disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200264793-A2.  
XX  
PD 22-AUG-2002.  
XX  
PE 03-JAN-2002; 2002WO-US000056.  
XX  
PR 03-JAN-2001; 2001US-0259552P.  
XX  
PR 09-JAN-2001; 2001US-0260544P.  
XX  
PR 20-MAR-2001; 2001US-0277405P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Casman SJ, Edinger SR, Ellerman K, Smithson G, Kekuda R;  
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PI Muralidhara P;  
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DR WPI; 2002-643487/69.